XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX
PD 25-APR-2002.
XX
PF 28-SEP-2001; 2001WO-JP008574.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX
DR WPI; 2002-372311/40.
XX
PT Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
PS Example 1; Page 109; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2589
AAL49948
ID AAL49948 standard; DNA; 17 BP.
XX
AC AAL49948;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human B1153 expression in allergic disease related PCR primer GT15A.
XX
KW Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN WO200250269-A1.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-JP011286.
XX
PR 21-DEC-2000; 2000JP-00389476.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX
DR WPI; 2002-713252/77.
XX
PT Examination of allergic diseases comprises detecting gene B1153 over-
PT expressed in T cells of allergy patients for diagnosis treatment and
PT investigation of atopic skin inflammation and asthma.
XX
PS Example 6; Page 81; 102pp; Japanese.
XX
CC The present invention relates to a method of examining allergic diseases
CC which comprises comparing the expression level of gene B1153 in allergy
CC patients with the expression level in healthy subjects. The method is
CC useful for the treatment, prevention, diagnosis and study of allergic
CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2590
AAL49949/c
ID AAL49949 standard; DNA; 17 BP.
XX
AC AAL49949;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human B1153 expression in allergic disease related PCR primer GT15C.
XX
KW Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN WO200250269-A1.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-JP011286.
XX
PR 21-DEC-2000; 2000JP-00389476.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX
DR WPI; 2002-713252/77.
XX
PT Examination of allergic diseases comprises detecting gene B1153 over-
PT expressed in T cells of allergy patients for diagnosis treatment and
PT investigation of atopic skin inflammation and asthma.
XX
PS Example 6; Page 82; 102pp; Japanese.
XX
CC The present invention relates to a method of examining allergic diseases
CC which comprises comparing the expression level of gene B1153 in allergy
CC patients with the expression level in healthy subjects. The method is
CC useful for the treatment, prevention, diagnosis and study of allergic
CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention

```
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2591
AAL47234
ID   AAL47234 standard; DNA; 17 BP.
XX
AC   AAL47234;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 2.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
XX
PF   11-OCT-2001; 2001WO-JP008937.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
PI   Takahashi E;
XX
DR   WPI; 2002-372313/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   intersectin 2 gene showing different expression particularly significant
PT   increase in eosinophils in patients.
XX
PS   Example 1; Page 52; 90pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   with intersectin 2 gene or a gene with equivalent function of intersectin
CC   2 as an indicator gene, which comprises determining the expression level
CC   of the gene in the eosinophils in a patient, and comparing the expression
CC   level with that in the eosinophils of a healthy individual. The method is
CC   for examining allergic diseases, particularly atopic dermatitis, which is
CC   also applicable in screening candidate compounds for remedies. The
CC   present sequence is an anchor primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2592
AAL47235/c
ID   AAL47235 standard; DNA; 17 BP.
XX
AC   AAL47235;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 3.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
XX
PF   11-OCT-2001; 2001WO-JP008937.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
PI   Takahashi E;
XX
DR   WPI; 2002-372313/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   intersectin 2 gene showing different expression particularly significant
PT   increase in eosinophils in patients.
XX
PS   Example 1; Page 53; 90pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   with intersectin 2 gene or a gene with equivalent function of intersectin
CC   2 as an indicator gene, which comprises determining the expression level
CC   of the gene in the eosinophils in a patient, and comparing the expression
CC   level with that in the eosinophils of a healthy individual. The method is
CC   for examining allergic diseases, particularly atopic dermatitis, which is
CC   also applicable in screening candidate compounds for remedies. The
CC   present sequence is an anchor primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2593
ABK49757/c
ID   ABK49757 standard; DNA; 17 BP.
XX
AC   ABK49757;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human atopic dermatitis cDNA related PCR primer GT15c.
XX
KW   Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW   allergic disease; antiallergic; dermatological; GT15c.
XX
OS   Synthetic.
XX
PN   WO200226962-A1.
```

XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 55; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15c PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2594
ABK49756
ID ABK49756 standard; DNA; 17 BP.
XX
AC ABK49756;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15a.
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15a.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 54; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15a PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2595
ABX79793/c
ID ABX79793 standard; cDNA; 17 BP.
XX
AC ABX79793;
XX
DT 17-APR-2003 (first entry)
XX
DE EST polymorphic DNA repeat polynucleotide #118.
XX
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS Homo sapiens.
XX
PN US6472154-B1.
XX
PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX
DR WPI; 2003-208818/20.
XX
PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
PS Example; Col 483; 588pp; English.
XX

CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 GAAAAAAAAAAAAAAA 1

RESULT 2596
ADB04270
ID ADB04270 standard; DNA; 17 BP.
XX
AC ADB04270;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5256.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5256; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 CTTTTTTTTTTTTTTT 17

RESULT 2597
ADB04272
ID ADB04272 standard; DNA; 17 BP.
XX
AC ADB04272;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5258.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5258; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX

```
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2598
ADB04272/c
ID   ADB04272 standard; DNA; 17 BP.
XX
AC   ADB04272;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5258.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5258; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2599
ACC64866
ID   ACC64866 standard; DNA; 17 BP.
XX
AC   ACC64866;
XX
DT   01-JUL-2003  (first entry)
XX
DE   Murine oligonucleotide associated with tumour supression, SEQ ID 2113.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; ss.
XX
OS   Mus musculus.
XX
PN   WO2003025176-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004210.
XX
PR   17-SEP-2001; 2001FR-00011979.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-333167/31.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; Page 278; 738pp; French.
XX
CC   The present invention relates to murine oligonucleotides (ACC62754-
CC   ACC68806), which are associated with tumour suppression, tumour
CC   reversion, apoptosis and virus resistance. The oligonucleotides are
CC   useful as (1) as probes and primers for detecting, identifying,
CC   quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC   gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC   recombinant polypeptides. The oligonucleotides are useful for preparation
CC   of pharmaceuticals for prevention and/or treatment of viral diseases that
CC   are characterised by development of tumours or cell degeneration,
CC   specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ   Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2074 ATCTGACACACTCTAA 2089
              ||||||||||||||||
Db          2 ATCTGACACACTCTAA 17


RESULT 2600
ABZ70578
ID   ABZ70578 standard; DNA; 17 BP.
XX
AC   ABZ70578;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Primer.
XX
KW   Aspergillus phoenices; oxalate decarboxylase; APOXD; transgenic plant;
```

KW crop protection; primer; ss.
XX
OS Synthetic.
XX
PN CA2350328-A1.
XX
PD 26-DEC-2002.
XX
PF 26-JUN-2001; 2001CA-02350328.
XX
PR 26-JUN-2001; 2001CA-02350328.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Scelonge C, Bidney D;
XX
DR WPI; 2003-248733/25.
XX
PT New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT phoenices, for degrading oxalic acid, identifying transformed plant
PT cells, and preventing pathogenic disease in plants.
XX
PS Disclosure; Page 50; 60pp; English.
XX
CC The present sequence is that of a primer used in the invention. The
CC invention relates to a novel nucleic acid (see ABZ70560) encoding
CC Aspergillus phoenices oxalate decarboxylase (APOXD) (see ABP72475). The
CC gene and its encoded protein are useful in degrading oxalate, in
CC diagnostic assays, for protecting plants against disease, and as a
CC selectable marker
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTT 17

RESULT 2601
ABZ70578/c
ID ABZ70578 standard; DNA; 17 BP.
XX
AC ABZ70578;
XX
DT 23-MAY-2003 (first entry)
XX
DE Primer.
XX
KW Aspergillus phoenices; oxalate decarboxylase; APOXD; transgenic plant;
KW crop protection; primer; ss.
XX
OS Synthetic.
XX
PN CA2350328-A1.
XX
PD 26-DEC-2002.
XX
PF 26-JUN-2001; 2001CA-02350328.
XX
PR 26-JUN-2001; 2001CA-02350328.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Scelonge C, Bidney D;
XX
DR WPI; 2003-248733/25.
XX
PT New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT phoenices, for degrading oxalic acid, identifying transformed plant
PT cells, and preventing pathogenic disease in plants.
XX
PS Disclosure; Page 50; 60pp; English.
XX
CC The present sequence is that of a primer used in the invention. The
CC invention relates to a novel nucleic acid (see ABZ70560) encoding
CC Aspergillus phoenices oxalate decarboxylase (APOXD) (see ABP72475). The
CC gene and its encoded protein are useful in degrading oxalate, in
CC diagnostic assays, for protecting plants against disease, and as a
CC selectable marker
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 17 AAAAAAAAAAAAAAAA 2

RESULT 2602
ADC84469/c
ID ADC84469 standard; DNA; 17 BP.
XX
AC ADC84469;
XX
DT 01-JAN-2004 (first entry)
XX
DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.
XX
KW Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2003159071-A.
XX
PD 03-JUN-2003.
XX
PF 22-NOV-2001; 2001JP-00358366.
XX
PR 22-NOV-2001; 2001JP-00358366.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2003-818678/77.
XX
PT New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX
PS Example 3; SEQ ID NO 2; 43pp; Japanese.
XX
CC The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2603
ADC84468
ID ADC84468 standard; DNA; 17 BP.
XX
AC ADC84468;
XX
DT 01-JAN-2004 (first entry)
XX
DE PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
XX
KW Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2003159071-A.
XX
PD 03-JUN-2003.
XX
PF 22-NOV-2001; 2001JP-00358366.
XX
PR 22-NOV-2001; 2001JP-00358366.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR WPI; 2003-818678/77.
XX
PT New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX
PS Example 3; SEQ ID NO 1; 43pp; Japanese.
XX
CC The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2604
ADE77745/c
ID ADE77745 standard; DNA; 17 BP.
XX
AC ADE77745;
XX
DT 29-JAN-2004 (first entry)
XX
DE DNA oligo (SeqID 5) related to the human B1799 gene.
XX
KW ss; allergic disease; B1799; antiallergic; antiinflammatory;
KW dermatological; gene therapy; atopic dermatitis.
XX
OS Unidentified.
XX
PN WO2003083139-A1.
XX
PD 09-OCT-2003.
XX
PF 25-FEB-2003; 2003WO-JP002047.
XX
PR 03-APR-2002; 2002JP-00100908.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN AGENCY NATION.
XX
PI Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;
XX
DR WPI; 2003-804076/75.
XX
PT Examining allergic diseases, such as atopic dermatitis, comprises
PT comparing the expression levels of gene B1799 in T cells in a patient and
PT a healthy individual.
XX
PS Example 1; SEQ ID NO 5; 87pp; Japanese.
XX
CC This invention relates to a novel method for screening and examining
CC allergic diseases by the use of B1799 as the indicator gene.
CC Specifically, it comprises determining the expression level of this
CC indicator gene in a biological sample obtained from the patient, and
CC identifying differential expression (increased expression of B1799) in
CC comparison to that observed in a healthy individual. The present
CC invention describes the B1799 protein as antiallergic, antiinflammatory
CC and dermatological. As such, through the use of gene therapy, this method
CC can be used to treat allergic diseases particularly atopic dermatitis.
CC Furthermore, it is useful for determining a diagnosis that is convenient
CC and non-invasive, and is also applicable in high throughput screening to
CC identify candidate compounds for additional remedies. This
CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human
CC B1799 gene of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2605
ABK13935
ID ABK13935 standard; DNA; 18 BP.
XX
AC ABK13935;
XX
DT 21-MAY-2002 (first entry)
XX
DE 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
PR 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G;
XX

DR WPI; 2002-217065/27.
XX
PT Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
PS Disclosure; Fig 1; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the production of a single pattern characteristic of a sample,
CC employing a Type II restriction enzyme (i.e. HaeII) in the methods of the
CC present invention
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
||||||||||||||||
Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2606
ACF36339
ID ACF36339 standard; DNA; 18 BP.
XX
AC ACF36339;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA fragment.
XX
KW Gene variant identification; restriction enzyme; HaeII; ds.
XX
OS Synthetic.
XX
PN WO2003064689-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000255.
XX
PR 29-JAN-2002; 2002US-0352245P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Lonnerberg P, Oldin M, Linnarsson S, Ernfors P;
XX
DR WPI; 2003-627619/59.
XX
PT Determining polyadenylation sites within transcribed gene sequences
PT present in a sample comprises assigning to gene fragments gene candidates
PT within a database by comparing signals in the dataset with the database.
XX
PS Example; Fig 2; 81pp; English.
XX
CC The invention relates to determining the presence of and/or identifying a
CC polyadenylation site within a sequence of a transcribed gene or variants
CC present in a sample. The method involves assigning to gene fragments gene
CC candidates within a database by comparing signals in the dataset with the
CC database, the database comprising data representing mRNAs with known
CC polyA sites and/or 'virtual genes' representing a possible
CC polyadenylation site within an actual gene. The method is useful for
CC determining the presence of and/or identifying a polyadenylation site or
CC alternative polyadenylation sites within a sequence of a transcribed gene
CC or sequences of transcribed gene variants present or potentially present
CC in a sample, in identifying gene features, particularly in identifying
CC differences between sequence variants that occur in a population of
CC nucleic acid molecules, especially in identifying or discovering polyA
CC site usage or determining polyA site usage in a nucleic acid sample, and
CC gene variants arising from alternative polyA sites. The present sequence
CC represents a double stranded product DNA fragment
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
||||||||||||||||
Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2607
ACF36364
ID ACF36364 standard; DNA; 18 BP.
XX
AC ACF36364;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW electrophoresis; type II restriction enzyme; HaeII; ds.
XX
OS Synthetic.
XX
PN WO2003064691-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000843.
XX
PR 29-JAN-2002; 2002US-0352215P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
PI Montelius A;
XX
DR WPI; 2003-618365/58.
XX
PT Producing a population of double-stranded product DNA molecules, useful
PT for mRNA profiling, comprises amplification by nested polymerase chain
PT reaction.
XX
PS Example; Fig 1; 105pp; English.
XX
CC The invention relates to producing a population of double-stranded
CC product DNA molecules comprising amplification by a nested PCR method.
CC The method is useful in profiling mRNA transcribed in a system under
CC investigation. The oligonucleotides are used as size standards in
CC electrophoresis, and as internal controls allowing for calculation of
CC relative amounts of material present. The present sequence represents a
CC double stranded product DNA, which aids in outlining an approach to
CC production of a single pattern characteristic of a sample, employing a
CC type II restriction enzyme (HaeII)
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;

```
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2608
AAN30173/c
ID   AAN30173 standard; DNA; 18 BP.
XX
AC   AAN30173;
XX
DT   05-APR-1992  (first entry)
XX
DE   Sequence derived from the L1 region of the bovine papillomavirus (bPV)
DE   type 1a genome.
XX
KW   Diagnostioc reagent; vaccine; medicine; wart; tumour; ss.
XX
OS   Bovine papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .18
FT                   /*tag=  a
XX
PN   EP92456-A.
XX
PD   26-OCT-1983.
XX
PF   01-APR-1983;   83EP-00901081.
XX
PR   05-APR-1982;   82FR-00005887.
XX
PA   (INSP ) INST PASTEUR.
PA   (DANO/) DANOS O.
XX
PI   Danos O,  Katinka M,  Yaniv M;
XX
DR   WPI; 1983-802979/44.
DR   P-PSDB; AAP30313.
XX
PT   DNA fragment coding for Papillomavirus antigenic proteins - and derived
PT   immunogen, vaccine and antibody.
XX
PS   Claim 6; Page 16; 25pp; French.
XX
CC   The inventors claim DNA fragments capable of expressing, in a host, a
CC   prod. contg. at least one antigenic determinant of papillomavirus (PV),
CC   (see AAN30170-N30173). Also claimed are immunogens consisting of at least
CC   one peptide sequence coded for by the DNA fragments (see AAP30310-
CC   P30313), vaccines contg. the immunogens and antibodies raised from them.
CC   The vaccines are useful in human and veterinary medicine and the
CC   antibodies are useful as diagnostic reagents. The DNA fragments are most
CC   esp. derived from the L1 region of human PV type 1a
XX
SQ   Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         18 TTTTTTTTTTTTTTTT 3


RESULT 2609
AAF75596
ID   AAF75596 standard; DNA; 18 BP.
XX
AC   AAF75596;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Binary encoded sequence tag method anchored primer #1.
XX
KW   Binary encoded sequence tag; BEST; nucleic acid analysis;
KW   gene expression; adaptor; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200112855-A2.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-US022164.
XX
PR   13-AUG-1999;   99US-0148870P.
PR   06-APR-2000; 2000US-00544713.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Kaufman JC,  Roth ME,  Lizardi PM,  Feng L,  Latimer DR;
XX
DR   WPI; 2001-202878/20.
XX
PT   Producing binary sequence tags, useful for analyzing nucleic acid
PT   sequence tags, gene expression or gene-expression patterns, involves
PT   generating nucleic acid fragments, which are mixed with offset adaptors
PT   and adaptor-indexers.
XX
PS   Disclosure; Page 100; 101pp; English.
XX
CC   The present invention describes a method of producing binary sequence
CC   tags from nucleic acid fragments in a sample, involving incubating the
CC   sample with cleaving reagents, mixing offset adaptors with the sample,
CC   incubating with more cleaving reagents and mixing the sample with adaptor
CC   -indexers where the adaptors are coupled to binary sequence tags. The
CC   method is useful in sequence analysis, including analysis and comparison
CC   of gene expression, nucleic acid samples and genomes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2610
AAV54170
ID   AAV54170 standard; cDNA; 18 BP.
XX
AC   AAV54170;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 7.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
```

```
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
                ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2611
AAV54175/c
ID   AAV54175 standard; cDNA; 18 BP.
XX
AC   AAV54175;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 12.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 51; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2612
AAV54173
ID   AAV54173 standard; cDNA; 18 BP.
XX
AC   AAV54173;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 10.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
                ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2613
AAV54169/c
ID   AAV54169 standard; cDNA; 18 BP.
XX
AC   AAV54169;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 6.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
```

XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 49; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2614
AAV54172/c
ID AAV54172 standard; cDNA; 18 BP.
XX
AC AAV54172;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 9.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 50; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 17 GAAAAAAAAAAAAAAA 2

RESULT 2615
AAV54167
ID AAV54167 standard; cDNA; 18 BP.
XX
AC AAV54167;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 4.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 48; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2616
AAV35391

ID AAV35391 standard; DNA; 18 BP.
XX
AC AAV35391;
XX
DT 13-OCT-1998 (first entry)
XX
DE HIV-1 gag protein DNA primer #4.
XX
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX
OS Synthetic.
XX
PN WO9822596-A1.
XX
PD 28-MAY-1998.
XX
PF 19-NOV-1997; 97WO-JP004216.
XX
PR 19-NOV-1996; 96JP-00323412.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (JAPG) NIPPON ZEON KK.
XX
PI Kojima A, Kurata T, Yasuda A;
XX
DR WPI; 1998-312481/27.
XX
PT Recombinant vaccinia virus containing fusion HIB gag gene - for
PT production in host cells of gag protein for use as vaccine.
XX
PS Example 1; Page 64; 84pp; Japanese.
XX
CC AAV35388-V35414 are primers used in a method which results in a
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC region (30-300 bases in length) of a retroviral gene other than the gag
CC gene. The gag gene may be altered so as to produce a gag protein modified
CC from the natural sequence by the addition, deletion or substitution of at
CC least 1 amino acid residue. The fusion gene is inserted into a region of
CC a vaccinia virus not essential to its propagation, to give a recombinant
CC vaccinia virus vector which is used to transform a host cell (such as
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC culturing the host cell produces particulate structures containing the
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC protein particles may be used in the production of vaccines for
CC protecting against infection with retroviruses such as HIV
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 3 CTTTTTTTTTTTTTTT 18

RESULT 2617
AAZ90649
ID AAZ90649 standard; DNA; 18 BP.
XX
AC AAZ90649;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #10.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 2 TTTTTTTTTTTTTTTA 17

RESULT 2618
AAZ90642/c
ID AAZ90642 standard; DNA; 18 BP.
XX
AC AAZ90642;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #3.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51

```
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2619
AAZ90640
ID   AAZ90640 standard; DNA; 18 BP.
XX
AC   AAZ90640;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #1.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTTA 17


RESULT 2620
AAZ90645/c
ID   AAZ90645 standard; DNA; 18 BP.
XX
AC   AAZ90645;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #6.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2621
AAZ90643
ID   AAZ90643 standard; DNA; 18 BP.
XX
AC   AAZ90643;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #4.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
```

```
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTA 17


RESULT 2622
AAZ90651/c
ID   AAZ90651 standard; DNA; 18 BP.
XX
AC   AAZ90651;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #12.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         17 GAAAAAAAAAAAAAAA 2


RESULT 2623
AAA58385
ID   AAA58385 standard; DNA; 18 BP.
XX
AC   AAA58385;
XX
DT   01-NOV-2000  (first entry)
XX
DE   Polynucleotide # 1 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999;   99WO-US026612.
XX
PR   10-NOV-1998;   98US-0107828P.
PR   09-NOV-1999;   99US-00437076.
XX
PA   (BIOC-) BIOCRYSTAL LTD.
XX
PI   Barbera-Guillem E,  Nelson MB,  Castro S;
XX
DR   WPI; 2000-376593/32.
XX
PT   Functionalized nanocrystal carrying polynucleotide, used for detecting
PT   target analyte, forms dendrimers with complementary nanocrystals to
PT   amplify the fluorescent signal.
XX
PS   Example 3; Page 68; 72pp; English.
XX
CC   The present invention relates to functionalised nanocrystals for use in
CC   nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC   proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC   attached to their surfaces with one end of the polynucleotide extending
CC   outwardly from the nanocrystal. The present sequence is one such
CC   polynucleotide. These nanocrystals are used with a second series of
CC   nanocrystals, which have polynucleotides complementary to the first
CC   polynucleotides, so that the respective complementary strands hybridise
CC   to each other and form a dendrimer. This dendrimer produces a signal
CC   which can then be detected e.g. fluorescence. The present sequence is
CC   composed mainly of Adenine bases. This sequence may therefore be used
CC   with a polynucleotide composed mainly of Thymine bases (AAA58386)
XX
SQ   Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          3 GAAAAAAAAAAAAAAA 18


RESULT 2624
ABK51158
ID   ABK51158 standard; DNA; 18 BP.
XX
AC   ABK51158;
XX
DT   30-JUL-2002  (first entry)
XX
DE   Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX
KW   Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
KW   cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
KW   reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS   Human cytomegalovirus.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 17
FT                   /*tag=  a
FT                   /label= n
```

```
FT                   /note= "n= dATP, dCTP or dGTP"
XX
PN   EP1201765-A2.
XX
PD   02-MAY-2002.
XX
PF   15-OCT-2001; 2001EP-00124604.
XX
PR   16-OCT-2000; 2000US-0240750P.
XX
PA   (AXXI-) AXXIMA PHARM AG.
XX
PI   Schubart D,  Habenberger P,  Stein-Gerlach M,  Bevec D;
XX
DR   WPI; 2002-373930/41.
XX
PT   Identifying agents for treatment or prevention of cytomegalovirus
PT   infection, comprises contacting test compound with cellular kinase and
PT   detecting change in cellular kinase activity.
XX
PS   Example 1; Page 13; 49pp; English.
XX
CC   The present invention relates to a new method for identifying compounds
CC   for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC   related diseases. The method of the invention comprises contacting a test
CC   compound with at least one of the cellular kinases RICK, RIP, Nck-
CC   Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
CC   activity. The method of the invention can be used to treat and/or prevent
CC   CMV infections and related diseases. Oligonucleotides that can detect the
CC   specified kinases can also be used for diagnosis of infection. The
CC   present nucleic acid sequence represents human CMV reverse transcriptase
CC   (RT)-PCR primer TXN that was used in the methods of the invention for
CC   preparation of radioactively labelled cDNA probes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 2625
ABK51158/c
ID   ABK51158 standard; DNA; 18 BP.
XX
AC   ABK51158;
XX
DT   30-JUL-2002  (first entry)
XX
DE   Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX
KW   Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
KW   cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
KW   reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS   Human cytomegalovirus.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 17
FT                   /*tag=  a
FT                   /label= n
FT                   /note= "n= dATP, dCTP or dGTP"
XX
PN   EP1201765-A2.
XX
PD   02-MAY-2002.
XX
PF   15-OCT-2001; 2001EP-00124604.
XX
PR   16-OCT-2000; 2000US-0240750P.
XX
PA   (AXXI-) AXXIMA PHARM AG.
XX
PI   Schubart D,  Habenberger P,  Stein-Gerlach M,  Bevec D;
XX
DR   WPI; 2002-373930/41.
XX
PT   Identifying agents for treatment or prevention of cytomegalovirus
PT   infection, comprises contacting test compound with cellular kinase and
PT   detecting change in cellular kinase activity.
XX
PS   Example 1; Page 13; 49pp; English.
XX
CC   The present invention relates to a new method for identifying compounds
CC   for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC   related diseases. The method of the invention comprises contacting a test
CC   compound with at least one of the cellular kinases RICK, RIP, Nck-
CC   Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
CC   activity. The method of the invention can be used to treat and/or prevent
CC   CMV infections and related diseases. Oligonucleotides that can detect the
CC   specified kinases can also be used for diagnosis of infection. The
CC   present nucleic acid sequence represents human CMV reverse transcriptase
CC   (RT)-PCR primer TXN that was used in the methods of the invention for
CC   preparation of radioactively labelled cDNA probes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 2626
AAD52799
ID   AAD52799 standard; DNA; 18 BP.
XX
AC   AAD52799;
XX
DT   14-MAY-2003  (first entry)
XX
DE   Primer used to prepare radioactively labelled cDNA probes from RNA.
XX
KW   Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW   cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW   prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW   CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW   TME; BSE; Gerstmann-Straussler-Scheinker syndrome; GSS; Alpers syndrome;
KW   fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic;
KW   Alzheimer's disease; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200293164-A2.
XX
PD   21-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-EP005420.
XX
PR   16-MAY-2001; 2001EP-00111858.
PR   29-MAY-2001; 2001US-0293528P.
PR   13-JUL-2001; 2001EP-00117113.
PR   18-JUL-2001; 2001US-0305898P.
XX
PA   (AXXI-) AXXIMA PHARM AG.
XX
PI   Stein-Gerlach M,  Salassidis K,  Bacher G,  Mueller S;
XX
DR   WPI; 2003-120714/11.
```

XX
PT New pyridylpyrimidine derivatives useful in the treatment or prevention
PT of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease
PT (CJD).
XX
PS Example; Page 38; 96pp; English.
XX
CC The invention relates to novel pyridylpyrimidine derivatives and methods
CC of detecting prion infections and/or prion disease in an individual or in
CC cells, cell cultures and/or cell lysates. The method involves adding at
CC least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-
CC pyrimidine derivative to the sample or in cells, cell cultures and/or
CC cell lysates and detecting the activity of at least one human cellular
CC protein kinases (e.g., FGF-R1 (also known as flg, Fl-1, Flt-2, b-FGFR),
CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also
CC known as c-abl), clk1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also
CC known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL
CC (also known as MCP83) and PTP-zeta, the cellular signal transduction
CC molecules HSP80 and GPIR-1. The invention is useful for regulating the
CC production of prions in cells and in the manufacture of pharmaceutical
CC composition for prophylaxis and/or treatment of infectious disease (e.g.
CC Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy
CC (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy
CC (BSE), variant CJD, Gerstmann-Straussler-Scheinker syndrome (GSS), fatal
CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,
CC vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans
CC or ruminants. The present DNA sequence is a primer used to prepare
CC radioactively labelled cDNA probes from RNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
||||||||||||||||
Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2627
AAD52799/c
ID AAD52799 standard; DNA; 18 BP.
XX
AC AAD52799;
XX
DT 14-MAY-2003 (first entry)
XX
DE Primer used to prepare radioactively labelled cDNA probes from RNA.
XX
KW Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW TME; BSE; Gerstmann-Straussler-Scheinker syndrome; GSS; Alpers syndrome;
KW fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic;
KW Alzheimer's disease; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200293164-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-EP005420.
XX
PR 16-MAY-2001; 2001EP-00111858.
PR 29-MAY-2001; 2001US-0293528P.
PR 13-JUL-2001; 2001EP-00117113.
PR 18-JUL-2001; 2001US-0305898P.
XX
PA (AXXI-) AXXIMA PHARM AG.
XX
PI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;
XX
DR WPI; 2003-120714/11.
XX
PT New pyridylpyrimidine derivatives useful in the treatment or prevention
PT of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease
PT (CJD).
XX
PS Example; Page 38; 96pp; English.
XX
CC The invention relates to novel pyridylpyrimidine derivatives and methods
CC of detecting prion infections and/or prion disease in an individual or in
CC cells, cell cultures and/or cell lysates. The method involves adding at
CC least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-
CC pyrimidine derivative to the sample or in cells, cell cultures and/or
CC cell lysates and detecting the activity of at least one human cellular
CC protein kinases (e.g., FGF-R1 (also known as flg, Fl-1, Flt-2, b-FGFR),
CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also
CC known as c-abl), clk1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also
CC known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL
CC (also known as MCP83) and PTP-zeta, the cellular signal transduction
CC molecules HSP80 and GPIR-1. The invention is useful for regulating the
CC production of prions in cells and in the manufacture of pharmaceutical
CC composition for prophylaxis and/or treatment of infectious disease (e.g.
CC Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy
CC (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy
CC (BSE), variant CJD, Gerstmann-Straussler-Scheinker syndrome (GSS), fatal
CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,
CC vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans
CC or ruminants. The present DNA sequence is a primer used to prepare
CC radioactively labelled cDNA probes from RNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 16 AAAAAAAAAAAAAAAA 1

RESULT 2628
ABZ89487
ID ABZ89487 standard; DNA; 20 BP.
XX
AC ABZ89487;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.

XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4729; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 5 AAAAAAAAAAAAAAAA 20

RESULT 2629
ABZ85532
ID ABZ85532 standard; DNA; 20 BP.
XX
AC ABZ85532;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.

XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 774; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 5 AAAAAAAAAAAAAAAA 20

RESULT 2630
AAT73293/c
ID AAT73293 standard; DNA; 20 BP.
XX
AC AAT73293;
XX
DT 12-DEC-1997 (first entry)
XX
DE Primer for pUC19 DNA amplification.
XX
KW primer; PCR; polymerase chain reaction; sequencing; walking;
KW complementary extension reaction; low redundancy; universal primer; ss.
XX
OS Synthetic.
XX
PN EP767240-A2.
XX
PD 09-APR-1997.
XX
PF 17-SEP-1996; 96EP-00114907.
XX
PR 18-SEP-1995; 95JP-00238141.
PR 30-JAN-1996; 96JP-00013634.
XX
PA (HITA) HITACHI LTD.
XX
PI Kambara H, Okano K;
XX

```
DR   WPI; 1997-205424/19.
XX
PT   Efficient sequencing of long DNA by fragment walking - with simultaneous
PT   sequencing of restriction enzyme fragment and adjacent region of intact
PT   DNA, avoids the need for cloning and requires fewer primers.
XX
PS   Example 1; Page 23; 50pp; English.
XX
CC   A method for DNA analysis based on a complementary extension reaction
CC   using a DNA polymerase, comprises a combination of fragment walking and
CC   DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC   restriction enzyme and the targeted DNA sequence can be determined
CC   directly from the digested DNA fragments. By exploring the overlapping
CC   sequence of the determined base sequence, the overall base sequence of a
CC   lengthy DNA can be determined with low redundancy without cloning or
CC   subcloning. In addition, the method can be done with commercially
CC   available universal primers or with fewer primers than required in
CC   existing methods. AAT73291-92 are primers used in determination of the
CC   pUC19 sequence. Primer extension was carried out using 16 primers
CC   AAT73293
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         16 GAAAAAAAAAAAAAAA 1


RESULT 2631
AAX93567
ID   AAX93567 standard; DNA; 20 BP.
XX
AC   AAX93567;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1602; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTT 2099
                ||||||||||||||||
Db          5 CTCTAAACCCCGTGTT 20


RESULT 2632
AAD15533/c
ID   AAD15533 standard; DNA; 20 BP.
XX
AC   AAD15533;
XX
DT   15-NOV-2001  (first entry)
XX
DE   Human C-Raf protein target DNA #4.
XX
KW   Human; C-Raf protein; genetic disease; antisense target; therapeutic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200161030-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US004732.
XX
PR   14-FEB-2000; 2000US-00504653.
XX
PA   (BOLL/) BOLLON A P.
PA   (GRAY/) GRAY D M.
PA   (JUSE/) JU-SEOG L.
XX
PI   Bollon AP,  Gray DM,  Ju-Seog L;
XX
DR   WPI; 2001-529916/58.
XX
PT   Selecting optimal subsequence antisense targets for inhibition of mRNA
PT   expression of target mRNA for the therapeutic treatment of genetic
PT   disease.
XX
PS   Example 2; Page 17; 87pp; English.
XX
CC   The invention relates to a method for selecting optimal subsequence
CC   antisense targets. The method involves preparing an antisense
CC   oligonucleotide capable of inhibiting mRNA expression of target mRNA
CC   sequences, as well as antisense oligonucleotides capable of binding DNA.
CC   The antisense and antigene libraries are useful for preparing therapeutic
CC   agents for the treatment of genetic disease. The present DNA sequence is
CC   human C-Raf protein target DNA related to the invention. Note: The
CC   present sequence is shown as DNA in the specification; however, in vivo,
CC   this target sequence would be mRNA
XX
SQ   Sequence 20 BP; 3 A; 5 C; 10 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        505 GCTGCCCTCGCACCAC 520
                ||||||||||||||||
Db         16 GCTGCCCTCGCACCAC 1
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RESULT 2633
AAC82924/c
ID   AAC82924 standard; DNA; 20 BP.
XX
AC   AAC82924;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #8.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              ||||||||||||||||
Db         16 TTGAAAAAAAAAAAAA 1


RESULT 2634
AAC82922
ID   AAC82922 standard; DNA; 20 BP.
XX
AC   AAC82922;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #6.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTAAC 2189
              ||||||||||||||||
Db          1 TTTTTTTTTTTTAAC 16


RESULT 2635
AAD33499
ID   AAD33499 standard; DNA; 20 BP.
XX
AC   AAD33499;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS27-20-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
```

```
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2636
AAD33499/c
ID   AAD33499 standard; DNA; 20 BP.
XX
AC   AAD33499;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS27-20-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2637
AAD35095
ID   AAD35095 standard; DNA; 20 BP.
XX
AC   AAD35095;
XX
DT   25-JUL-2002  (first entry)
XX
DE   HT15-C downstream PCR primer used for identification of genes.
XX
KW   Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
KW   sex discrimination; infertility treatment; chromosomal manipulation;
KW   sperm separation; gene therapy; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   EP1195382-A2.
XX
PD   10-APR-2002.
XX
PF   02-OCT-2001; 2001EP-00123259.
XX
PR   03-OCT-2000; 2000JP-00303994.
XX
PA   (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
PA   (UYGU-) UNIV GUNMA.
XX
PI   Aizawa A,  Kawakami A,  Kondo T;
XX
DR   WPI; 2002-354153/39.
XX
PT   New X-chromosome gene expressed in haploid cells of the testis, useful
PT   for gene diagnosis, discrimination of sex, separation of sperm,
PT   infertility treatment and chromosomal manipulation.
XX
PS   Example 1; Page 4; 28pp; English.
XX
CC   The present invention relates to genes located on the X-chromosome of
CC   mammals. These genes are specifically expressed in haploid cells of the
CC   testis and encode amino acid sequences having homology with the amino
CC   acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences
CC   of the invention are used for gene diagnosis, discrimination of sex,
CC   separation of sperm, infertility treatment and chromosomal manipulation,
CC   especially in livestock. They are also used in gene therapy. The present
CC   DNA sequence is a PCR primer which is used for the identification of
CC   genes by differential display method
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          4 CTTTTTTTTTTTTTTT 19


RESULT 2638
AAD35095/c
ID   AAD35095 standard; DNA; 20 BP.
XX
AC   AAD35095;
XX
```

DT 25-JUL-2002 (first entry)
XX
DE HT15-C downstream PCR primer used for identification of genes.
XX
KW Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
KW sex discrimination; infertility treatment; chromosomal manipulation;
KW sperm separation; gene therapy; PCR; primer; ss.
XX
OS Unidentified.
XX
PN EP1195382-A2.
XX
PD 10-APR-2002.
XX
PF 02-OCT-2001; 2001EP-00123259.
XX
PR 03-OCT-2000; 2000JP-00303994.
XX
PA (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
PA (UYGU-) UNIV GUNMA.
XX
PI Aizawa A, Kawakami A, Kondo T;
XX
DR WPI; 2002-354153/39.
XX
PT New X-chromosome gene expressed in haploid cells of the testis, useful
PT for gene diagnosis, discrimination of sex, separation of sperm,
PT infertility treatment and chromosomal manipulation.
XX
PS Example 1; Page 4; 28pp; English.
XX
CC The present invention relates to genes located on the X-chromosome of
CC mammals. These genes are specifically expressed in haploid cells of the
CC testis and encode amino acid sequences having homology with the amino
CC acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences
CC of the invention are used for gene diagnosis, discrimination of sex,
CC separation of sperm, infertility treatment and chromosomal manipulation,
CC especially in livestock. They are also used in gene therapy. The present
CC DNA sequence is a PCR primer which is used for the identification of
CC genes by differential display method
XX
SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 20 GAAAAAAAAAAAAAAA 5

RESULT 2639
ABZ89873/c
ID ABZ89873 standard; DNA; 20 BP.
XX
AC ABZ89873;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5115; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTT 2178
||||||||||||||||
Db 16 TCCTTTTTTTTTTTTT 1

RESULT 2640
ABZ89014/c
ID ABZ89014 standard; DNA; 20 BP.
XX
AC ABZ89014;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX

```
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4256; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db         20 TTTTTTTTTTTTTTTA 5


RESULT 2641
AAZ09196/c
ID   AAZ09196 standard; DNA; 21 BP.
XX
AC   AAZ09196;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Oligonucleotide 8 for DNA analysis.
XX
KW   Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   JP11196874-A.
XX
PD   27-JUL-1999.
XX
PF   14-JAN-1998;   98JP-00005399.
XX
PR   14-JAN-1998;   98JP-00005399.
XX
PA   (HITA ) HITACHI LTD.
XX
DR   WPI; 1999-496652/42.
XX
PT   Analysis of DNA fragment - comprises addition of known common
PT   oligonucleotide, amplification of resultant DNA fragment and analysis and
PT   labelling of amplified DNA.
XX
PS   Example 1; Page 12; 17pp; Japanese.
XX
CC   This invention descibes a novel method for the analysis of a DNA fragment
CC   which comprises: (i) addition of a known common oligonucleotide sequence
CC   to at least one terminal of each DNA fragment, (ii) amplification of the
CC   resultant DNA fragment as a primer using a first common primer containing
CC   a complementary nucleotide sequence to the above mentioned known common
CC   oligonucleotide sequence, a second common primer containing a
CC   complementary nucleotide sequence to the prepared known common
CC   oligonucleotide sequence optionally having been introduced with
CC   complementary nucleotide sequence at a terminal, and a specific primer
CC   capable of hybridisation with a DNA fragment containing whole or part of
CC   the gene having known sequence, to give amplified DNA, (iii) analysis of
CC   the amplified DNA to find the information of the DNA fragment, in which
CC   the specific primer is designed to prepare fragments of the common first
CC   and second primers and to give short fragment of amplified DNA and (iv)
CC   labelling them to make their differentiation. Differentiation of
CC   informations of known and unknown genes readily provides information of
CC   unknown gene and simultaneous monitoring of signals derived from minor
CC   genes. Furthermore, labelling of DNAs according to functions of known
CC   genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC   used to illustrate the method of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         21 AAAAAAAAAAAAAAAA 6


RESULT 2642
ABL57071
ID   ABL57071 standard; DNA; 21 BP.
XX
AC   ABL57071;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .21
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 1-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
```

PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Dubertret B, Calame M, Libchaber A;
XX
DR WPI; 2002-404569/43.
XX
PT Sensitively detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.
XX
PS Example 3; Page 62; 62pp; English.
XX
CC The present sequence is that of a perfectly matched target sequence for a
CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC a nanoparticle. In the native state, the probe forms a hairpin
CC conformation with hybridised termini. The proximity of the fluorophore
CC and quencher (gold nanoparticle) in the molecular beacon results in
CC little or no detectable fluorescence. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, such as the
CC present sequence, the hairpin undergoes a conformational change resulting
CC in an increase in fluorescence, the extent of which is proportional to
CC the amount of target sequence present. Single mismatches can be detected.
CC The invention relates generally to the use of metal surface quenchers
CC such as particles or films for high sensitivity applications in, for
CC example, detection and diagnostic systems
XX
SQ Sequence 21 BP; 15 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 1 GAAAAAAAAAAAAAAA 16

RESULT 2643
ABS97317/c
ID ABS97317 standard; DNA; 21 BP.
XX
AC ABS97317;
XX
DT 23-DEC-2002 (first entry)
XX
DE Aryl hydrocarbon nuclear translocation receptor sequencing primer #6.
XX
KW Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 6; Page 109; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention
XX
SQ Sequence 21 BP; 3 A; 4 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAA 2798
||||||||||||||||
Db 16 TTGAAAAAAAAAAAAA 1

RESULT 2644
AAD33500
ID AAD33500 standard; DNA; 21 BP.
XX
AC AAD33500;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS26-21-0003 probe for calibration of molecular array data.

XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 1 AAAAAAAAAAAAAAAA 16

RESULT 2645
AAD33500/c
ID AAD33500 standard; DNA; 21 BP.
XX
AC AAD33500;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS26-21-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2181
||||||||||||||||
Db 16 TTTTTTTTTTTTTTTT 1

RESULT 2646
AAD33501
ID AAD33501 standard; DNA; 22 BP.
XX
AC AAD33501;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS25-22-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 22 BP; 16 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2647
AAD33501/c
ID   AAD33501 standard; DNA; 22 BP.
XX
AC   AAD33501;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS25-22-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 22 BP; 16 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2648
AAT33701/c
ID   AAT33701 standard; DNA; 23 BP.
XX
AC   AAT33701;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Primer #1 for tissue or cell derived RNA.
XX
KW   PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
KW   molecular indexing; class IIS restriction enzyme; cancer; causative gene;
KW   viral infection; hereditary disease; agricultural gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "hydroxylated"
XX
PN   EP735144-A1.
XX
PD   02-OCT-1996.
XX
PF   26-MAR-1996;   96EP-00104817.
XX
PR   28-MAR-1995;   95JP-00069695.
PR   20-JUL-1995;   95JP-00184006.
PR   12-SEP-1995;   95JP-00234122.
XX
PA   (SHKJ ) RES DEV CORP JAPAN.
XX
PI   Kato K;
XX
DR   WPI; 1996-435619/44.
XX
PT   Molecular indexing of DNA - using restriction enzymes, PCR amplification
PT   and electrophoresis to analyse DNA fragments.
XX
PS   Claim 3; Page 14; 20pp; English.
XX
CC   AAT33701-T33703 represent amplification primers used in the reverse-
CC   transcription of tissue or cell derived mRNA, in the method of the
CC   invention. The method of the invention is a molecular indexing method,
CC   and comprises digesting the cDNA amplified by these sequences with a
CC   class IIS restriction enzyme. Each resultant cDNA fragment is then
CC   ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
CC   cohesive to all possible overhangs), and digesting the products with two
CC   further class IIS restriction enzymes. These steps are repeated (but the
CC   enzyme used for the first step is different in each) to produce two
CC   further cDNA samples. The ligation samples are then recovered using
CC   streptavidin-coated paramagnetic beads, removing the strand complementary
CC   to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
CC   (such as this sequence) are then used to amplify the cDNA samples. The
CC   amplified products are separated, and the sizes of the fragments obtained
CC   is recorded. The method can be used for the analysis and diagnosis or
CC   diseases such as cancers or viral infections, for the search and
CC   isolation of the genes of physiologically active substances that are
CC   potential pharmaceuticals, or causative genes of hereditary diseases, as
CC   well as for the isolation of genes for improving agricultural products.
CC   Using this method, it is possible to classify (index) DNA into groups in
CC   a short period of time without duplication
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 2649
AAV61554/c
ID   AAV61554 standard; DNA; 23 BP.
XX
AC   AAV61554;
XX
```

DT 08-DEC-1998 (first entry)
XX
DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW gene expression; internal standard; calibration curve; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN EP870842-A2.
XX
PD 14-OCT-1998.
XX
PF 07-APR-1998; 98EP-00302726.
XX
PR 07-APR-1997; 97JP-00088495.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kato K;
XX
DR WPI; 1998-523164/45.
XX
PT Determination of gene expression levels - using combinations of different
PT cDNA samples tagged with different PCR adaptors.
XX
PS Example 2; Page 9; 22pp; English.
XX
CC The present sequence represents a primer which was used to synthesise
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC AAV61555 and AAV61556 were added to both mouse liver-derived and mouse
CC kidney-derived total RNA to generate single-stranded cDNA. These primers
CC were used in the method of the invention to determine the amount ratio
CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC be quantitatively determined, and because internal standards are not
CC required to prepare a calibration curve, it is a quicker and less
CC laborious process
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 22 AAAAAAAAAAAAAAAA 7

RESULT 2650
AAA08407/c
ID AAA08407 standard; DNA; 23 BP.
XX
AC AAA08407;
XX
DT 13-JUL-2000 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO:1.
XX
KW Detection; primer; adapter; probe; hybridisation; gene cluster;
KW fractionation; ss.
XX
OS Synthetic.
XX
PN JP2000055914-A.
XX
PD 25-FEB-2000.
XX
PF 13-AUG-1998; 98JP-00228944.
XX
PR 13-AUG-1998; 98JP-00228944.
XX
PA (TAIS) TAISHO PHARM CO LTD.
XX
DR WPI; 2000-368733/32.
XX
PT Gene detection method involves hybridizing probe opposite to objective
PT gene out of fractional gene cluster.
XX
PS Example 1; Page 9; 11pp; Japanese.
XX
CC The present invention describes a gene detection method which comprises
CC fractionating using a probe opposite to the objective gene which is
CC hybridised out of fractioned gene cluster. The objective gene detected
CC belongs to the group of objective genes contained in the sample. The
CC method is used for gene detection by fractionation of cDNA by molecular
CC index method using specific primer. It provides high detection
CC sensitivity of objective gene. AAA08407 to AAA08414 represent
CC oligonucleotides used in the exemplification of the present invention
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 22 AAAAAAAAAAAAAAAA 7

RESULT 2651
ABA99682/c
ID ABA99682 standard; DNA; 23 BP.
XX
AC ABA99682;
XX
DT 31-MAY-2002 (first entry)
XX
DE Murine osteoporosis/arthro-rheumatism associated gene PCR primer DAPA1.
XX
KW Osteoporosis; murine; treatment; arthro-rheumatism; PCR; primer; ss.
XX
OS Mus musculus.
XX
PN JP2002051782-A.
XX
PD 19-FEB-2002.
XX
PF 09-AUG-2000; 2000JP-00241413.
XX
PR 09-AUG-2000; 2000JP-00241413.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2002-288360/33.
XX
PT Preventing or treating an agent for osteoporosis or arthro-rheumatism.
XX
PS Example 2; Page 38; 44pp; Japanese.
XX
CC This invention describes a novel method for testing the effect of a
CC substance as a preventive or treating agent for osteoporosis or arthro-
CC rheumatism. This sequence represents a PCR primer used in the
CC amplification of a gene encoding a protein associated with osteoporosis
CC or arthro-rheumatism which is described in the disclosure of the
CC invention
XX
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

```
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 2652
AAT33703/c
ID   AAT33703 standard; DNA; 23 BP.
XX
AC   AAT33703;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Primer #3 for tissue or cell derived RNA.
XX
KW   PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
KW   molecular indexing; class IIS restriction enzyme; cancer; causative gene;
KW   viral infection; hereditary disease; agricultural gene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "hydroxylated"
XX
PN   EP735144-A1.
XX
PD   02-OCT-1996.
XX
PF   26-MAR-1996;   96EP-00104817.
XX
PR   28-MAR-1995;   95JP-00069695.
PR   20-JUL-1995;   95JP-00184006.
PR   12-SEP-1995;   95JP-00234122.
XX
PA   (SHKJ ) RES DEV CORP JAPAN.
XX
PI   Kato K;
XX
DR   WPI; 1996-435619/44.
XX
PT   Molecular indexing of DNA - using restriction enzymes, PCR amplification
PT   and electrophoresis to analyse DNA fragments.
XX
PS   Claim 3; Page 14; 20pp; English.
XX
CC   AAT33701-T33703 represent amplification primers used in the reverse-
CC   transcription of tissue or cell derived mRNA, in the method of the
CC   invention. The method of the invention is a molecular indexing method,
CC   and comprises digesting the cDNA amplified by these sequences with a
CC   class IIS restriction enzyme. Each resultant cDNA fragment is then
CC   ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
CC   cohesive to all possible overhangs), and digesting the products with two
CC   further class IIS restriction enzymes. These steps are repeated (but the
CC   enzyme used for the first step is different in each) to produce two
CC   further cDNA samples. The ligation samples are then recovered using
CC   streptavidin-coated paramagnetic beads, removing the strand complementary
CC   to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
CC   (such as this sequence) are then used to amplify the cDNA samples. The
CC   amplified products are separated, and the sizes of the fragments obtained
CC   is recorded. The method can be used for the analysis and diagnosis or
CC   diseases such as cancers or viral infections, for the search and
CC   isolation of the genes of physiologically active substances that are
CC   potential pharmaceuticals, or causative genes of hereditary diseases, as
CC   well as for the isolation of genes for improving agricultural products.
CC   Using this method, it is possible to classify (index) DNA into groups in
CC   a short period of time without duplication
XX
SQ   Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 2653
AAV61556/c
ID   AAV61556 standard; DNA; 23 BP.
XX
AC   AAV61556;
XX
DT   08-DEC-1998  (first entry)
XX
DE   Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
XX
KW   Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
KW   kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;
KW   gene expression; internal standard; calibration curve; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   EP870842-A2.
XX
PD   14-OCT-1998.
XX
PF   07-APR-1998;   98EP-00302726.
XX
PR   07-APR-1997;   97JP-00088495.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kato K;
XX
DR   WPI; 1998-523164/45.
XX
PT   Determination of gene expression levels - using combinations of different
PT   cDNA samples tagged with different PCR adaptors.
XX
PS   Example 2; Page 9; 22pp; English.
XX
CC   The present sequence represents a primer which was used to synthesise
CC   Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC   AAV61554 and AAV61555 were added to both mouse liver-derived and mouse
CC   kidney-derived total RNA to generate single-stranded cDNA. These primers
CC   were used in the method of the invention to determine the amount ratio
CC   between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC   that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC   tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC   be quantitatively determined, and because internal standards are not
CC   required to prepare a calibration curve, it is a quicker and less
CC   laborious process
XX
SQ   Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 2654
AAA08409/c
ID   AAA08409 standard; DNA; 23 BP.
XX
AC   AAA08409;
```

```
XX
DT   13-JUL-2000  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO:3.
XX
KW   Detection; primer; adapter; probe; hybridisation; gene cluster;
KW   fractionation; ss.
XX
OS   Synthetic.
XX
PN   JP2000055914-A.
XX
PD   25-FEB-2000.
XX
PF   13-AUG-1998;   98JP-00228944.
XX
PR   13-AUG-1998;   98JP-00228944.
XX
PA   (TAIS ) TAISHO PHARM CO LTD.
XX
DR   WPI; 2000-368733/32.
XX
PT   Gene detection method involves hybridizing probe opposite to objective
PT   gene out of fractional gene cluster.
XX
PS   Example 1; Page 9; 11pp; Japanese.
XX
CC   The present invention describes a gene detection method which comprises
CC   fractionating using a probe opposite to the objective gene which is
CC   hybridised out of fractioned gene cluster. The objective gene detected
CC   belongs to the group of objective genes contained in the sample. The
CC   method is used for gene detection by fractionation of cDNA by molecular
CC   index method using specific primer. It provides high detection
CC   sensitivity of objective gene. AAA08407 to AAA08414 represent
CC   oligonucleotides used in the exemplification of the present invention
XX
SQ   Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         22 AAAAAAAAAAAAAAAA 7


RESULT 2655
AAZ99839
ID   AAZ99839 standard; DNA; 23 BP.
XX
AC   AAZ99839;
XX
DT   12-JUL-2000  (first entry)
XX
DE   Nucleotide sequence of reverse transcription primer.
XX
KW   Mono-length cDNA library; differential display; gene expression;
KW   gene identification; drug response; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200014273-A2.
XX
PD   16-MAR-2000.
XX
PF   26-AUG-1999;   99WO-CA000789.
XX
PR   03-SEP-1998;   98US-00145936.
XX
PA   (SIGN-) SIGNALGENE INC.
XX
PI   Belouchi AM,  Fournier H,  Gee M,  Gauvreau D;
XX
DR   WPI; 2000-257012/22.
XX
PT   Determining differential display of gene expression, useful for
PT   monitoring drug responses at the gene expression level and locating genes
PT   involved in a particular response, by comparisons between mono-length
PT   cRNA libraries.
XX
PS   Example 3; Page 48; 73pp; English.
XX
CC   The present sequence represents a primer used for reverse transcription
CC   of mRNA to produce cDNA. The cDNA is used for cDNA library production, in
CC   the course of the invention. The specification describes a method of
CC   determining differential display of gene expression, by comparison of
CC   mono-length cRNA libraries. These libraries are probe hybridised to
CC   accessible ordered arrays to determine differential hybridisation display
CC   sites between mono-length segment libraries and to locate genes of
CC   expression differential. The methods are useful for determining
CC   differential hybridisation display sites between mono-length segment
CC   libraries and to locate genes of expression differential. The methods are
CC   also useful in gene identification related to complex traits. The methods
CC   also permit monitoring drug responses at the gene expression level and
CC   locating genes involved in a particular response. The methods are also
CC   useful for pharmacogenomic research in evaluating how variability in
CC   genetic background influences positive or negative response to a drug
XX
SQ   Sequence 23 BP; 0 A; 4 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          8 CTTTTTTTTTTTTTTT 23


RESULT 2656
AAD33502
ID   AAD33502 standard; DNA; 23 BP.
XX
AC   AAD33502;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS24-23-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
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CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 23 BP; 17 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2657
AAD33502/c
ID   AAD33502 standard; DNA; 23 BP.
XX
AC   AAD33502;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS24-23-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 23 BP; 17 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2658
AAI65187/c
ID   AAI65187 standard; DNA; 24 BP.
XX
AC   AAI65187;
XX
DT   12-DEC-2001  (first entry)
XX
DE   Human gap connexin 10 PCR primer #1.
XX
KW   Human; gap connexin 10; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; gene therapy; malignant tumour;
KW   PCR primer; haemopathy; HIV infection; immunological disease;
KW   inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200172818-A1.
XX
PD   04-OCT-2001.
XX
PF   26-MAR-2001; 2001WO-CN000511.
XX
PR   29-MAR-2000; 2000CN-00115275.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-602853/68.
XX
PT   Human gap connexin 10 polynucleotide and polypeptide, useful in diagnosis
PT   and treatment of malignant tumor, hemopathy, HIV infection, immunological
PT   diseases and various inflammatory diseases.
XX
PS   Example 2; Page 12; 36pp; Chinese.
XX
CC   The present invention relates to human gap connexin 10 (see AAI65186 and
CC   AAG78856). The protein and its coding sequence are useful in the
CC   diagnosis and treatment of malignant tumours, haemopathy, HIV infection,
CC   immunological diseases and various inflammations. The present sequence is
CC   a PCR primer which was used in an example from the present invention
XX
SQ   Sequence 24 BP; 2 A; 0 C; 3 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         23 AAAAAAAAAAAAAAAA 8


RESULT 2659
ABK11020/c
ID   ABK11020 standard; DNA; 24 BP.
XX
AC   ABK11020;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Gamma-COP13 polypeptide, RT-PCR primer #2.
XX
KW   Gamma-COP13; cytostatic; haemostatic; virucide; immunomodulatory;
KW   antiinflammatory; malignant tumour; haemopathy; inflammation;
KW   human immunodeficiency virus; HIV; immunological disease;
KW   reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200202616-A1.
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```
XX
PD   10-JAN-2002.
XX
PF   11-JUN-2001; 2001WO-CN000961.
XX
PR   14-JUN-2000; 2000CN-00116482.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-090536/12.
XX
PT   Gamma-cop 13 polypeptide and encoded polynucleotide, used in diagnosis
PT   and treatment of malignant tumors, hemopathy, human immunodeficiency
PT   virus infection, immunological diseases and inflammation.
XX
PS   Example 2; Page 11; 33pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide (I), of gamma-COP13 and
CC   the polynucleotide (II) encoding it. (I) and (II) are used in diagnosis
CC   and treatment of malignant tumour, haemopathy, human immunodeficiency
CC   virus (HIV) infection, immunological diseases and various inflammations.
CC   The present sequence represents a reverse transcriptase (RT)-PCR primer
CC   used to isolate the coding sequence of gamma-COP13 polypeptide
XX
SQ   Sequence 24 BP; 3 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
              |||   |||||| ||| |||||||
Db         24 AGATAAGAAAAATAAATAAAAAAA 1


RESULT 2660
AAV82670/c
ID   AAV82670 standard; DNA; 24 BP.
XX
AC   AAV82670;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Primer used to identify cDNA encoding ST38.2.
XX
KW   Rat; chemokine; ST38.2; chemotaxis; leucocyte-activating; inflammation;
KW   immune response; brain injury; trauma; ischaemia;
KW   autoimmune inflammation; multiple sclerosis; stroke;
KW   rheumatoid arthritis; meningitis; encephalitis; PCR primer; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   WO9849309-A1.
XX
PD   05-NOV-1998.
XX
PF   23-APR-1998;   98WO-EP002405.
XX
PR   30-APR-1997;   97EP-00107135.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Lesslauer W,  Utansschneitz U;
XX
DR   WPI; 1999-009430/01.
XX
PT   New chemokine ST38.2 with chemotactic and leucocyte-activating properties
PT   - used to treat inflammation and immune responses and to identify
PT   specific modulators.
XX
PS   Example 3; Page 28; 64pp; English.
XX
CC   PCR primers AAV82670-71 were used to amplify cDNA encoding a novel rat
CC   chemokine designated ST38.2. In addition, primer AAV82670 was used to
CC   reverse transcribe rat RNA. The protein has chemotactic and leucocyte-
CC   activating properties. ST38.2 is involved in inflammation and immune
CC   responses, particularly inflammatory response to brain injury (trauma,
CC   ischaemia or autoimmune inflammation) but also in multiple sclerosis,
CC   stroke, rheumatoid arthritis and infections (particularly meningitis and
CC   encephalitis)
XX
SQ   Sequence 24 BP; 2 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         24 AAAAAAAAAAAAAAAA 9


RESULT 2661
ABL40114/c
ID   ABL40114 standard; DNA; 24 BP.
XX
AC   ABL40114;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human natriuretic peptide acceptor 10 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; natriuretic peptide acceptor 10; malignant tumour; blood disease;
KW   HIV infection; immunity disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1323830-A.
XX
PD   28-NOV-2001.
XX
PF   16-MAY-2000; 2000CN-00115724.
XX
PR   16-MAY-2000; 2000CN-00115724.
XX
PA   (SHAN-) SHANGHAI BODE GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-148833/20.
XX
PT   New polypeptide-human natriuretic peptide acceptor 10 and polynucleotides
PT   for coding same.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The present invention describes human natriuretic peptide acceptor 10
CC   (I). The present invention also describes a method for producing (I)
CC   through DNA recombination techniques. (I) and the polynucleotide encoding
CC   it can be used in the treatment of several diseases such as malignant
CC   tumours, blood diseases, HIV infection and immunity diseases and various
CC   inflammations. The present sequence represents a PCR primer for human
CC   natriuretic peptide acceptor 10, which is used in an example from the
CC   present invention
XX
SQ   Sequence 24 BP; 2 A; 5 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              ||||||||||||||||
```

```
Db         22 TGAAAAAAAAAAAAAA 7


RESULT 2662
ABQ79142
ID   ABQ79142 standard; DNA; 24 BP.
XX
AC   ABQ79142;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Primer #2 related to human eukaryotic initial factor -2 protein.
XX
KW   Human; eukaryotic initial factor -2; (elF-2); tumour; virus infection;
KW   development disorder; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1340547-A.
XX
PD   20-MAR-2002.
XX
PF   31-AUG-2000; 2000CN-00119830.
XX
PR   31-AUG-2000; 2000CN-00119830.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-436441/47.
XX
PT   Polypeptide-human eukaryotic initiation factor-2 (eIF-2)-associated
PT   protein 74.14 and polynucleotide encoding it.
XX
PS   Example 2; Page 18 (Disclosure); 36pp; Chinese.
XX
CC   This invention relates to a novel polypeptide-human eukaryotic initial
CC   factor -2 (elF-2)-associated protein 74.14 and the application of the
CC   polypeptide in treating diseases such as tumours, virus infection
CC   abnormalities and development disorders. The present sequence represents
CC   a primer related to the novel human eukaryotic initial factor -2 (elF-2)-
CC   associated protein
XX
SQ   Sequence 24 BP; 4 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
             ||| ||||| |||||| ||| | |
Db          1 TTTATTTTTATTTTTTATTTCATT 24


RESULT 2663
AAQ43999
ID   AAQ43999 standard; DNA; 24 BP.
XX
AC   AAQ43999;
XX
DT   25-MAR-2003  (revised)
DT   28-OCT-1993  (first entry)
XX
DE   HIV-1 LTR region antisense oligonucleotide Dx.
XX
KW   Purine; pyrimidine; tracts; therapeutic; diagnostic; control;
KW   gene expresssion; mRNA synthesis suppression;
KW   human immunodeficiency virus; ss.
XX
OS   Synthetic.
XX
PN   WO9312230-A1.
XX
PD   24-JUN-1993.
XX
PF   11-DEC-1992;   92WO-US010792.
XX
PR   13-DEC-1991;   91US-00808452.
PR   21-JAN-1992;   92US-00826934.
XX
PA   (STRI ) SRI INT.
XX
PI   Jayasena SD,  Johnston BH;
XX
DR   WPI; 1993-214172/26.
XX
PT   New oligo:nucleotide(s) forming triple helix with target nucleic acid -
PT   contain purine and pyrimidine tracts in specific orientations, useful
PT   therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
XX
PS   Disclosure; Fig 12b; 101pp; English.
XX
CC   The sequence is that of the antisense oligonucleotide Dx which is
CC   designed to target HIV-1 LTR region nucleotides 5786-8887. It may be
CC   useful for therapeutic or diagnostic control of gene expression, e.g.
CC   suppression of mRNA synthesis in the HIV-1 genome. When appropriately
CC   labelled it can also be used as a probe, and attachment of cleavage
CC   agents caused permanent inactivation of the target by site-specific
CC   cleavage. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 24 BP; 0 A; 8 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTT 2178
              | || | ||||||||||  |||||
Db          1 TCTTCTCCTCCTTTTTCCTTTT 24


RESULT 2664
AAX26962/c
ID   AAX26962 standard; DNA; 24 BP.
XX
AC   AAX26962;
XX
DT   24-JUN-1999  (first entry)
XX
DE   PCR primer used to amplify autoimmune regulator-1 (AIR-1) cDNA.
XX
KW   Autoimmune regulator-1; AIR-1; immune maturation; immune response;
KW   disease; autoimmune polyendocrinopathy candidiasis ectodermal dystrophy;
KW   APECED; autoimmune polyglandular syndrome type I; APS I; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9915559-A1.
XX
PD   01-APR-1999.
XX
PF   23-SEP-1998;   98WO-FI000749.
XX
PR   23-SEP-1997;   97FI-00003762.
XX
PA   (FIIM-) FINNISH IMMUNOTECHNOLOGY LTD.
XX
PI   Krohn K,  Heino M,  Peterson P,  Scott H,  Antonarakis S,  Lalioti M;
PI   Shimizu N,  Kudoh J;
XX
DR   WPI; 1999-244390/20.
XX
PT   Autoimmune regulator 1 (AIR1) DNA sequence.
XX
```

```
PS   Example 5; Page 16; 59pp; English.
XX
CC   PCR primers AAX26957-62 were used to amplify human autoimmune regulator-1
CC   (AIR-1) cDNA fragments. The amplified products were used as probes. The
CC   peptide was used to raise antibodies against AIR-1. The AIR polypeptides
CC   and polynucleotides can be used in methods for the diagnosis and
CC   treatment of diseases related to immune maturation and regulation of
CC   immune response towards self and nonself. They can be used particularly
CC   in the diagnosis and treatment of autoimmune polyendocrinopathy
CC   candidiasis ectodermal dystrophy (APECED) (also known as autoimmune
CC   polyglandular syndrome type I (APS I))
XX
SQ   Sequence 24 BP; 6 A; 8 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1591 CTGGGAACCCCTCCTGGCCTGGGG 1614
                | |||| || ||||| ||||||  |
Db         24 CCGGGAGCCTCTCCTTGCCTGGTG 1


RESULT 2665
AAZ49466
ID   AAZ49466 standard; DNA; 24 BP.
XX
AC   AAZ49466;
XX
DT   04-APR-2000  (first entry)
XX
DE   Gene specific sense primer used to clone 3'end of human Kv6.2 gene.
XX
KW   Voltage gated potassium channel; Kv6.2; human; excitability; ion flux;
KW   resting potential; alpha subunit; modulator; hearing/vision problem;
KW   migraine; central nervous system; CNS; seizure; neuroprotective agent;
KW   psychotic disorder; reporter; treatment; detection; antibody; probe;
KW   PCR primer; gene specific sense primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200001811-A1.
XX
PD   13-JAN-2000.
XX
PF   30-JUN-1999;   99WO-US014945.
XX
PR   01-JUL-1998;   98US-0091466P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ;
XX
DR   WPI; 2000-126937/11.
XX
PT   New voltage-gated potassium channel alpha subunit, useful for identifying
PT   modulators of voltage-gated channel activity useful for treating central
PT   nervous system disorders e.g. migraines and as neuroprotective agents.
XX
PS   Example 2; Page 62; 80pp; English.
XX
CC   The present DNA sequence is the gene specific sense primer, used in a
CC   single round of 3'RACE PCR, to clone the 3'end of the human Kv6.2 gene
CC   from human whole brain tissue. This primer specifically binds to the P
CC   region of the human Kv6.2 gene. Kv6.2 DNA sequence can be used to produce
CC   specific primers or probes for detection purposes. Modulator compounds
CC   that can modulate the ion flux through heteromeric voltage-gated
CC   potassium channels, are used as neuroprotective agents and for treating
CC   CNS disorders, such as migraines, hearing and vision problems, psychotic
CC   disorders and seizures. Kv6.2 can also be used as reporter molecules in
CC   assays and to produce antibodies
XX
SQ   Sequence 24 BP; 4 A; 7 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1216 CATGCTATTGGCGGCCCAGCAACT 1239
                |||  ||||||| || |||  || ||
Db          1 CATCCTATTGGTGGGCCATCATCT 24


RESULT 2666
AAC70288/c
ID   AAC70288 standard; DNA; 24 BP.
XX
AC   AAC70288;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #79.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 24 BP; 7 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1963 CTAAATATTTACCTTGAAAAAAAG 1986
                || || ||||  |||||| |||||
Db         24 CTCAACATTTGTCTTGAACAAAAG 1


RESULT 2667
AAC67230/c
ID   AAC67230 standard; DNA; 24 BP.
```

XX
AC AAC67230;
XX
DT 09-APR-2001 (first entry)
XX
DE Fibrosis modulator related oligonucleotide #5.
XX
KW Fibrosis modulator; fibronectin; FN EIIIA domain; scarring;
KW wound healing; fibroplasia; epidermolysis bullosa; burn; graft;
KW PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200076456-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016366.
XX
PR 14-JUN-1999; 99US-0139020P.
PR 02-JUN-2000; 2000US-00139020.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Van De Water L, Wieder KG, Liao Y, Classen JM;
XX
DR WPI; 2001-091313/10.
XX
PT Novel mutant fibronectin polypeptide useful for promoting or inhibiting
PT fibrosis or scarring.
XX
PS Disclosure; Fig 16; 73pp; English.
XX
CC The present invention provides mutant fibronectin (FN) proteins where the
CC mutation does not alter the conformation of the C-C' loop or the EIIIA
CC domain. These can be used to modulate fibrosis, to inhibit adhesions and
CC vascular restenosis, to treat fibroplasia, epidermolysis bullosa, burns
CC and impaired wound healing and to promote engraftment
XX
SQ Sequence 24 BP; 6 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1168 AACCAGACCTCATCTTGGAGGACG 1191
||||||| | || |||||||| |
Db 24 AACCAGATCCGATTTTGGAGGATG 1

RESULT 2668
AAH44680
ID AAH44680 standard; DNA; 24 BP.
XX
AC AAH44680;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human Kazal type inhibitory factor 35 PCR primer 2 SEQ ID NO:4.
XX
KW Human; Kazal type inhibitory factor 35; malignant tumour; haemopathy;
KW human immunodeficiency virus; HIV infection; immunological disease;
KW inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1301765-A.
XX
PD 04-JUL-2001.
XX
PF 29-DEC-1999; 99CN-00127224.
XX
PR 29-DEC-1999; 99CN-00127224.
XX
PA (UYFU-) UNIV FUDAN.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-550471/62.
XX
PT New polypeptide-human kazal type inhibitory factor 35 for treating
PT malignant tumor, hemopathy, human immunodeficiency virus infection,
PT immunological diseases and various inflammations.
XX
PS Example 3; Page 17 (Disclosure); 31pp; Chinese.
XX
CC The present invention discloses a new kind of polypeptide designated
CC human Kazal type inhibitory factor 35. Also described are polynucleotides
CC encoding this polypeptide, and a DNA recombination process to produce the
CC polypeptide. The present invention also describes a method of applying
CC the polypeptide to treat various diseases, such as malignant tumour,
CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
CC diseases and various inflammations. The present sequence represents a PCR
CC primer used in the isolation of human Kazal type inhibitory factor 35,
CC which is used in an example from the present invention
XX
SQ Sequence 24 BP; 1 A; 0 C; 4 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2160 TTCTCCTTTTTTTTTTTTTTTTT 2183
|| | |||||||||||||| ||
Db 1 TTGTGGGTTTTTTTTTTTTTATT 24

RESULT 2669
AAF30562/c
ID AAF30562 standard; DNA; 24 BP.
XX
AC AAF30562;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human Factor V gene PCR primer A11 F5(253)-24D.
XX
KW Factor V; human; FV gene; bi-directional PCR; Bi-PASA; mutation;
KW zygosity; homozygote; heterozygote; genetic screening; diagnosis;
KW venous thromboembolism; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6207425-B1.
XX
PD 27-MAR-2001.
XX
PF 10-SEP-1998; 98US-00150900.
XX
PR 11-SEP-1997; 97US-0058575P.
XX
PA (CITY) CITY OF HOPE.
XX
PI Liu Q, Sommer SS;
XX
DR WPI; 2001-256850/26.
XX
PT Conducting a bi-directional polymerase chain reaction amplification of
PT specific alleles, involves amplifying DNA containing one or both of two
PT alleles using an outer pair of primers and an inner pair of primers.
XX
PS Example; Col 7-8; 22pp; English.
XX
CC The present sequence is that of human Factor V (FV) gene primer A11
CC F5(253)-24D, used in bi-directional PCR amplification of specific alleles

CC (Bi-PASA). Its name indicates an A primer for FV (F5), the 5' end
CC beginning at base 253 of exon 10 of the FV gene (see AAF30549) and
CC proceeding downstream for 24 bases. It also includes a G8C2 tail, and the
CC first base from the 3' end is a mutated A nucleotide. A mutation in FV
CC gene exon 10 is associated with venous thromboembolism. Detection of this
CC mutation was used to demonstrate Bi-PASA. In Bi-PASA, 2 outer primers (P
CC and Q) and 2 inner primers (A and B) are used. A and B are each specific
CC for different alleles. P is complementary to the antisense strand of both
CC alleles in a region upstream of the sequence difference (mismatch). Q is
CC complementary to the sense strand of both alleles in a region downstream
CC of the mismatch. In heterozygotes, 3 segments are amplified: a segment of
CC size AQ resulting from 1 allele, another of size PB resulting from the
CC 2nd allele, and a combined segment of size PQ. In homozygotes, segment PQ
CC and either segments AQ or PB amplify. P, Q, A and B primers for the FV
CC gene are given in AAF30550-74. Under optimal PCR conditions, the relative
CC yield of DNA products obtained using the present primer is good, as
CC indicated by a very strong DNA band on agarose gels. Bi-PASA provides a
CC one-tube method for simultaneously differentiating homozygotes and
CC heterozygotes. It can detect small deletions and insertions as well as
CC single base changes. Bi-PASA is also used to perform population
CC screening, haplotype analysis, patient screening and carrier testing. The
CC method is rapid, reproducible, inexpensive, non-isotopic and amenable to
CC automation
XX
SQ Sequence 24 BP; 3 A; 7 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy         16 TGCGTGTCCAGTGACCCGGACAGC 39
              ||| ||||||| ||||| | | ||
Db         24 TGCCTGTCCAGGGACCCCGCCCGC 1
```

RESULT 2670
AAL47095
ID AAL47095 standard; DNA; 24 BP.
XX
AC AAL47095;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human proliferating cell antigen P120-51-59 cDNA PCR primer #1.
XX
KW Human; proliferating cell antigen P120-51.59; cancer; infection;
KW autoimmune disease; embryonic development deformity; gene therapy;
KW cytostatic; antimicrobial; immunosuppressive; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233078-A1.
XX
PD 25-APR-2002.
XX
PF 17-SEP-2001; 2001WO-CN001430.
XX
PR 18-SEP-2000; 2000CN-00125265.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-340238/37.
XX
PT New isolated proliferating cell antigen P120-51.59 polypeptide for
PT diagnosing and treating embryonic development deforming, tumor,
PT infection, and autoimmune disease.
XX
PS Example 3; Page 19; 36pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC proliferating cell antigen P120-51.59. The sequences can be used in the
CC treatment of cancer, infection, autoimmune diseases and embryonic
CC development deformities. The present sequence is a PCR primer for the
CC coding sequence of the invention
XX
SQ Sequence 24 BP; 9 A; 0 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2116 GGTTTTAGGAAACTTGTAGAAACG 2139
              |||||| ||||| |  |||||| |
Db          1 GGTTTTTGGAAATTGATAGAAAAG 24
```

RESULT 2671
ABV74361
ID ABV74361 standard; DNA; 24 BP.
XX
AC ABV74361;
XX
DT 05-FEB-2003 (first entry)
XX
DE Signalase 10.01 PCR primer SEQ ID NO 4.
XX
KW Signalase 10.01; enzyme; tumour; haemopathy; cytostatic; HIV; infection;
KW human immunodeficiency virus; immunological disease; inflammation; PCR;
KW primer; ss.
XX
OS Unidentified.
XX
PN CN1345975-A.
XX
PD 24-APR-2002.
XX
PF 22-SEP-2000; 2000CN-00125348.
XX
PR 22-SEP-2000; 2000CN-00125348.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-539373/58.
XX
PT New polypeptide-signalase 10.01 for treating malignant tumor, hemopathy,
PT human immunodeficiency virus infection, immunological disease and various
PT inflammations.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to signalase 10.01, a polynucleotide encoding the
CC polypeptide and producing the polypeptide by DNA recombinant technology.
CC The invention also discloses curing several diseases, such as malignant
CC tumour, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological disease and various inflammations using the polypeptide.
CC The invention also discloses an antagonist for resisting the polypeptide
CC and its therapeutic action and application of the polynucleotide encoding
CC the new signalase 10.01. The present sequence is that of a signalase
CC 10.01 PCR primer, useful in examples of the invention
XX
SQ Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2168 TTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||| ||||||  | | ||
Db          1 TTTTTTTTCTTTTTTCCTGATTT 24
```

RESULT 2672

```
ABV74361/c
ID   ABV74361 standard; DNA; 24 BP.
XX
AC   ABV74361;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Signalase 10.01 PCR primer SEQ ID NO 4.
XX
KW   Signalase 10.01; enzyme; tumour; haemopathy; cytostatic; HIV; infection;
KW   human immunodeficiency virus; immunological disease; inflammation; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   CN1345975-A.
XX
PD   24-APR-2002.
XX
PF   22-SEP-2000; 2000CN-00125348.
XX
PR   22-SEP-2000; 2000CN-00125348.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-539373/58.
XX
PT   New polypeptide-signalase 10.01 for treating malignant tumor, hemopathy,
PT   human immunodeficiency virus infection, immunological disease and various
PT   inflammations.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to signalase 10.01, a polynucleotide encoding the
CC   polypeptide and producing the polypeptide by DNA recombinant technology.
CC   The invention also discloses curing several diseases, such as malignant
CC   tumour, haemopathy, human immunodeficiency virus (HIV) infection,
CC   immunological disease and various inflammations using the polypeptide.
CC   The invention also discloses an antagonist for resisting the polypeptide
CC   and its therapeutic action and application of the polynucleotide encoding
CC   the new signalase 10.01. The present sequence is that of a signalase
CC   10.01 PCR primer, useful in examples of the invention
XX
SQ   Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
             || | |  |||||| |||||||||
Db         24 AAATCAGGAAAAAAGAAAAAAAAA 1


RESULT 2673
ABL56688
ID   ABL56688 standard; DNA; 24 BP.
XX
AC   ABL56688;
XX
DT   30-JUL-2002  (first entry)
XX
DE   PCR primer #2 for human class III MHC 61 cDNA.
XX
KW   Human; class III MHC 61; immunological disease; inflammation;
KW   organ transplantation; gene therapy; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226828-A1.
XX
PD   04-APR-2002.
XX
PF   02-JUL-2001; 2001WO-CN001116.
XX
PR   07-JUL-2000; 2000CN-00117015.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-281324/32.
XX
PT   Human class III MHC 61 and encoding polynucleotide, used in diagnosis and
PT   treatment of immunological diseases and inflammation and in organ
PT   transplantation.
XX
PS   Example 3; Page 13; 40pp; Chinese.
XX
CC   PCR primers ABL56687-88 were used to amplify cDNA encoding human class
CC   III MHC 61. The polypeptide and polynucleotide are used in diagnosis and
CC   treatment of immunological diseases and inflammation and in organ
CC   transplantation. The polynucleotide may also be used for gene therapy
XX
SQ   Sequence 24 BP; 10 A; 2 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1913 AACAATACCTTTTTTTTCAGTGTT 1936
              || |||||||||| || | | ||
Db          1 AAAAATACCTTTTTATTAATTATT 24


RESULT 2674
AAD26271
ID   AAD26271 standard; DNA; 24 BP.
XX
AC   AAD26271;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human caspase-12 cDNA 5' clones amplifying KW256 PCR primer.
XX
KW   Human; cysteine-dependent aspartate-specific proteases; caspase-12;
KW   Parkinson's disease; ulcerative colitis; cytostatic; glomerulonephritis;
KW   inflammatory bowel disease; hypersensitivity; rheumatoid arthritis; ALS;
KW   amyotrophic lateral sclerosis; bronchitis; inflammatory; cardiovascular;
KW   neurodegenerative disease; Crohn's disease; Alzheimer's disease; cancer;
KW   allergic rhinitis; cell proliferative disorder; asthma; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200185961-A2.
XX
PD   15-NOV-2001.
XX
PF   08-MAY-2001; 2001WO-US015103.
XX
PR   09-MAY-2000; 2000US-0203162P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Kletzien RF,  Reardon IM,  Weiland KL;
XX
DR   WPI; 2002-082900/11.
XX
PT   New human caspase-12 polynucleotides and polypeptides, useful for
PT   screening modulators of caspase activity, e.g. inhibitors, especially for
PT   treating e.g. inflammatory, cardiovascular or neurodegenerative diseases,
PT   or cancer.
XX
PS   Example 1; Page 194; 207pp; English.
```

```
XX
CC   The invention relates to purified, isolated caspase-12 polypeptides and
CC   their polynucleotides. Cysteine-dependent aspartate-specific proteases
CC   (caspases) are a family of proteases that cleave their substrates at
CC   aspartic acid-X bonds. They are highly specific endopeptidases that
CC   catalyse limited proteolysis. Caspase-12 polypeptides are useful for
CC   screening modulators of caspase activity. Caspase12 inhibitors are useful
CC   for preventing or treating disorders involving inappropriate apoptosis,
CC   cardiovascular diseases, neurodegenerative disorders (Alzheimer's disease
CC   Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis
CC   (ALS)); inflammatory diseases (systemic inflammatory conditions and
CC   conditions associated locally with migration and attraction of monocytes,
CC   leukocytes and/or neutrophils); autoimmune diseases (rheumatoid or
CC   reactive arthritis, acute glomerulonephritis, chronic glomerulonephritis,
CC   inflammatory bowel diseases such as Crohn's disease, ulcerative colitis
CC   and necrotising enterocolitis); allergic reactions (allergic asthma,
CC   chronic bronchitis, acute and delayed hypersensitivity, allergic rhinitis
CC   and cell proliferative disorder (cancer). Cancers that may be treated
CC   comprise lymphomas, carcinomas or hormone-dependent tumours. The present
CC   sequence is a PCR primer used for amplifying human caspase-12 cDNA 5'
CC   clones
XX
SQ   Sequence 24 BP; 3 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        129 GATTTAACTGGCGACTGTTTTGGG 152
              | ||||||| || ||||  |||||
Db          1 GCTTTAACTTGCCACTGGGTTGGG 24


RESULT 2675
AAD33504
ID   AAD33504 standard; DNA; 24 BP.
XX
AC   AAD33504;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS23-24-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 2676
AAD33504/c
ID   AAD33504 standard; DNA; 24 BP.
XX
AC   AAD33504;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS23-24-0003 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 2677
ABN86391
ID   ABN86391 standard; DNA; 24 BP.
```

XX
AC ABN86391;
XX
DT 21-OCT-2002 (first entry)
XX
DE Basophilic nucleoprotein polypeptide 45.32 cDNA isolating primer 2.
XX
KW Basophilic nucleoprotein polypeptide 45.32; cytostatic; human; RT-PCR;
KW embryonic development; growth; tumour; immunological disease; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1341659-A.
XX
PD 27-MAR-2002.
XX
PF 07-SEP-2000; 2000CN-00125081.
XX
PR 07-SEP-2000; 2000CN-00125081.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-520726/56.
XX
PT A human basophilic nucleoprotein polypeptide 45.32, useful for curing
PT e.g. tumors and immunological disease.
XX
PS Example 2; Page 16 (disclosure); 33pp; Chinese.
XX
CC The invention relates to a human basophilic nucleoprotein polypeptide
CC 45.32 and encoding polynucleotide. The polypeptide can be expressed by
CC standard DNA recombination technology. The polypeptide is useful for
CC curing several diseases, such as embryonic development disturbance,
CC growth development disturbance disease, tumour and immunological disease.
CC The present sequence represents a RT-PCR primer for isolating the human
CC basophilic nucleoprotein polypeptide 45.32 cDNA
XX
SQ Sequence 24 BP; 6 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTTTTA 2187
| ||| | |||||| ||||| |||
Db 1 CATTTATATTTTTTATTTTTATTA 24

RESULT 2678
ABZ57032/c
ID ABZ57032 standard; DNA; 24 BP.
XX
AC ABZ57032;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human kinesin light chain 14.74 RT-PCR primer, SEQ ID NO:3.
XX
KW Human; kinesin light chain 14.74; recombinant production; gene therapy;
KW diabetes; hyperthyroidism; arrhythmia; tumour; cancer; infection;
KW cardiant; cytostatic; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1364772-A.
XX
PD 21-AUG-2002.
XX
PF 10-JAN-2001; 2001CN-00105134.
XX
PR 10-JAN-2001; 2001CN-00105134.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-000484/01.
XX
PT New human kinesin light chain 14.74 polypeptide and its encoding
PT polynucleotide, useful in the treatment of cancer and diabetes.
XX
PS Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to human kinesin light chain 14.74 (ABP58652) and
CC nucleic acids encoding it (ABZ57031). The protein has a molecular weight
CC of 15 kD. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. Kinesin
CC light chain 14.74 can be used in the treatment of a variety of diseases
CC such as diabetes, hyperthyroidism, arrhythmia, tumours and infections.
CC Sequences ABZ57032-ABZ57033 represent reverse transcription-PCR (RT-PCR)
CC primers used in an exemplification of the invention to isolate human
CC kinesin light chain 14.74 cDNA
XX
SQ Sequence 24 BP; 1 A; 5 C; 17 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 411 CGTACGCCGCCGCCATCAACCCCC 434
| | |||||||||||| | |||||
Db 24 CCTCCGCCGCCGCCAGCGCCCCCC 1

RESULT 2679
ABZ23085/c
ID ABZ23085 standard; DNA; 24 BP.
XX
AC ABZ23085;
XX
DT 14-APR-2003 (first entry)
XX
DE Human GPCR 10823 PCR primer SEQ ID NO:29.
XX
KW Human; guanosine triphosphate-binding protein-coupled receptor; GPCR;
KW G protein-coupled receptor; clinical diagnosis; drug development;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO2002103006-A1.
XX
PD 27-DEC-2002.
XX
PF 18-JUN-2002; 2002WO-JP006058.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
PI Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
DR WPI; 2003-167516/16.
XX
PT Novel guanosine triphosphate-binding protein-coupled receptors encoded
PT GRCR sequences obtained by automated system search, applicable in
PT clinical diagnosis and drug development.
XX
PS Example 6; Page 58; 200pp; Japanese.
XX
CC The present invention describes a guanosine triphosphate-binding protein-
CC coupled receptor (G protein-coupled receptor, GPCR). The GPCRs can be

CC used in clinical diagnosis and drug development. The present sequence
CC represents a PCR primer for a human GPCR, which is used in an example
CC from the present invention
XX
SQ Sequence 24 BP; 6 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1472 GCTGATTCTAACAAAACCCTGGAG 1495
||| |||| ||||| | ||||||
Db 24 GCTAGTTCTCACAAAGCTCTGGAG 1

RESULT 2680
ACD27468
ID ACD27468 standard; cDNA; 24 BP.
XX
AC ACD27468;
XX
DT 15-SEP-2003 (first entry)
XX
DE Human LTBP 1 binding protein PN9826 cDNA fragment #16.
XX
KW Human; ss; LTBP1; PN9826; angiogenesis; metastasis; adhesion;
KW latent transforming growth factor beta binding protein 1; cell growth;
KW cancer; diabetes; Alzheimer's disease; asthma; atherosclerosis;
KW infectious disease; hepatitis; pneumonia; hypertension;
KW inflammatory disorder; obesity; tissue ischaemia; wound healing;
KW coronary artery disease; peripheral vascular disease;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN US2003036163-A1.
XX
PD 20-FEB-2003.
XX
PF 10-JUL-2002; 2002US-00195142.
XX
PR 10-JUL-2001; 2001US-0304323P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Wettstein DA, Mauck KA;
XX
DR WPI; 2003-512249/48.
DR P-PSDB; ABU62831.
XX
PT New PN9826 polypeptide and nucleic acid encoding the polypeptide, useful
PT in screening assays to select modulators of PN9826 for treating or
PT preventing diseases or disorders such as cancer, diabetes, Alzheimer's
PT disease or asthma.
XX
PS Claim 1; Page 66; 69pp; English.
XX
CC The invention relates to a new isolated PN9826 polypeptide (a latent
CC transforming growth factor beta binding protein 1, LTBP1) or its fragment
CC appearing as ABU62815-ABU62833 or an amino acid sequence that is at least
CC 95% identical to the sequences above and capable of interacting with
CC LTBP1. Also included are the nucleic acids encoding the LTBP1 proteins, a
CC nucleic acid vector comprising the isolated PN9826 nucleic acid, a host
CC cell containing the nucleic acid vector, a microarray comprising the
CC isolated PN9826 nucleic acid and an isolated antibody immunoreactive with
CC an LTBP1 polypeptide appearing as ABU2819-ABU2821. The PN9826 nucleic
CC acids and proteins are useful in screening assays to select modulators of
CC PN9826 and the protein complexes formed by PN9826 and latent transforming
CC growth factor beta binding protein 1 (LTBP1). The modulators are useful
CC in modulating the functions and activities of PN9826 and protein
CC complexes containing PN9826, e.g. angiogenesis, metastasis, or cell
CC growth and adhesion. The proteins and protein-protein interactions in
CC which they participate are potential drug targets useful in identifying
CC new drugs for treating or preventing diseases or disorders such as
CC cancer, diabetes, Alzheimer's disease, asthma, atherosclerosis,
CC infectious diseases (e.g. hepatitis or pneumonia), hypertension,
CC inflammatory disorders, obesity, tissue ischaemia (e.g. coronary artery
CC disease), peripheral vascular disease, neurodegenerative disorders, or
CC impaired wound healing. Detecting PN9826 nucleic acid, polypeptide and/or
CC protein complexes is useful for diagnosing the diseases mentioned above.
CC The present sequence encodes a PN9826 fragment
XX
SQ Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 191 GTCAAGTACGAAGAGGACTGCGAG 214
|||| ||||| ||||||| | ||
Db 1 GTCACCTACGATGAGGACTACCAG 24

RESULT 2681
ADE86193
ID ADE86193 standard; DNA; 24 BP.
XX
AC ADE86193;
XX
DT 29-JAN-2004 (first entry)
XX
DE Ret gene chair quadruplex DNA.
XX
KW quadruplex DNA; gene therapy; cancer; cytostatic; RET; human; ds.
XX
OS Homo sapiens.
XX
PN WO2003087317-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010658.
XX
PR 05-APR-2002; 2002US-0370358P.
PR 20-AUG-2002; 2002US-0404966P.
PR 20-MAR-2003; 2003US-0456637P.
XX
PA (CYTE-) CYTERNEX INC.
PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI Siddiqui-Jain A, Grand CL, Bearss DJ, Hurley LH, Farrell TJ;
XX
DR WPI; 2003-853947/79.
XX
PT Identifying a compound that modulates the biological activity of a native
PT quadruplex DNA for treating colorectal cancer comprises determining the
PT presence or absence of interaction between the candidate compound and the
PT test quadruplex DNA.
XX
PS Disclosure; Fig 8A; 69pp; English.
XX
CC The present sequence is that of a quadruplex structure-forming DNA
CC sequence from the nuclease hypersensitivity element (NHE) in the
CC regulatory regions of the human RET gene. Certain mutations in quadruplex
CC forming nucleotides sequences have been shown to destabilise quadruplex
CC structure and are associated with cancer. Methods are provided for
CC identifying quadruplex nucleotide sequences having destabilising guanine
CC substitutions, for determining whether a subject is at risk of developing
CC or having cancer, pharmacogenomic methods for targeting appropriate
CC prevention or therapeutic regiments, methods for screening molecules that
CC interact with stabilised and destabilised quadruplexes, and therapeutic
CC methods for treating cancers, such as antisense nucleic acid cancer
CC therapy that specifically targets DNA in subjects having a quadruplex-
CC destabilising mutation.
XX
SQ Sequence 24 BP; 1 A; 4 C; 19 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 16;  DB 1;  Length 24;
  Best Local Similarity   79.2%;  Pred. No. 2.9e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 AAGGCCCGCGCGCGGCGGGGGCGG 63
              | || | | ||| ||||||||||
Db          1 AGGGGCGGGGCGGGGCGGGGGCGG 24


RESULT 2682
AAC95686/c
ID   AAC95686 standard; DNA; 25 BP.
XX
AC   AAC95686;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #21.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
              | |||  |  ||||||||||||||
Db         24 TGGAAAAGGTAAAAAAAAAAAAAA 1


RESULT 2683
AAC96367/c
ID   AAC96367 standard; DNA; 25 BP.
XX
AC   AAC96367;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #99.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 50; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
              | |||  |  ||||||||||||||
Db         24 TGGAAAAGGTAAAAAAAAAAAAAA 1


RESULT 2684
ABK87632/c
ID   ABK87632 standard; DNA; 25 BP.
XX
AC   ABK87632;
XX
DT   24-SEP-2002  (first entry)
XX
DE   BamT15C PCR primer.
XX
KW   Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
KW   rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
KW   viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
OS   Unidentified.
XX
PN   WO200251999-A1.
XX
PD   04-JUL-2002.
XX
PF   21-DEC-2001; 2001WO-JP011293.
XX
PR   21-DEC-2000; 2000JP-00388739.
XX
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```
PA   (MOCH ) MOCHIDA PHARM CO LTD.
PA   (KAZU-) KAZUSA DNA RES INST.
XX
PI   Ohara O,  Nagase T,  Negishi T,  Mizushima S,  Furusako S;
XX
DR   WPI; 2002-519957/55.
XX
PT   Human spleen-originated cDNA library-isolated atopic dermatitis-
PT   associated gene, which encodes a protein, useful in diagnosis and
PT   screening of preventives or remedies for e.g. atopic dermatitis.
XX
PS   Example 1; Page 45; 88pp; Japanese.
XX
CC   The present invention relates to a new DNA containing a fully defined 568
CC   base sequence given in the specification. The polynucleotides and
CC   proteins of the invention are useful in diagnosis and screening of
CC   preventives or remedies for atopic dermatitis. The invention can also be
CC   used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
CC   nephritis, arteriosclerosis, allergic diseases, viral diseases,
CC   inflammatory colitis, bronchitis and skin diseases. The present nucleic
CC   acid sequence represents a PCR primer used in the methods of the
CC   invention
XX
SQ   Sequence 25 BP; 1 A; 6 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         25 GAAAAAAAAAAAAAAA 10


RESULT 2685
AAC96038
ID   AAC96038 standard; DNA; 25 BP.
XX
AC   AAC96038;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #5.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||| ||   || |
Db          1 TTTTTTTTTTTTTATTCGGAATT 24


RESULT 2686
AAC96204/c
ID   AAC96204 standard; DNA; 25 BP.
XX
AC   AAC96204;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #171.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              ||||||||||||||||
Db         16 TGAAAAAAAAAAAAAA 1
```

RESULT 2687
AAC95828
ID AAC95828 standard; DNA; 25 BP.
XX
AC AAC95828;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #8.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 40; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 5 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 25;
Best Local Similarity 79.2%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTTTAACTT 2191
||||||||||||| ||| | || |
Db 1 TTTTTTTTTTTTATTTCTCCACAT 24

RESULT 2688
AAH39959
ID AAH39959 standard; DNA; 25 BP.
XX
AC AAH39959;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2755.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 64; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 16 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 25;
Best Local Similarity 79.2%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
||| | ||||||||||||||||
Db 1 TAGTCTCTTAAAAAAAAAAAAAAA 24

RESULT 2689
AAC96753/c
ID AAC96753 standard; DNA; 25 BP.
XX
AC AAC96753;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #130.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.

```
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 56; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 5 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
              || ||||  |  ||||||||||||
Db         24 AGTATTGGGACCAAAAAAAAAAAA 1


RESULT 2690
AAC96423/c
ID   AAC96423 standard; DNA; 25 BP.
XX
AC   AAC96423;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #25.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 4 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAA 2799
              |||  |  || ||||||||||||||
Db         24 GTTCTATGTGGAAAAAAAAAAAAA 1


RESULT 2691
AAC95851
ID   AAC95851 standard; DNA; 25 BP.
XX
AC   AAC95851;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #31.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 41; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
```

```
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||  |  |  ||  |||
Db          1 TTTTTTTTTTTTGTCAATCTGTGA 24


RESULT 2692
AAC96884/c
ID   AAC96884 standard; DNA; 25 BP.
XX
AC   AAC96884;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #89.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 59; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2803
              |||  ||   |  ||||||||||||||
Db         24 GAACTGGTTATAAAAAAAAAAAAA 1


RESULT 2693
AAC96213
ID   AAC96213 standard; DNA; 25 BP.
XX
AC   AAC96213;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #180.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 3 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||  ||||   ||  |
Db          1 TTTTTTTTTTTTCAACTCATAAGG 24


RESULT 2694
AAC96028/c
ID   AAC96028 standard; DNA; 25 BP.
XX
AC   AAC96028;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #40.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
```

```
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 25;
  Best Local Similarity   79.2%;  Pred. No. 3.1e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAA 2803
              ||| ||   | ||||||||||||||
Db         24 GAACTGGTTATAAAAAAAAAAAAA 1


RESULT 2695
AAA62140/c
ID   AAA62140 standard; DNA; 26 BP.
XX
AC   AAA62140;
XX
DT   06-AUG-2003  (revised)
DT   10-NOV-2000  (first entry)
XX
DE   A. auricaliformis (RT-) PCR primer.
XX
KW   PCR primer; RT-PCR primer; plant genetic marker; plant breeding; ss.
XX
OS   Acacia auriculiformis.
XX
PN   AU9960643-A.
XX
PD   01-JUN-2000.
XX
PF   24-NOV-1999;   99AU-00060643.
XX
PR   25-NOV-1998;   98JP-00333469.
XX
PA   (REAS-) RES ASSOC REFORESTATION TROPICAL FOREST.
XX
PI   Hibino T,  Koshiyama J;
XX
DR   WPI; 2000-412598/36.
XX
PT   Method for obtaining plant DNA fragments useful as novel genetic markers,
PT   comprising digesting plant DNA, subjecting fragments to genome
PT   subtraction and screening the polymorphic fragments.
XX
PS   Example 1; Page 13; 21pp; English.
XX
CC   The present sequence is a primer for Acacia auricaliformis. This sequence
CC   was used in RT-PCR reactions to produce cDNA from A. auricaliformis RNA.
CC   The resulting cDNA was amplified via PCR using the present sequence and
CC   another PCR primer (see AAA62141). The PCR product was used as an
CC   expression probe. The expression probe was used to obtain desired DNA
CC   fragments. The plant genetic fragments obtained by this method may be
CC   useful as markers in plant breeding. In addition, genes encoding the DNA
CC   fragments or their promoter regions may be used to modify expression.
CC   (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 26 BP; 1 A; 4 C; 5 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2696
AAZ25387/c
ID   AAZ25387 standard; DNA; 26 BP.
XX
AC   AAZ25387;
XX
DT   16-DEC-1999  (first entry)
XX
DE   Infectious pancreatic necrosis virus PCR primer #1.
XX
KW   Infectious pancreatic necrosis virus; IPNV; strain West Buxton;
KW   strain SP; segment A; segment B; nonpathogenic; Birnavirdae family;
KW   infection; live attenuated vaccine; aquaculture industry; Rainbow trout;
KW   Brook trout; Atlantic salmon; PCR primer; ss.
XX
OS   Synthetic.
OS   Infectious pancreatic necrosis virus.
XX
PN   WO9950419-A2.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US004285.
XX
PR   31-MAR-1998;   98US-0080178P.
XX
PA   (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI   Vakharia VN,  Yao K;
XX
DR   WPI; 1999-591321/50.
XX
PT   Preparing nonpathogenic infectious pancreatic necrosis virus, IPNV,
PT   useful for producing attenuated virus for vaccines useful in the
PT   aquaculture industry.
XX
PS   Example 1; Page 21; 63pp; English.
XX
CC   A method has been developed for preparing nonpathogenic, infectious
CC   pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA
CC   containing the IPNV genome segments A and B where A is modified to
CC   prevent expression of an arginine-rich non-structural (NS) protein; 2)
CC   transcribing the cDNA to produce RNA; 3) incubating the host cells in a
CC   culture medium; and 4) isolating live IPNV from the culture medium. The
CC   method is useful to produce live nonpathogenic IPNV, useful to study
CC   viral pathogenesis and for the production of live, nonpathogenic IPNV
CC   vaccines, since it was demonstrated that the NS protein-deficient virus
CC   could replicate but did not invoke a pathological response in hosts.
CC   Combination vaccines may also be produced by combining the IPNV with
CC   bacterial antigens (especially from gram negative bacteria e.g. Aeromonas
CC   salmonicida) and/or antigens from aquatic viruses other than Birnaviruses
CC   (the family to which IPNV belongs) e.g. infectious haematopoietic
CC   necrosis virus. The method may also be used to generate a nonpathogenic
CC   chimeric virus when the cDNA of segment A encodes epitopic determinants
CC   from at least two different IPNV strains. IPNV causes a highly contagious
CC   and destructive disease of juvenile Rainbow and Brook trout and Atlantic
CC   salmon (e.g. highly virulent strains can cause more than 90 % mortality
CC   in hatchery stocks less than 4 months old and survivors can remain
CC   lifelong carriers and reservoirs of infection); IPNV is therefore a
CC   pathogen of major economic importance to the aquaculture industry. The
CC   present sequence represents an IPNV PCR primer used in an example from
```

```
CC   the present invention
XX
SQ   Sequence 26 BP; 0 A; 6 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAAA 11


RESULT 2697
AAX23572
ID   AAX23572 standard; DNA; 27 BP.
XX
AC   AAX23572;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Deletion sequence oligonucleotide 25.
XX
KW   Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW   probe; cellular adhesion modulator; cellular proliferation modulator;
KW   human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW   HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911820-A1.
XX
PD   11-MAR-1999.
XX
PF   01-SEP-1998;   98WO-US018084.
XX
PR   02-SEP-1997;   97US-00923771.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Chen D,  Srivatsa GS;
XX
DR   WPI; 1999-205198/17.
XX
PT   New compositions comprising sensor arrays made up of unique probe
PT   oligonucleotides - useful for characterizing a sample of target deletion
PT   oligonucleotides.
XX
PS   Example 1; Page 98; 163pp; English.
XX
CC   This invention describes a novel composition comprising a number of
CC   sensor arrays, where each array comprises a unique probe oligonucleotide,
CC   which is the reverse complement of part of a unique target
CC   oligonucleotide present in a mixture of target deletion sequence
CC   oligonucleotides. The compositions form a method for characterizing a
CC   sample of target deletion oligonucleotides which are labelled and
CC   hybridize with the probe oligonucleotides of the sensor arrays. Such
CC   oligonucleotides and their targets are represented in AAX23548-X23709.
CC   Oligonucleotides characterized by the method form pharmaceutical
CC   compositions that are useful for modulating cellular adhesion or
CC   proliferation, and being active against a eukaryotic pathogen, a human
CC   retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC   retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC   Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC   characterization of deletion sequence oligonucleotides having related,
CC   but different nucleobase sequences, and quantification of different
CC   species of deletion sequence ("target") oligonucleotides in a mixture.
CC   Also, if the specificity of the oligonucleotide's nucleobase sequence for
CC   its reverse complement is not modified, the method may be performed using
CC   oligodeoxynucleotides
XX
SQ   Sequence 27 BP; 7 A; 2 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTA 16


RESULT 2698
AAD49491
ID   AAD49491 standard; DNA; 27 BP.
XX
AC   AAD49491;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Oligonucleotide #2 used to clone C3Basic3 reverse HIV Tat protein.
XX
KW   Drug delivery construct; axon growth; nerve injury; ischaemic damage;
KW   stroke injury; gene therapy; neuroleptic; neuroprotective; ss.
XX
OS   Unidentified.
XX
PN   WO200283179-A2.
XX
PD   24-OCT-2002.
XX
PF   08-APR-2002; 2002WO-CA000480.
XX
PR   12-APR-2001; 2001CA-02342970.
PR   13-NOV-2001; 2001CA-02362004.
PR   15-JAN-2002; 2002CA-02367636.
XX
PA   (BIOA-) BIOAXONE THERAPEUTIQUE INC.
XX
PI   Mckerracher L;
XX
DR   WPI; 2003-092963/08.
XX
PT   New drug delivery construct comprising a transport and active agent
PT   region, useful for the manufacture of a pharmaceutical composition for
PT   treating nerve injury.
XX
PS   Example 14; Page 86; 188pp; English.
XX
CC   The invention relates to a new drug delivery construct comprises at least
CC   one transport agent region and an active agent region. The transport
CC   agent region is able to facilitate the uptake of the active agent region
CC   into a cell. The active agent region is an active therapeutic agent
CC   region able to facilitate axon growth and an analogue. The drug delivery
CC   construct is useful for suppressing the inhibition of neuronal axon
CC   growth, facilitating axon growth, treating nerve injury, treating
CC   ischaemic damage related to stroke injury. The drug delivery construct
CC   and the drug conjugate are useful for the manufacture of a pharmaceutical
CC   composition for treating nerve injury. The invention is useful in gene
CC   therapy. The present sequence is an oligonucleotide used to clone
CC   C3Basic3 reverse HIV Tat protein
XX
SQ   Sequence 27 BP; 0 A; 7 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 16;  DB 1;  Length 27;
  Best Local Similarity   79.2%;  Pred. No. 3.5e+03;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              |||||| ||| || ||||| || |
Db          4 TCCTTTGTTTCTTCTTTTTCTTCT 27


RESULT 2699
AAD33514
ID   AAD33514 standard; DNA; 28 BP.
```

XX
AC AAD33514;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS19-28-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 1 AAAAAAAAAAAAAAAA 16

RESULT 2700
AAD33516
ID AAD33516 standard; DNA; 29 BP.
XX
AC AAD33516;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS18-29-0003 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2801
||||||||||||||||
Db 1 AAAAAAAAAAAAAAAA 16

RESULT 2701
ADC65905/c
ID ADC65905 standard; DNA; 34 BP.
XX
AC ADC65905;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA oligonucleotide #38.
XX
KW RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW cation-mediated delivery; bacterial infection; viral infection;
KW drug resistant infection; double stranded DNA oligomer; ss.
XX
OS Synthetic.
XX
PN US2003087241-A1.
XX
PD 08-MAY-2003.
XX
PF 30-NOV-2001; 2001US-00997931.
XX
PR 15-APR-1993; 93US-00047860.
PR 23-FEB-1995; 95US-00393439.
PR 26-FEB-1997; 97US-00805631.
PR 11-MAY-2000; 2000US-00569344.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 2003-755141/71.
XX
PT Synthesizing RNA oligonucleotide involves combining single-stranded
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
PT template.
XX

PS Example 18; SEQ ID NO 38; 78pp; English.
XX
CC The invention relates to a method for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesising an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an
CC oligonucleotide used in the method of the invention.
XX
SQ Sequence 34 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 6 Other;

Query Match 0.6%; Score 16; DB 1; Length 34;
Best Local Similarity 88.9%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||| ||| ||||
Db 33 AAAAAAAAANAAANAAAA 16

RESULT 2702
ADE27346
ID ADE27346 standard; RNA; 19 BP.
XX
AC ADE27346;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:290.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 290; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 15 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 2e+03;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAAAAAA 2798
||| : |||||||||||||
Db 1 GAAUCUAAAAAAAAAAAAA 19

RESULT 2703
ADE27636/c
ID ADE27636 standard; RNA; 19 BP.
XX
AC ADE27636;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:580.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 580; 139pp; English.

```
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 2 A; 1 C; 1 G; 0 T; 15 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAA 2798
              ||||  ||||||||||||
Db         19 GAATCTAAAAAAAAAAAAA 1


RESULT 2704
AAS05713/c
ID   AAS05713 standard; DNA; 20 BP.
XX
AC   AAS05713;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Polypyrimidine Crick strand oligonucleotide.
XX
KW   reverse phase triplex forming oligonucleotide; RP-TFO;
KW   protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW   SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
OS   Synthetic.
XX
PN   WO200132929-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US030534.
XX
PR   03-NOV-1999;   99US-0163356P.
PR   03-NOV-1999;   99US-0163416P.
PR   21-DEC-1999;   99US-0171348P.
PR   07-JUL-2000; 2000US-0216579P.
XX
PA   (CYGE-) CYGENE INC.
PA   (OSTE/) OSTE C C.
XX
PI   Oste CC,  Ramberg ER;
XX
DR   WPI; 2001-343488/36.
XX
PT   Analyzing target nucleic acid sequences, useful for population genetics,
PT   drug development and diagnosing cancer, comprises hybridizing triple
PT   forming oligonucleotide and probe to target sequence.
XX
PS   Example 2; Page 66; 141pp; English.
XX
CC   The sequence is a polypyrimidine oligonucleotide for binding a second
CC   reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to
CC   the target SNP used to analyse Factor V Leiden SNP using the method of
CC   the invention. The invention relates to analysing target nucleic acid
CC   sequences comprising restricting isolated DNA, hybridising at least one
CC   triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to
CC   form a protected nucleic acid sequence (PNAS) tail structure, hybridising
CC   the captured structure with a single nucleotide polymorphisms (SNP)
CC   identification probe and determining the SNP score. The methods can be
CC   used for analysing target nucleic acid sequences, especially genomic DNA
CC   sequences, to determine if they contain SNPs or short tandem repeats
CC   (STRs). The methods can be used to detect SNPs for use in population
CC   genetics, drug development, forensics, cancer, genetic disease research,
CC   genomic analysis, diagnostics and therapeutics in humans, plants and
CC   animals
XX
SQ   Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||| || ||||||||||||
Db         20 AAATAAGAAAAAAAAAAAA 2


RESULT 2705
AAF83959/c
ID   AAF83959 standard; DNA; 20 BP.
XX
AC   AAF83959;
XX
DT   06-AUG-2001  (first entry)
XX
DE   BAP28 gene fragment amplifying primer BAP28polyTcourt.
XX
KW   BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100669-A2.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-IB001183.
XX
PR   25-JUN-1999;   99US-0141323P.
PR   18-JAN-2000; 2000US-0176880P.
XX
PA   (GEST ) GENSET.
XX
PI   Barry C,  Bougueleret L,  Chumakov I,  Cohen-Akenine A;
XX
DR   WPI; 2001-367032/38.
XX
PT   New BAP28 polynucleotides and polypeptides overexpressed in prostate
PT   cancer cells for diagnosing prostate tumors, e.g. by hybridization or
PT   polymerase chain reaction assays.
XX
PS   Example; Page 347; 349pp; English.
XX
CC   The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
CC   sequences and regulatory region located at the 3' and 5' ends of the
CC   BAP28 coding region. The BAP28 polypeptides can be expressed by standard
CC   recombinant methodology. BAP28 polynucleotides and polypeptides have been
CC   found to be over expressed in prostate tumour cells, therefore levels of
CC   BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
CC   reaction (PCR)) to diagnose patient suffering from or susceptible to
CC   prostate cancer. Antibodies specific for the BAP28 polypeptides are
CC   useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
CC   useful in genetic analysis. Sequences AAF83934-963 represent primers for
CC   the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on
CC   the opposite of the coding strand of BAP28)
XX
SQ   Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAA 2800
              ||  ||||||||||||||||
Db         19 ATACAAAAAAAAAAAAAAA 1


RESULT 2706
ABZ88564/c
ID   ABZ88564 standard; DNA; 20 BP.
XX
AC   ABZ88564;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3806; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||| | |
Db         20 TTTTTTTTTTTTTTTTCTGT 2


RESULT 2707
ABZ85535
ID   ABZ85535 standard; DNA; 20 BP.
XX
AC   ABZ85535;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 777; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||| |||||
Db          1 AAAAAAAAGAAAAGAAAAA 19


RESULT 2708
AAQ37797/c
ID   AAQ37797 standard; DNA; 20 BP.
XX
AC   AAQ37797;
XX
DT   25-MAR-2003  (revised)
DT   09-JAN-2003  (revised)
DT   01-JUL-1993  (first entry)
XX
DE   Antisense oligonucleotide #4 for treating Aberrant Programming diseases.
XX
KW   diagnosis; treatment; cancer; neoplasm; tumour; growth; malignancy; AIDS;
KW   myeloproliferative diseases; myelodysplasias; atherosclerosis;
KW   antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO9303770-A1.
XX
PD   04-MAR-1993.
XX
PF   24-AUG-1992;   92WO-US007133.
XX
PR   23-AUG-1991;   91US-00748997.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Smith LJ;
XX
DR   WPI; 1993-093733/11.
XX
PT   Treating aberrant programming diseases, e.g. AIDS or cancer - by
PT   administering an expression vector, double stranded
PT   oligo:deoxy:nucleotide or anti-sense oligo:deoxy:nucleotide.
XX
PS   Claim 13; Page 64; 73pp; English.
XX
CC   This sequence represents an antisense oligonucleotide. Presumably it is
CC   used in a claimed method for the treatment of an individual having an
CC   Aberrant Programming disease, but this is not clear in the specification.
CC   (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2709
AAQ48269
ID   AAQ48269 standard; DNA; 20 BP.
XX
AC   AAQ48269;
XX
DT   25-MAR-2003  (revised)
DT   16-FEB-1994  (first entry)
XX
DE   Glucocerebrosidase gene exon 5 3' sense PCR primer.
XX
KW   Mutant; polymerase chain reaction; PvuII polymorphism; detection;
KW   screening method; GC alleles; Gaucher's disease; amplification; ss.
XX
OS   Synthetic.
XX
PN   EP558257-A1.
XX
PD   01-SEP-1993.
XX
PF   23-FEB-1993;   93EP-00301301.
XX
PR   24-FEB-1992;   92US-00841652.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Beutler E;
XX
DR   WPI; 1993-274677/35.
XX
PT   Detection of Gaucher's disease - by screening DNA for a substitution of
PT   adenine for guanine at position 1 of gluco:cerebrosidase gene intron 2.
XX
PS   Example 2; Page 15; 42pp; English.
XX
CC   The sequence is that of a 3' sense PCR primer corresponding to nucleotide
CC   positions 316 through 335 of glucocerebrosidase exon 11 (nt 6912 - nt
CC   6931). It was used in a PCR amplification of a 3' fragment of amplified
CC   1226G/?Pv1.1-/Pv1.1+ genotype cDNA comprising a portion of the leader
CC   sequence of cDNA corresponding to the 5' portion of exon 1 and extended
CC   through most of the cDNA corresponding to exon 9 of the genomic sequence.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        109 TGGGGGCTGGGGGGATCCT 127
              ||||||||||||||||  ||
Db          2 TGGGGGCTGGGGGGACACT 20


RESULT 2710
AAQ68872/c
ID   AAQ68872 standard; DNA; 20 BP.
XX
AC   AAQ68872;
XX
DT   25-MAR-2003  (revised)
DT   31-MAY-1995  (first entry)
XX
DE   Oligonucleotide (SA12/m1) used as control in antisense therapy.
XX
KW   Oligonucleotide; antisense; self paired; nuclease resistant;
KW   dermatological disorders; viral infection; cancer; atopical dermatitis;
KW   psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
KW   hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
KW   elastase; bone marrow graft; ss.
XX
OS   Synthetic.
XX
PN   FR2703053-A1.
XX
PD   30-SEP-1994.
XX
PF   26-MAR-1993;   93FR-00003514.
XX
PR   26-MAR-1993;   93FR-00003514.
XX
PA   (GEST ) GENSET.
```

```
XX
PI   Vasseur M,  Blumenfeld M,  Meguenni S,  Poddevin B;
XX
DR   WPI; 1994-312170/39.
XX
PT   New oligo:nucleotide(s) self paired at one or both ends - have improved
PT   resistance to nuclease(s) and reduced toxicity, useful as anti:sense
PT   molecules for treating dermatological disorders, virus infections,
PT   cancer, etc.
XX
PS   Example 1; Fig 4a; 40pp; French.
XX
CC   New hooked or semi-hooked oligonucleotides (see AAQ68869-71, AAQ68873,
CC   AAQ68875, AAQ68877, AAQ68879 and AAQ68880) are useful as therapeutic
CC   antisense molecules for treating dermatological disorders (e.g. atopical
CC   dermatitis, psoriasis, melanoma, T cell lymphoma etc.) viral infections
CC   (e.g. herpes simplex, papilloma, hepatitis or HIV); or cancer (when
CC   directed against an oncogene), due to their ability to hybridise with
CC   target nucleic acid. They can be used ex vivo, e.g., to treat bone marrow
CC   grafts. They can also be used for diagnosis or in cosmetics e.g. to block
CC   mRNA coding proteins involved in the ageing process such as collagenase
CC   or elastase. This linear antisense oligonucleotide is used as a control
CC   to see whether the hooked and semi-hooked oligonucleotides exhibit a
CC   greater resistance to exonucleases than linear oligonucleotides. (Updated
CC   on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
CC   PA field.)
XX
SQ   Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
                ||||  | ||||||||||||
Db         19 CTTTCTATTTTTTTTTTTT 1


RESULT 2711
AAT44565/c
ID   AAT44565 standard; mRNA; 20 BP.
XX
AC   AAT44565;
XX
DT   04-FEB-1997  (first entry)
XX
DE   Antisense oligo OL(1)P53 targetting p53 oncogene mRNA.
XX
KW   antisense; protease; tumour; metastasis; inhibition; breast cancer;
KW   phosphorothioate; cell invasion; urokinase; non-toxic; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /note= "phosphorothioate backbone"
XX
PN   US5552390-A.
XX
PD   03-SEP-1996.
XX
PF   09-DEC-1993;   93US-00164200.
XX
PR   09-DEC-1993;   93US-00164200.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Scholar EM,  Iversen PL;
XX
DR   WPI; 1996-412096/41.
XX
PT   Anti:sense oligo:nucleotide(s) to murine urokinase mRNA - for inhibiting
PT   tumour cell invasion and metastasis.
XX
PS   Example 1; Col 5-6; 14pp; English.
XX
CC   AAT44560-77 are antisense phosphorothioate oligonucleotides (PONs)
CC   complementary to the mRNA of protease enzymes involved in tumour
CC   invasion. Urokinase (UK) is important in metastasis of tumours and PONs
CC   to urokinase plasminogen activator (UPA) have demonstrated in vivo and in
CC   vitro reduction of metastasis of breast cell cancer. The present
CC   sequence, which is complementary to exon 10 of p53 mRNA has been
CC   administered to mouse, rat and rhesus monkey for toxicity evaluation. All
CC   studies used dose exposure escalating studies and no major toxicity was
CC   observed
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| |||||| |||
Db         19 GAGCCAGGGGGGGAGCAGGG 1


RESULT 2712
AAT93630/c
ID   AAT93630 standard; DNA; 20 BP.
XX
AC   AAT93630;
XX
DT   03-FEB-1998  (first entry)
XX
DE   Human p53 oncogene phosphorothioate oligonucleotide.
XX
KW   Phosphorothioate; antisense oligonucleotide; p53 oncogene;
KW   oligonucleotide technology; immunostimulatory response; cancer;
KW   B cell proliferation; therapeutic formulation; cyclodextrin;
KW   HIV infection; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /note= "comprises phosphorothioate backbone"
XX
PN   WO9710005-A2.
XX
PD   20-MAR-1997.
XX
PF   19-AUG-1996;   96WO-US013311.
XX
PR   12-SEP-1995;   95US-00527126.
XX
PA   (HYBR-) HYBRIDON INC.
XX
PI   Zhao Q,  Temsamani J,  Agrawal S;
XX
DR   WPI; 1997-202011/18.
XX
PT   Reduction of immuno:stimulatory responses to phosphoro:thioate
PT   oligo:nucleotide or protein - by admin. of the oligo:nucleotide or
PT   protein and at least one cyclodextrin.
XX
PS   Example 1; Page 41; 50pp; English.
XX
CC   The present sequence is of an antisense phosphorothioate linked
CC   deoxyribonucleic acid oligonucleotide that binds to the human p53
CC   oncogene. Although antisense oligonucleotide technology provides new
CC   therapy for many diseases, some antisense oligonucleotides containing
CC   phosphorothioate linkages exhibit an immunostimulatory response, causing
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CC   B cell proliferation and an antibody response. Reduction of this
CC   immunostimulatory response comprises administration of a therapeutic
CC   formulation containing the phosphorothioate oligonucleotide or protein,
CC   and at least one cyclodextrin. The immune response of the mammal is
CC   monitored. Phosphorothioate oligonucleotides are useful in treatment of
CC   cancer, inherited conditions and HIV infection
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2713
AAT88465/c
ID   AAT88465 standard; DNA; 20 BP.
XX
AC   AAT88465;
XX
DT   05-DEC-1997  (first entry)
XX
DE   Phosphorothioate linked human p53 gene oligonucleotide.
XX
KW   Phosphorothioate; methylphosphonate linkage; immune response reduction;
KW   pathogenic infection; genetic; hereditary; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .20
FT                   /*tag=  a
FT                   /note= "phosphorothioate linked"
XX
PN   WO9706253-A1.
XX
PD   20-FEB-1997.
XX
PF   09-JUL-1996;   96WO-US011439.
XX
PR   04-AUG-1995;   95US-00511536.
XX
PA   (HYBR-) HYBRIDON INC.
XX
PI   Agrawal S,  Temsamani J,  Zhao Q;
XX
DR   WPI; 1997-154260/14.
XX
PT   Reducing immunostimulatory effects of phosphoro:thioate
PT   oligo:nucleotide(s) - comprises modifying terminal structures, e.g. by
PT   introducing methyl:phosphonate linkages or ribonucleotide(s).
XX
PS   Example 1; Page 28; 42pp; English.
XX
CC   AAT88463-T88465 are phosphorothioate linked oligonucleotides that are
CC   complementary to HIV-1 gag and pol regions and human p53 respectively.
CC   They are used as controls for an experiment for identifying
CC   phosphorothioate oligonucleotides with reduced immunostimulatory
CC   response. Such oligonucleotides can be used to treat pathogenic
CC   infections and diseases with a genetic component e.g. cancer and
CC   inherited conditions. They can be administered in a therapeutic
CC   formulation and the mammal's immune response monitored; in such a
CC   formulation the activity of the oligonucleotides may also be enhanced by
CC   the addition of other active factors and agents, and combinations of the
CC   oligonucleotides could be directed at different regions of a pathogen
CC   genome or an overexpressed target gene
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2714
AAV47686
ID   AAV47686 standard; DNA; 20 BP.
XX
AC   AAV47686;
XX
DT   20-NOV-1998  (first entry)
XX
DE   Unmethylated CpG dinucleotide 2001.
XX
KW   Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
KW   natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW   pulmonary disorder; asthma; environmentally induced airway disease;
KW   bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW   inflammatory bowel disease; ss.
XX
OS   Synthetic.
XX
PN   WO9837919-A1.
XX
PD   03-SEP-1998.
XX
PF   25-FEB-1998;   98WO-US003678.
XX
PR   28-FEB-1997;   97US-0039405P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Schwartz DA,  Krieg AM;
XX
DR   WPI; 1998-480941/41.
XX
PT   Use of nucleic acids containing an unmethylated CpG - for treating a
PT   subject having or at risk of having an acute decrement in air flow or
PT   inhibiting an inflammatory response.
XX
PS   Claim 35; Page 27; 65pp; English.
XX
CC   This sequence represents an unmethylated CpG dinucleotide, and can be
CC   used in the method of the invention. The method is for treating a subject
CC   having, or at risk of having an acute decrement in air flow, comprising
CC   administering a nucleic acid sequence containing at least one
CC   unmethylated CpG. The nucleic acids containing an unmethylated CpG
CC   dinucleotide affect an immune response in a subject by activating natural
CC   killer cells (NK) or redirecting a subject's immune response from a Th2
CC   to a Th1 response by inducing monocytic and other cells to produce Th1
CC   cytokines. They can be used to treat pulmonary disorders having an
CC   immunologic component, such as asthma or environmentally induced airway
CC   disease. They can also be used to treat diseases associated with Gram-
CC   positive bacterial infections or endotoxaemia including bacterial
CC   meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC   and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
CC   abscess, haemorrhagic shock, disseminated intravascular coagulation, or
CC   an inflammatory response to lipopolysaccharide
XX
SQ   Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0,  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| |||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20
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RESULT 2715
AAV18923/c
ID   AAV18923 standard; DNA; 20 BP.
XX
AC   AAV18923;
XX
DT   07-JUL-1998  (first entry)
XX
DE   Phosphorothioate oligonucleotide 3.
XX
KW   Human serum albumin; biological agent; specific tissue site;
KW   protein-encapsulated; insoluble gas-filled microbubble; ss;
KW   site specific delivery; gene therapy vector; anti-sense;
KW   anti-gene type strategy.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .20
FT                   /*tag= a
FT                   /note= "Phosphorothioate analogues of polynucleotide have
FT                   chiral internucleoside linkage in one of the non-bridging
FT                   ligands is sulphur"
XX
PN   WO9800172-A2.
XX
PD   08-JAN-1998.
XX
PF   20-JUN-1997;   97WO-US010766.
XX
PR   28-JUN-1996;   96US-00670999.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Porter T,  Iversen PL;
XX
DR   WPI; 1998-086738/08.
XX
PT   Delivery of biological agents to a target site - by administration of a
PT   solution of protein-encapsulated insoluble gas-filled micro-bubbles
PT   conjugated to the biological agent.
XX
PS   Example 2; Page 17; 30pp; English.
XX
CC   This nucleotide sequence is used in the method of the invention for
CC   delivering a biological agent to specific tissue sites, by forming a
CC   solution of protein-encapsulated, insoluble gas-filled microbubbles
CC   attached to the biological agent. The method of the invention can be used
CC   for the site specific delivery of biologically active agents such as
CC   therapeutics or diagnostics. The method is particularly useful for
CC   delivery of nucleotide sequences in the form of gene therapy vectors, or
CC   anti-sense of anti-gene type strategies to ultimately alter gene
CC   expressions in target cells
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2716
AAV22438
ID   AAV22438 standard; DNA; 20 BP.
XX
AC   AAV22438;
XX
DT   08-JUL-1998  (first entry)
XX
DE   Antisense oligonucleotide designed to target the R2 message.
XX
KW   R2 subunit; ribonucleotide reductase; ras pathway; cell proliferation;
KW   tumour cell; antisense; growth; inhibition; sensitivity; hydroxyurea;
KW   chemotherapeutic drug; methotrexate; PALA; treatment; phosphorothioate;
KW   ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .2
FT                   /*tag= a
FT                   /note= "phosphorothioate linkage"
FT   modified_base   4. .5
FT                   /*tag= b
FT                   /note= "phosphorothioate linkage"
FT   modified_base   8. .9
FT                   /*tag= c
FT                   /note= "phosphorothioate linkage"
FT   modified_base   11. .12
FT                   /*tag= d
FT                   /note= "phosphorothioate linkage"
FT   modified_base   14. .15
FT                   /*tag= e
FT                   /note= "phosphorothioate linkage"
FT   modified_base   17. .18
FT                   /*tag= f
FT                   /note= "phosphorothioate linkage"
FT   modified_base   19. .20
FT                   /*tag= g
FT                   /note= "phosphorothioate linkage"
XX
PN   WO9805769-A2.
XX
PD   12-FEB-1998.
XX
PF   01-AUG-1997;   97WO-CA000540.
XX
PR   02-AUG-1996;   96US-0023040P.
PR   07-MAR-1997;   97US-0039959P.
XX
PA   (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI   Wright JA,  Young AH;
XX
DR   WPI; 1998-145609/13.
XX
PT   Antisense oligonucleotides to ribonucleotide reductase genes - used to
PT   modulate tumour growth and inhibit tumour cell proliferation.
XX
PS   Claim 4; Page 38; 79pp; English.
XX
CC   AAV22429-530 represent antisense oligonucleotides which are targeted
CC   against the mRNA of the R2 subunit sequence of ribonucleotide reductase.
CC   Aberrant expression of the R2 gene can determine the malignant
CC   characteristics of cells. Altered R2 expression was found to cooperate
CC   with ras in mechanisms of malignant progression, and recombinant R2
CC   expression resulted in increased membrane associated Raf-1 protein. These
CC   results suggest that R2 cooperates with Raf-1 and Rac-1, thereby
CC   affecting ras pathways and cell proliferation. Suppression of R2 gene
CC   expression was found to reduce transformed properties of tumour cells.
CC   The antisense oligonucleotides can be used for modulating tumour cell
CC   growth, or for inhibiting tumour cell proliferation. They can also be
CC   used for increasing the sensitivity of neoplastic cells to
CC   chemotherapeutic drugs (especially to hydroxyurea, methotrexate (MTX),
CC   and PALA). The antisense oligonucleotides may be used to treat
CC   proliferative disorders including leukaemias, lymphomas, sarcomas,
CC   melanomas, various other forms of cancer, papillomas, arthrosclerosis,
CC   psoriasis, polythemia, mastocytosis, autoimmune diseases, angiogenesis,
CC   bacterial infections and viral infections (including HIV hepatitis, or
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CC   herpes infections)
XX
SQ   Sequence 20 BP; 3 A; 11 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        348 CCCCTCCCTACCAGCAGCT 366
              |||||| || |||||||||
Db          1 CCCCTCACTCCCAGCAGCT 19


RESULT 2717
AAV74243
ID   AAV74243 standard; DNA; 20 BP.
XX
AC   AAV74243;
XX
DT   20-MAR-2003  (revised)
DT   15-MAR-1999  (first entry)
XX
DE   CpG-N motif O-ODN 2001 DNA.
XX
KW   CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation; ODN;
KW   viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW   toxin; tumour suppressor; cytokine; apoptotic protein; interferon;
KW   hormone; clotting factor; ligand; receptor; oligodeoxynucleotide; ss.
XX
OS   Synthetic.
XX
PN   WO9852581-A1.
XX
PD   26-NOV-1998.
XX
PF   20-MAY-1998;   98WO-US010408.
XX
PR   20-MAY-1997;   97US-0047209P.
PR   20-MAY-1997;   97US-0047233P.
XX
PA   (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (QIAG-) QIAGEN GMBH.
XX
PI   Davis HL,  Krieg AM,  Schorr J,  Wu T;
XX
DR   WPI; 1999-059712/05.
XX
PT   Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
PT   enhancing the immunostimulatory effect of an antigen or enhancing the
PT   expression of a therapeutic polypeptide.
XX
PS   Example 1; Page 64; 109pp; English.
XX
CC   AAV74237-V74253 are oligodeoxynucleotide (ODN) primers used to describe a
CC   method for enhancing the immunostimulatory effect of an antigen encoded
CC   by nucleic acid contained in a nucleic acid construct. The method
CC   involves determining the CpG-N and CpG-S motifs present in the construct,
CC   removing neutralising CpG (CpG-N) motifs and optionally inserting
CC   stimulatory CpG (CpG-S) motifs in the construct, thereby producing a
CC   nucleic acid construct having enhanced immunostimulatory efficacy. The
CC   method can be used for immunisation against viral antigens, e.g. from
CC   hepatitis B virus (HBV), bacterial antigens or an antigen derived from a
CC   parasite. They can also be used for expression of a therapeutic
CC   polypeptide, e.g. growth factors, toxins, tumour suppressors, cytokines,
CC   apoptotic proteins, interferons, hormones, clotting factors, ligands and
CC   receptors. (Updated on 20-MAR-2003 to correct PA field.)
XX
SQ   Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 2718
AAX27854/c
ID   AAX27854 standard; DNA; 20 BP.
XX
AC   AAX27854;
XX
DT   02-JUN-1999  (first entry)
XX
DE   PCR primer for mutant lipase coding sequence.
XX
KW   Lipase; mutant; methyl (2R,3S)-3-(4-methoxyphenyl)glycidate;
KW   (-)-MPGM production; PCR primer; ss.
XX
OS   Synthetic.
OS   Pseudomonas sp.
XX
PN   JP10304875-A.
XX
PD   17-NOV-1998.
XX
PF   08-MAY-1997;   97JP-00117353.
XX
PR   08-MAY-1997;   97JP-00117353.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
DR   WPI; 1999-232450/20.
XX
PT   New lipase protein - useful for production of methyl (2R,3S)-3-(4-
PT   methoxyphenyl)glycidate ((-)-MPGM).
XX
PS   Example 1; Page 6; 15pp; Japanese.
XX
CC   This sequence is a PCR primer for DNA encoding the mutant lipase protein
CC   of the invention. The lipase can be used for the production of methyl
CC   (2R,3S)-3-(4-methoxyphenyl)glycidate ((-)-MPGM). Microbes transformed
CC   with the DNA sequence can produce (-)-MPGM of high optical purity
XX
SQ   Sequence 20 BP; 7 A; 2 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1914 ACAATACCTTTTTTTTCAG 1932
              |||| |||||||| |||||
Db         20 ACAACACCTTTTTGTTCAG 2


RESULT 2719
AAA39400/c
ID   AAA39400 standard; DNA; 20 BP.
XX
AC   AAA39400;
XX
DT   15-SEP-2000  (first entry)
XX
DE   Human p53 antisense oligonucleotide OL(1)p53 SEQ ID NO:2.
XX
KW   Human; p53; antisense oligonucleotide; morpholino; phosphorothioate;
KW   phosphorodiamidate; proliferative cell disorder; cancer; stroke;
KW   hypotoxic state; ischaemia; peptide nucleic acid; phosphoramidate;
KW   restenosis; cytostatic; antipsoriatic; vasotropic; cerebroprotective;
KW   antiinflammatory; opthalmalogical; antiasthmatic; HPV; infection;
KW   human papilloma virus; asthma; keratoconjunctivitis; psoriasis;
KW   organ transplant; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200024885-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-US024758.
XX
PR   26-OCT-1998;   98US-0105695P.
XX
PA   (AVIB-) AVI BIOPHARMA INC.
XX
PI   Iversen PL;
XX
DR   WPI; 2000-350729/30.
XX
PT   Antisense oligonucleotides for treating disease states characterized by
PT   induction of p53 e.g. cancer and restenosis.
XX
PS   Claim 1; Page 20; 27pp; English.
XX
CC   The present invention describes an oligonucleotide (I) which is a
CC   morpholino oligonucleotide, a peptide nucleic acid, a 2'-O-allyl or 2'-O-
CC   alkyl modified oligonucleotide or a N3'-->P5' phosphoramidate
CC   oligonucleotide with a defined base sequence given in AAA39399 or
CC   AAA39400. Also described is a method of treating a disease state
CC   characterised by p53 induction in a mammalian subject comprising
CC   administering (I). (I) has cytostatic, antipsoriatic, vasotropic,
CC   cerebroprotective, antiinflammatory, opthalmalogical and antiasthmatic
CC   activities. The oligonucleotides are useful for treating disease states
CC   characterised by induction of p53 in a human subject where the disease
CC   state is preferably cancer or results from an ischaemic or
CC   ischaemic/reperfusive injury. Other disease states which can be treated
CC   include proliferative cell disorders e.g. restenosis, human papilloma
CC   virus (HPV)-infected cells, asthma, keratoconjunctivitis and psoriasis
CC   and hypoxic states induced by ischaemic attacks e.g. stroke or organ
CC   transplant. Morpholino oligomers and C-5-propyne pyrimidine-modified
CC   oligonucleotide are particularly effective RNA-binding molecules and
CC   distort the RNA helix which disrupts ribosomal binding
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||||  ||||||  |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2720
AAA94536
ID   AAA94536 standard; DNA; 20 BP.
XX
AC   AAA94536;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antisense oligonucleotide #20976 targeted to human G-alpha-S1.
XX
KW   G-alpha-S1; infection; inflammation; tumour; antisense; human;
KW   phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KW   Gs-alpha short form; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally the internucleotide linkages are
FT                   phosphorothioate"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
XX
PN   US6110664-A.
XX
PD   29-AUG-2000.
XX
PF   25-JUN-1999;   99US-00344914.
XX
PR   25-JUN-1999;   99US-00344914.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-586346/55.
XX
PT   New antisense compounds for modulating the expression of G-alpha-S1,
PT   especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
PT   prevent or delay infection, inflammation or tumor formation.
XX
PS   Claim 3; Col 40; 37pp; English.
XX
CC   The present invention relates to antisense compounds 8-30 bases long
CC   targeted to a coding region, a stop codon, or a 3' untranslated region of
CC   human G-alpha-S1 (see AAA94451). The antisense compounds specifically
CC   hybridize with and inhibit the expression of human G-alpha-S1. The
CC   antisense compounds are useful for diagnostics, therapeutics and
CC   prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC   formation. Particularly, the antisense oligonucleotides are useful for
CC   treating humans prone to a disease or condition associated with
CC   expression of G-alpha-S1. The present sequence an antisense
CC   oligonucleotide targeted to the 3' untranslated region of human G-alpha-
CC   S1
XX
SQ   Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2265 TATTTATTTCAGATGTTTC 2283
              ||||||||||  ||||||
Db          1 TATTTATTTCATTTGTTTC 19


RESULT 2721
AAZ77398/c
ID   AAZ77398 standard; DNA; 20 BP.
XX
AC   AAZ77398;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:11754.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
```

```
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 9; Page 2736; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 20 BP; 2 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAAATG 1501
              ||||||||||||  ||| ||
Db         20 CAAAACCCTGGAAAAACTG 2


RESULT 2722
AAA91253
ID   AAA91253 standard; DNA; 20 BP.
XX
AC   AAA91253;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Antisense IGFBP-5 inhibitor #59.
XX
KW   Insulin-like growth factor binding protein-5; IGFBP-5; human;
KW   antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
KW   breast cancer; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200105435-A2.
XX
PD   25-JAN-2001.
XX
PF   19-JUL-2000; 2000WO-CA000853.
XX
PR   19-JUL-1999;   99US-0144495P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (MIYA/) MIYAKE H.
XX
PI   Gleave M;
XX
DR   WPI; 2001-168448/17.
XX
PT   Composition for treating hormone-regulated cancer, e.g. breast and
PT   prostatic tumors, comprising an antisense oligonucleotide that inhibits
PT   expression of insulin like growth factor binding protein-5 by hormone-
PT   regulated tumor cells.
XX
PS   Disclosure; Page 44; 45pp; English.
XX
CC   This sequence represents an antisense oligonucleotide targeted against
CC   human insulin-like growth factor binding protein-5 (IGFBP-5). The
CC   invention relates to a composition for treatment of hormone-regulated
CC   cancer, comprising an antisense oligonucleotide (such as this sequence)
CC   which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.
CC   The compositions is useful for delaying progression of hormone-regulated
CC   tumour cells such as prostatic cancer cells or breast cancer cells, to an
CC   androgen-independent state, by treating hormone sensitive tumour cells
CC   with the antisense sequence which inhibits expression of IGFBP-5 by the
CC   tumour cells. The composition can also be used for treating a hormone-
CC   responsive cancer in an individual, and administering the composition to
CC   the individual after initiation of hormone-withdrawal to induce apoptotic
CC   cell death of hormone-responsive tumour cells, and therefore delaying the
CC   progression of hormone-responsive cancer cells to a hormone-independent
CC   state in the individual. It can also be used for inhibiting or delaying
CC   metastatic boney progression of an IGF-1 sensitive tumour in a mammal, by
CC   administering the composition to inhibit the expression of IGFBP-5 by the
CC   hormone-responsive cancer cells, and therefore inhibiting or delaying
CC   metastatic boney progression of the tumour
XX
SQ   Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       451 CACAGGCAGCCAGCAGCAG 469
             ||  ||||  ||||||||||
Db         2 CATAGGCGGCCAGCAGCAG 20


RESULT 2723
AAK95041
ID   AAK95041 standard; DNA; 20 BP.
XX
AC   AAK95041;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human cDNA clone-specific primer, SEQ ID NO: 4286.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
XX
```

PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Example 18; Page 129; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a primer used to amplify a human cDNA
CC clone provided in the invention
XX
SQ Sequence 20 BP; 8 A; 2 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2294 GAAAAGGGTAGGCACGAAG 2312
||||||||||||||| |||
Db 1 GAAAAGGGTAGGCAGCAAG 19

RESULT 2724
AAK95078
ID AAK95078 standard; DNA; 20 BP.
XX
AC AAK95078;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone-specific primer, SEQ ID NO: 4323.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Example 18; Page 130; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a primer used to amplify a human cDNA
CC clone provided in the invention
XX
SQ Sequence 20 BP; 8 A; 2 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2294 GAAAAGGGTAGGCACGAAG 2312
||||||||||||||| |||
Db 1 GAAAAGGGTAGGCAGCAAG 19

RESULT 2725
AAF99116
ID AAF99116 standard; DNA; 20 BP.
XX
AC AAF99116;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #232.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 43; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGCAG 69

```
                  ||||||| |||||||||  |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 2726
AAH91454/c
ID   AAH91454 standard; DNA; 20 BP.
XX
AC   AAH91454;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human inflammatory bowel disease associated polymorphic site #529.
XX
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW   chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    12
FT                   /*tag=  a
FT                   /note= "SNP, optionally insertion or deletion at this
FT                   position"
XX
PN   WO200142511-A2.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US033632.
XX
PR   10-DEC-1999;   99US-0170257P.
PR   10-APR-2000; 2000US-0196046P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI   Daly M,  Hudson TJ,  Lander ES,  Rioux J,  Siminovitch K;
XX
DR   WPI; 2001-367874/38.
XX
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay.
XX
PS   Claim 1; Page 61; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention
XX
SQ   Sequence 20 BP; 17 A; 0 C; 2 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              \\\\ \\\ \\\\\ |||||
Db         20 TTTTCTTTNTTTTTCTTTTT 1


RESULT 2727
AAH44608/c
ID   AAH44608 standard; DNA; 20 BP.
XX
AC   AAH44608;
XX
DT   05-NOV-2001  (first entry)
XX
DE   20-mer p53 phosphorothioate antisense oligonucleotide SEQ ID NO:2.
XX
KW   Antisense oligonucleotide; phosphorothioate; p53; cytostatic;
KW   gene expression inhibitor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
XX
PN   US6265389-B1.
XX
PD   24-JUL-2001.
XX
PF   25-JUN-1998;   98US-00104549.
XX
PR   31-AUG-1995;   95US-00521744.
PR   22-SEP-1997;   97US-00934830.
XX
PA   (ALKE-) ALKERMES CONTROLLED THERAPEUTICS.
XX
PI   Burke PA;
XX
DR   WPI; 2001-556573/62.
XX
PT   Sustained release composition for oligonucleotides, e.g. antisense
PT   oligodeoxynucleotides, contains a biocompatible polymer, and an antisense
PT   oligonucleotide complexed with a metal cation.
XX
PS   Claim 9; Col 10; 13pp; English.
XX
CC   The present invention describes a sustained release composition,
CC   comprising a biocompatible polymer, and an antisense oligonucleotide,
CC   dispersed within the biocompatible polymer, and complexed with a metal
CC   cation. The present sequence represents a specifically claimed 20-mer p53
CC   phosphorothioate antisense oligonucleotide for use in the above
CC   composition. The composition has cytostatic activity and can be used as a
CC   gene expression inhibitor. The composition can be used for the sustained
CC   release of oligonucleotides, particularly antisense oligonucleotides. The
CC   antisense oligonucleotides are useful in the treatment of diseases, where
CC   a particular protein has been identified as critical for a disease to
CC   flourish
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| ||||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2728
ABK90841/c
ID   ABK90841 standard; DNA; 20 BP.
XX
AC   ABK90841;
XX
DT   05-NOV-2002  (first entry)
XX
DE   p53 antisense oligonucleotide.
XX
KW   p53; antisense; anti-leukaemic; ss.
XX
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate nucleotides"
XX
PN   US2002064557-A1.
XX
PD   30-MAY-2002.
XX
PF   29-MAR-2001; 2001US-00820587.
XX
PR   31-AUG-1995;   95US-00521744.
PR   22-SEP-1997;   97US-00934830.
PR   25-JUN-1998;   98US-00104549.
XX
PA   (ALKE-) ALKERMES CONTROLLED THERAPEUTICS.
XX
PI   Burke PA;
XX
DR   WPI; 2002-607110/65.
XX
PT   Composition for sustained release of oligonucleotide from a polymer
PT   matrix, comprises biocompatible polymer, and a metal cation-complexed
PT   oligonucleotide dispersed within the biocompatible polymer.
XX
PS   Example 1; Page 6; 13pp; English.
XX
CC   The invention relates to a new composition (I) for the sustained release
CC   of an oligonucleotide from a polymer matrix, comprising: (a) a
CC   biocompatible polymer; and (b) a metal cation-complexed oligonucleotide,
CC   dispersed within the biocompatible polymer. (I) is useful for providing a
CC   therapeutically effective amount of an oligonucleotide in a subject for a
CC   sustained period. The compositions are preferably useful for providing
CC   anti-leukaemic effects in vivo, where the antisense oligonucleotides in
CC   the composition are directed to genes involved in cellular
CC   transformation. The sustained release composition overcomes the problem
CC   of high initial release of an oligonucleotide, in particular an antisense
CC   oligodeoxynucleotide (ODN) which is not stabilised prior to incorporation
CC   into the polymeric matrix. Also, loss of activity of the oligonucleotide,
CC   such as an antisense ODN due to instability of the medicament, and
CC   chemical interactions between the oligonucleotide, and other components
CC   contained in or used in formulating the sustained release composition are
CC   substantially absent. The advantages also include increased patient
CC   compliance and acceptance by eliminating the need for repetitive
CC   administration, increased therapeutic benefit by eliminating fluctuations
CC   in oligonucleotide concentration in blood levels by providing a desirable
CC   release profile, and a potential lowering of the total amount of the
CC   oligonucleotide, in particular an antisense, ODN, necessary to provide a
CC   therapeutic benefit, by reducing these fluctuations. The present sequence
CC   represents an antisense oligonucleotide used in an example of the
CC   invention
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2729
ABN84654/c
ID   ABN84654 standard; DNA; 20 BP.
XX
AC   ABN84654;
XX
DT   29-OCT-2002  (first entry)
XX
DE   p53 antisense oligonucleotide.
XX
KW   Antisense; p53 sustained release; encapsulation; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
XX
PN   US2002064557-A1.
XX
PD   30-MAY-2002.
XX
PF   29-MAR-2001; 2001US-00820587.
XX
PR   31-AUG-1995;   95US-00521744.
PR   22-SEP-1997;   97US-00934830.
PR   25-JUN-1998;   98US-00104549.
XX
PA   (ALKE-) ALKERMES CONTROLLED THERAPEUTICS.
XX
PI   Burke PA;
XX
DR   WPI; 2002-607110/65.
XX
PT   Composition for sustained release of oligonucleotide from a polymer
PT   matrix, comprises biocompatible polymer, and a metal cation-complexed
PT   oligonucleotide dispersed within the biocompatible polymer.
XX
PS   Example 1; Page 6; 13pp; English.
XX
CC   The present sequence is an anti-p53 phosphorothioate antisense
CC   oligodeoxynucleotide (ODN). This antisense ODN was used in examples of
CC   the invention examining the encapsulation and sustained release of
CC   complexed ODN. The invention relates to a composition for the sustained
CC   release of oligonucleotides, especially antisense ODNs. The composition
CC   comprises a biocompatible polymer matrix into which a metal cation-
CC   complexed oligonucleotide is dispersed. Administration of the composition
CC   provides a therapeutically effective blood level of oligonucleotide in a
CC   subject for a sustained period. This overcomes the problem of high
CC   initial release of an oligonucleotide, in particular an antisense ODN,
CC   which is not stabilised prior to encapsulation. Loss of activity of the
CC   oligonucleotide, and chemical interactions between the oligonucleotide
CC   and other components contained in, or used in, formulating the sustained
CC   release composition are substantially absent. Patient compliance and
CC   acceptance are enhanced by eliminating the need for repetitive
CC   administration, and there is increased therapeutic benefit by eliminating
CC   fluctuations in oligonucleotide concentration in blood levels
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2730
ABS77759
ID   ABS77759 standard; DNA; 20 BP.
XX
AC   ABS77759;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #243.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
```

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 23; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGCAG 69
||||||| |||||||||| |
Db 2 GCGGCGGCGGCGGCGGCGG 20

RESULT 2731
ABT07490/c
ID ABT07490 standard; DNA; 20 BP.
XX
AC ABT07490;
XX
DT 14-NOV-2002 (first entry)
XX
DE Rat protein phosphatase 2 oligo inhibitor SEQ ID No 104.
XX
KW Cytostatic; antidiabetic; antisense therapy; aberrant insulin regulation;
KW protein phosphatase 2 catalytic beta subunit; antisense compound; cancer;
KW hyperproliferative disorder; diabetes; inflammation; tumour; rat; ds.
XX
OS Rattus norvegicus.
XX
PN WO200264737-A2.
XX
PD 22-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-US002805.
XX
PR 09-FEB-2001; 2001US-00780045.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-657588/70.
XX
PT New antisense oligonucleotides targeted to nucleic acid encoding Protein
PT Phosphatase 2 catalytic subunit beta, useful for treating diseases
PT related to Protein Phosphatase 2 catalytic subunit beta expression, such
PT as cancer.
XX
PS Example 16; Page 98; 137pp; English.
XX
CC The invention relates to a novel compound 8-50 nucleotides in length
CC targeted to a nucleic acid molecule encoding a protein phosphatase 2
CC catalytic beta subunit, where the compound specifically hybridises with
CC and inhibits the expression of protein phosphatase 2 catalytic beta
CC subunits, or specifically hybridises with at least an 8-nucleotide
CC portion of an active site on a nucleic acid molecule encoding a protein
CC phosphatase 2 catalytic beta subunit. The antisense compounds are useful
CC for modulating the expression of protein phosphatase 2 catalytic beta
CC subunits and for treating diseases or conditions associated with
CC expression of protein phosphatase 2 catalytic beta subunits, e.g.
CC aberrant insulin regulation or diabetes or a hyperproliferative disorder,
CC particularly cancer. The antisense compounds are also useful for
CC diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay
CC infection, inflammation or tumour formation, as research reagents and
CC kits, and in distinguishing between functions of various members of a
CC biological pathway. This polynucleotide sequence represents an
CC oligonucleotide inhibitor of rat protein phosphatase 2 catalytic beta
CC subunit mRNA levels of the invention. NOTE: This oligonucleotide contains
CC phosphorothioate residues and has 2'- MOE wings with a deoxy gap
XX
SQ Sequence 20 BP; 0 A; 15 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGCAG 69
||||||| |||||||||| |
Db 20 GCGGCGGCGGCGGCGGCGG 2

RESULT 2732
ABL39008
ID ABL39008 standard; DNA; 20 BP.
XX
AC ABL39008;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 410.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX

PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 199; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGCAG 69
||||||| ||||||||| |
Db 2 GCGGCGGCGGCGGCGGCGG 20

RESULT 2733
AAL42562/c
ID AAL42562 standard; DNA; 20 BP.
XX
AC AAL42562;
XX
DT 08-JUL-2002 (first entry)
XX
DE Humulus lupulus farnesyl pyrophosphate synthase PCR primer 12.
XX
KW Farnesyl pyrophosphate synthase protein; hop secondary metabolites;
KW hop based genetic engineering; drug application; ss; PCR; primer.
XX
OS Humulus lupulus.
XX
PN WO200231164-A1.
XX
PD 18-APR-2002.
XX
PF 05-OCT-2001; 2001WO-JP008816.
XX
PR 06-OCT-2000; 2000JP-00308054.
XX
PA (SAPB) SAPPORO BREWERIES LTD.
XX
PI Okada Y, Ito K;
XX
DR WPI; 2002-362680/39.
XX
PT Farnesyl pyrophosphate synthase protein and encoded nucleic acid with
PT promoter region specifically expressed in hop lupulin glandular hair,
PT useful in producing pharmacologically-active hop secondary metabolites.
XX
PS Example 2; Page 17; 49pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequence of the Humulus
CC lupulus farnesyl pyrophosphate synthase protein. The DNA and amino acid
CC sequences of the invention are useful in producing pharmacologically-
CC active hop secondary metabolites in vitro by transformant hop based
CC genetic engineering (e.g. for application in drugs). The present DNA
CC sequence represents a PCR primer specific for the gene sequence of the
CC Humulus lupulus farnesyl pyrophosphate synthase protein
XX
SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1561 GACTGCAAAAATCCTTCTC 1579
| |||| ||||||||||||
Db 20 GGCTGCCAAAATCCTTCTC 2

RESULT 2734
ABQ96037/c
ID ABQ96037 standard; DNA; 20 BP.
XX
AC ABQ96037;
XX
DT 28-OCT-2002 (first entry)
XX
DE Tumour suppression-related oligonucleotide #1688.
XX
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW viral infection; cell degeneration disease; neurodegeneration; ds;
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS Homo sapiens.
XX
PN FR2819824-A1.
XX
PD 26-JUL-2002.
XX
PF 23-JAN-2001; 2001FR-00000899.
XX
PR 23-JAN-2001; 2001FR-00000899.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Telerman A, Amson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 468; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral
CC resistance. (I) are useful as probes or primers for detecting,
CC identifying, measuring and/or amplifying nucleic acid sequences, as
CC antisense reagents and for recombinant production of polypeptides. (I),
CC polypeptides (II) encoded by (I), vector containing (I), cells containing
CC these vectors and antibodies (Ab) against (II) are all useful for
CC treatment/prevention of viral, tumour and cell degeneration diseases
CC (especially neurodegeneration, such as Alzheimer's disease and
CC schizophrenia). Analysing the expression of (I) is also useful for
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC (I) are used for studying the aetiology of these diseases (also immune
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC in the specification

```
XX
SQ   Sequence 20 BP; 17 A; 1 C; 1 G; 0 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTT 2178
              ||| | ||||||||| ||||
Db         20 TTTNTTCTTTTTTTTGTTTT 1


RESULT 2735
ABA97643/c
ID   ABA97643 standard; DNA; 20 BP.
XX
AC   ABA97643;
XX
DT   11-APR-2002  (first entry)
XX
DE   probe n.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATATA 2535
              |||||| || |||||||||
Db         20 GGTTTTTTTTATATATATA 2


RESULT 2736
ABZ91981/c
ID   ABZ91981 standard; DNA; 20 BP.
XX
AC   ABZ91981;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO0200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 7223; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 14 A; 1 C; 3 G; 1 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTT 2178
              |||| || |||| |||||||
Db         20 TTTCGCCNTTTTATTTTTTT 1


RESULT 2737
ABZ85436
ID   ABZ85436 standard; DNA; 20 BP.
XX
AC   ABZ85436;
XX
DT   17-OCT-2003  (first entry)
XX
```

```
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 678; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||  |||
Db             1 TTTTTTTTTTTTTTGAAAC 19


RESULT 2738
ABZ85668
ID   ABZ85668 standard; DNA; 20 BP.
XX
AC   ABZ85668;
XX
DT   17-OCT-2003  (first entry)
XX
```

```
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 910; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
                ||||  ||||||||||  |||
Db             2 CTTTCTTTTTTTTTTCTTT 20


RESULT 2739
ABZ92287
ID   ABZ92287 standard; DNA; 20 BP.
XX
AC   ABZ92287;
XX
DT   17-OCT-2003  (first entry)
XX
```

```
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 7529; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 6 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              ||||||  ||||||||||
Db          1 CTCCTTCCTTTTTTTTTTT 19


RESULT 2740
ABZ89545/c
ID   ABZ89545 standard; DNA; 20 BP.
XX
AC   ABZ89545;
XX
DT   17-OCT-2003  (first entry)
XX
```

```
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4787; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 15 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              ||||||||||||  ||  |||
Db         20 TTTTTTTTTTTTAAAATTT 2


RESULT 2741
ABZ22859/c
ID   ABZ22859 standard; DNA; 20 BP.
XX
AC   ABZ22859;
XX
DT   03-APR-2003  (first entry)
XX
```

DE Clonal T cell receptor gamma detection PCR primer TcellV-F(Vgamma1-8).
XX
KW Human; T cell receptor; TCR; neoplastic T-cell disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003001181-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019696.
XX
PR 21-JUN-2001; 2001US-00886227.
XX
PA (QUES-) QUEST DIAGNOSTICS INC.
XX
PI Samoszuk M, Zhu D;
XX
DR WPI; 2003-175302/17.
XX
PT Determining the clonality of a T-cell receptor (TCR) rearrangement in a
PT sample by polymerase chain reaction PCR and temporal temperature gradient
PT gel electrophoresis, useful for the diagnosis of neoplastic T-cell
PT disease.
XX
PS Disclosure; Fig 4; 31pp; English.
XX
CC The present invention describes a method (M1) for determining clonality
CC of a T cell receptor (TCR) rearrangement comprising extracting nucleic
CC acid, amplifying by PCR with two or more TCR-specific primers to provide
CC one or more TCR DNA fragments, and analysing the TCR DNA fragments using
CC an electrophoretic gel by temporal temperature gradient gel
CC electrophoresis (TTGE), where the presence of one or more discrete DNA
CC bands in the gel indicates the presence of a clonal TCR rearrangement.
CC Also described: (1) diagnosing (M2) a patient suspected of having a
CC neoplastic T-cell disease, comprising obtaining a sample from the
CC patient, and determining whether a clonal TCR gene rearrangement is
CC present in the sample by analysing the sample by (M1), where the presence
CC of the clonal TCR gene rearrangement indicates neoplastic T-cell disease;
CC (2) preparing (M3) a DNA migration marker for use in a TTGE gel,
CC comprising providing one or more TCR DNA segments having known migration
CC rates in the TTGE gel; and (3) a TTGE DNA migration marker, comprising a
CC substantially pure DNA molecule having a TCR gene sequence, and a buffer
CC suitable for loading on a TTGE gel. (M1-M3) and compositions are useful
CC for the diagnosis of neoplastic T-cell disease. The present sequence
CC represents a PCR primer used for the detection of clonal TCR-gamma
CC rearrangement, which is used in the exemplification of the present
CC invention
XX
SQ Sequence 20 BP; 4 A; 1 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1473 CTGATTCTAACAAAACCCT 1491
              ||||||| |||| ||||||
Db         19 CTGATTCCAACACAACCCT 1
```

RESULT 2742
ACD99549
ID ACD99549 standard; DNA; 20 BP.
XX
AC ACD99549;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #235.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 15; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20
```

RESULT 2743
ADA24235/c
ID ADA24235 standard; DNA; 20 BP.
XX
AC ADA24235;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human p53 oncogene antisense oligonucleotide SEQ ID NO:18.
XX
KW therapeutic oligonucleotide; double-stranded RNA; dsRNA; mobile protein;
KW cytostatic; immunosuppressive; virucide; anti-HIV; antibacterial;
KW cardiant; hyperproliferation; cancer; haematological; metastatic;
KW autoimmune disease; infection; endocrine; neural; cardiovascular;
KW pulmonary; reproductive system disorder; endocytosis; metabolic process;
KW murine; intracellular adhesion molecule 1; ICAM-1;
KW antisense oligonucleotide; phosphorothioate; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003069306-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004323.
XX
PR 13-FEB-2002; 2002US-0356053P.

```
XX
PA   (MEDB-) MEDBRIDGE INC.
XX
PI   Xie D;
XX
DR   WPI; 2003-646491/61.
XX
PT   Treating diseases with oligonucleotides or interfering RNA, useful e.g.
PT   for cancer or autoimmune diseases, covalently coupled to mobile proteins,
PT   in vivo or in vitro.
XX
PS   Claim 128; Page 12; 42pp; English.
XX
CC   The present invention describes a method for treating a disease by
CC   administering: (a) a therapeutic oligonucleotide (TON) or double-stranded
CC   RNA (dsRNA) that includes a reactive group (RG) that can react with a
CC   mobile protein (MP) to form a covalent conjugate of TON/dsRNA and MP; or
CC   (b) TON or dsRNA already conjugated to MP through a covalent bond. Also
CC   described: (1) TON of 15-30 bases that includes (i) a part that binds to
CC   target RNA or DNA and (ii) RG; (2) TON of 15-30 bases that includes a
CC   part that binds to target RNA or DNA and is conjugated to MP through a
CC   covalent link; (3) dsRNA that includes RG; and (4) dsRNA that is
CC   conjugated to MP through a covalent link. TON have cytostatic,
CC   immunosuppressive, virucide, anti-HIV, antibacterial and cardiant
CC   activities. The method is used to treat, or prevent, hyperproliferation
CC   (particularly cancers, solid or haematological, including prevention of
CC   metastatic spread); autoimmune diseases; viral or bacterial infections;
CC   endocrine, neural, cardiovascular, pulmonary or reproductive system
CC   disorders. Also where TON or dsRNA are labelled, they can be used for
CC   diagnosis and monitoring of therapy. When linked to a mobile protein,
CC   TON/dsRNA have better cell entry (via endocytosis or other parts of the
CC   mobile protein metabolic process) and longer therapeutic life, increased
CC   from hours to weeks (the result of increased resistance to nuclease),
CC   without loss of affinity for the target. In many cases immune response to
CC   TON/dsRNA is also reduced, as is non-specific binding to endogenous
CC   proteins. The present sequence represents a human p53 oncogene antisense
CC   oligonucleotide, which is a specifically claimed TON from the present
CC   invention.
XX
SQ   Sequence 20 BP; 0 A; 13 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              ||||||| |||||| |||
Db         19 GAGCCAGGGGGGAGCAGGG 1


RESULT 2744
ADB36618
ID   ADB36618 standard; DNA; 20 BP.
XX
AC   ADB36618;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #232.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 8; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 2745
ABS97317
ID   ABS97317 standard; DNA; 21 BP.
XX
AC   ABS97317;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Aryl hydrocarbon nuclear translocation receptor sequencing primer #6.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
```

```
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 6; Page 109; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a PCR
CC   primer used to amplify the sequences of the invention
XX
SQ   Sequence 21 BP; 3 A; 4 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACT 2190
                ||||||||||||  ||||
Db          1 TTTTTTTTTTTTTCAAACT 19


RESULT 2746
AAT80586/c
ID   AAT80586 standard; cDNA; 21 BP.
XX
AC   AAT80586;
XX
DT   04-NOV-1997  (first entry)
XX
DE   Anti-p53 phosphorothioate oligonucleotide OL(1)p53.
XX
KW   Antisense oligonucleotide; cancer; free hydroxy radical; inhibition;
KW   proliferation; malignant cell; p53; apoptosis; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .21
FT                   /*tag=  a
FT                   /note= "Linkages are phosphorothioate"
XX
PN   US5641754-A.
XX
PD   24-JUN-1997.
XX
PF   10-JAN-1994;   94US-00179655.
XX
PR   10-JAN-1994;   94US-00179655.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Iversen PL;
XX
DR   WPI; 1997-340973/31.
XX
PT   Method for killing cancer cells - by exposure to anti:sense
PT   oligo:nucleotide and to free hydroxy radicals.
XX
PS   Claim 2; Col 15; 12pp; English.
XX
CC   A novel method has been produced for killing cancer cells which involves
CC   exposing the cells to an antisense oligonucleotide and to free hydroxy
CC   radicals. The present sequence represents an antisense phosphorothioate
CC   oligonucleotide OL(1)p53 directed against a region in exon 10 of p53.
CC   This anti-p53 oligonucleotide is complementary to at least a portion of
CC   the mRNA transcript of the human p53 gene and is hybridisable to the mRNA
CC   transcript. The method is used to kill cancer cells. The treatment
CC   inhibits the proliferation or kills malignant but not normal cells. When
CC   the antisense oligonucleotide is one that downregulates the path by which
CC   the cancer cells repair oxidative damage to their DNA, the cells are
CC   rendered more susceptible to eradication upon exposure to the hydroxy
CC   radicals
XX
SQ   Sequence 21 BP; 0 A; 14 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
                ||||||| |||||| |||
Db         20 GAGCCAGGGGGGAGCAGGG 2


RESULT 2747
AAV67330/c
ID   AAV67330 standard; DNA; 21 BP.
XX
AC   AAV67330;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide fragment containing polymorphic site, WI-10681 (i).
XX
KW   ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW   cancer; inflammation; heart disease; CNS disease.
XX
OS   Homo sapiens.
XX
PN   WO9838846-A2.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;   98WO-US004571.
XX
PR   07-MAR-1997;   97US-00813159.
PR   28-MAR-1997;   97US-0042125P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
```

```
PI   Lipshutz RJ,  Chee M,  Fan J,  Berno A;
XX
DR   WPI; 1998-495419/42.
XX
PT   New nucleic acid segments containing polymorphic sites, or complements
PT   and methods of detecting a nucleic acid - for general use including
PT   diagnosis and monitoring of diseases.
XX
PS   Claim 1; Page 8; 42pp; English.
XX
CC   New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC   given in the specification (sequences of a polymorphic site), or the
CC   complement of the segment and a method of analysing a nucleic acid
CC   comprising determining the base occupying the polymorphic site of the
CC   polymorphic fragment sequences are disclosed in the specification. The
CC   information obtained from nucleic acid analysis by the method described
CC   is useful in diagnosis or monitoring of diseases like cancer,
CC   inflammation, heart disease, CNS diseases, and susceptibility to
CC   infection by microorganisms. In addition, the nucleic acid segments are
CC   useful in manufacturing medication in the treatment of prophylaxis of
CC   diseases, and also the use of the DNA segments as pharmaceutical
XX
SQ   Sequence 21 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2397 TATGCGTAATTTAATGGGGTC 2417
              | ||||||| : |||||||||
Db         21 TTTGCGTAAGWCAATGGGGTC 1


RESULT 2748
AAZ18450/c
ID   AAZ18450 standard; DNA; 21 BP.
XX
AC   AAZ18450;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Polymorphic fragment in region 5' to ASTH1I.
XX
KW   ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTHIJ; genetic locus;
KW   therapeutic; immunogen; polymorphism; ss.
XX
OS   Homo sapiens.
XX
PN   WO9937809-A1.
XX
PD   29-JUL-1999.
XX
PF   21-JAN-1998;   98WO-US001260.
XX
PR   21-JAN-1998;   98WO-US001260.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Brooks-Wilson AR,  Buckler A,  Cardon L,  Carey AH,  Galvin M;
PI   Miller A,  North M;
XX
DR   WPI; 1999-479058/40.
XX
PT   Mammalian asthma related genes, useful for diagnosis of a predisposition
PT   to development of asthma.
XX
PS   Disclosure; Page 63; 195pp; English.
XX
CC   The invention identifies a genetic locus ASTH1, associated with asthma,
CC   mapped to human chromosome 11p. ASTH1I and ASTHIJ are genes present
CC   within the locus, located close to each other on human chromosome 11p,
CC   and have similar patterns of expression, and common sequence motifs. The
CC   ASTH1 genes and fragments, encoded protein, genomic regulatory regions
CC   and anti-ASTH1 antibodies are useful in the identification of individuals
CC   predisposed to development of asthma, and for the modulation of gene
CC   activity in vivo for prophylactic and therapeutic purposes. The ASTH1
CC   protein is useful as an immunogen to raise specific antibodies, in drug
CC   screening for compositions that mimic or modulate ASTH1 activity or
CC   expression, including altered forms of ASTH1 protein, and as a
CC   therapeutic. Sequences AAZ18366-Z18509 represent polymorphisms in the
CC   ASTH1I and ASTH1J genes
XX
SQ   Sequence 21 BP; 8 A; 0 C; 2 G; 10 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1968 TATTTACCTTGAAAAAAAGA 1987
              ||||| |||| ||||||| |
Db         21 TATTTTCCTTNAAAAAAAAA 2


RESULT 2749
AAZ58827/c
ID   AAZ58827 standard; DNA; 21 BP.
XX
AC   AAZ58827;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human MUC12 gene specific primer MUC12F1.
XX
KW   Mucin; MUC11; MUC12; human; chromosome 7q22; epithelial inflammation;
KW   Crohn's disease; ulcerative colitis; asthma; chronic bronchitis;
KW   colorectal cancer; cystic fibrosis; inflammatory bowel disease;
KW   breast cancer; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004142-A1.
XX
PD   27-JAN-2000.
XX
PF   16-JUL-1999;   99WO-AU000579.
XX
PR   16-JUL-1998;   98AU-00004708.
XX
PA   (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA   (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX
PI   Williams SJ,  Antalis TM,  Mcguckin MA,  Gotley DC;
XX
DR   WPI; 2000-182416/16.
XX
PT   Novel MUC nucleic acid corresponding to mucin gene, useful for treating
PT   associated disease conditions e.g. colorectal, breast cancer, cystic
PT   fibrosis and inflammatory bowel disease.
XX
PS   Claim 21; Page 39; 103pp; English.
XX
CC   The invention provides mucin genes (MUC11 and MUC12) located on human
CC   chromosome 7q22. The mucin genes or its portion is used in detecting
CC   polymorphism, mutation, deletion, truncation and expansion in the gene or
CC   its gene transcript. Pharmaceutical compositions and gene therapy
CC   constructs comprising the mucin genes are used for treating disease
CC   conditions associated with aberrant Mucin expression, altered properties
CC   of mucus or epithelial inflammatory processes involving Mucins like
CC   Crohn's disease, ulcerative colitis, asthma, chronic bronchitis and
CC   colorectal cancer, cystic fibrosis, inflammatory bowel disease and breast
CC   cancer. The mucin genes and the polypeptides are used for determining
CC   these diseases or their predisposition. The MUC11 and MUC12 polypeptides
CC   are used for preparing antagonist and antibodies. Sequences AAZ58827-32
CC   represent human MUC11 and MUC12 gene specific primers
XX
SQ   Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        851 GGAAGATTGTCGCTCCTCA 869
              ||||||||||||| | |||
Db         19 GGAAGATTGTCGCCCTTCA 1


RESULT 2750
AAZ44349
ID   AAZ44349 standard; DNA; 21 BP.
XX
AC   AAZ44349;
XX
DT   04-APR-2000  (first entry)
XX
DE   Protein kinase inhibiting primer #11.
XX
KW   Antimicrobial; cytostatic; immunosuppressive; protein kinase;
KW   prophylactic; therapy; treatment; cancer; autoimmune disease;
KW   pathogenic microorganism; primer; ss.
XX
OS   Unidentified.
XX
PN   US5998596-A.
XX
PD   07-DEC-1999.
XX
PF   04-APR-1995;   95US-00416214.
XX
PR   04-APR-1995;   95US-00416214.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Bergan R,  Neckers L;
XX
DR   WPI; 2000-104623/09.
XX
PT   Oligonucleotides inhibiting protein kinase, useful for treating diseases
PT   such as cancer and autoimmune disease.
XX
PS   Example 3; Col 27-28; 26pp; English.
XX
CC   This invention describes novel purified aptameric oligonucleotides which
CC   have antimicrobial, cytostatic and immunosuppressive activity. The
CC   oligonucleotides are useful for binding to and preventing or inhibiting
CC   the biological function of a protein kinase or a target molecule and for
CC   detecting the presence or absence of a target molecule in biological
CC   samples. The oligonucleotides are also useful for prophylactic and
CC   therapeutic treatment of diseases such as cancer, autoimmune diseases and
CC   diseases caused by pathogenic microorganisms. This sequence represents a
CC   primer used in the method of the invention
XX
SQ   Sequence 21 BP; 0 A; 7 C; 14 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          2 GCGGCGGCGGCGGCGGCGG 20


RESULT 2751
AAF95374
ID   AAF95374 standard; DNA; 21 BP.
XX
AC   AAF95374;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #135.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 57; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 5 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        643 GGGCCTGGCCGAGAACCTG 661
              | ||||||||| ||||||
Db          2 GAGCCTGGCCGACAACCTG 20


RESULT 2752
AAH91825
ID   AAH91825 standard; DNA; 21 BP.
XX
AC   AAH91825;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human inflammatory bowel disease associated polymorphic site #900.
XX
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
```

KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 11
FT /*tag= a
FT /note= "SNP, optionally T or A at this position"
XX
PN WO200142511-A2.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033632.
XX
PR 10-DEC-1999; 99US-0170257P.
PR 10-APR-2000; 2000US-0196046P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
DR WPI; 2001-367874/38.
XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
PS Claim 1; Page 76; 463pp; English.
XX
CC The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention
XX
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2156 TTTTTTCTCCTTTTTTTTTT 2175
|| ||| || ||||||||||
Db 2 TTCTTTATCNTTTTTTTTTT 21

RESULT 2753
AAF75035/c
ID AAF75035 standard; DNA; 21 BP.
XX
AC AAF75035;
XX
DT 08-MAY-2001 (first entry)
XX
DE Primer #7.
XX
KW 5-hydroxy tryptamine receptor 1A; HTR1A; polymorphism; Tourette's;
KW neuropsychiatric; ss.
XX
OS Homo sapiens.
XX
PN WO200110884-A1.
XX
PD 15-FEB-2001.
XX
PF 01-AUG-2000; 2000WO-US040519.
XX
PR 06-AUG-1999; 99US-0147711P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Kliem SE, Nandabalan K, Stephens JC;
XX
DR WPI; 2001-191514/19.
XX
PT New 5-hydroxy tryptamine receptor 1A gene variants for studying
PT expression and biological function of the gene and for developing drugs
PT targeting 5-hydroxy tryptamine receptor 1A protein.
XX
PS Example 1; Page 32; 64pp; English.
XX
CC The present invention relates to 5-hydroxy tryptamine receptor 1A (HTR1A)
CC gene. HTR1A-encoding polynucleotides containing one or more of the novel
CC polymorphic sites are useful in studying the expression and biological
CC function of HTR1A, as well as in developing drugs targeting this protein.
CC In addition, information on the combinations of polymorphisms in the
CC HTR1A gene may have diagnostic and forensic applications. A polymorphic
CC variant of HTR1A is useful in studying the effect of the variation on the
CC biological activity of HTR1A as well as studying the binding affinity of
CC candidate drugs targeting HTR1A for the treatment of neuropsychiatric
CC diseases and Tourette's syndrome
XX
SQ Sequence 21 BP; 3 A; 9 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 682 CCAGATGGACGAGGTGCAG 700
| ||||||| |||||||||
Db 20 CAAGATGGATGAGGTGCAG 2

RESULT 2754
ABK99279/c
ID ABK99279 standard; RNA; 21 BP.
XX
AC ABK99279;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #9.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C

```
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 21 BP; 0 A; 14 C; 7 G; 0 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db         20 GCGGCGGCGGCGGCGGCGG 2


RESULT 2755
ABS98381
ID   ABS98381 standard; DNA; 21 BP.
XX
AC   ABS98381;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human multidrug resistance associated protein 3 polymorphic sequence #3.
XX
KW   Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 24; Page 152; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   polymorphic DNA sequence of the invention
XX
SQ   Sequence 21 BP; 7 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 21;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        979 GAAAAATGGAGGCCGGTCC 997
              || |||||||||| |||||
Db          1 GAGAAATGGAGGCAGGTCC 19


RESULT 2756
ABS66998
ID   ABS66998 standard; DNA; 21 BP.
XX
AC   ABS66998;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human MRP-1 polymorphic DNA region #260.
XX
KW   Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW   renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
```

PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 9; Page 84; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 3 A; 15 C; 2 G; 0 T; 0 U; 1 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 289 CCCCGCGCCACCCCTCTCCCA 309
||||||||||:||| ||||
Db 1 CCCCGCGCCAYCCCCACCCCA 21

RESULT 2757
ABS66997/c
ID ABS66997 standard; DNA; 21 BP.
XX
AC ABS66997;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #259.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Example 9; Page 84; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 0 A; 2 C; 15 G; 3 T; 0 U; 1 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 289 CCCCGCGCCACCCCTCTCCCA 309
||||||||||:||| ||||
Db 21 CCCCGCGCCAYCCCCACCCCA 1

RESULT 2758
AAF98936/c
ID AAF98936 standard; DNA; 22 BP.
XX
AC AAF98936;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #52.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Disclosure; Page 39; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

```
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         22 AAAAACAAAAAAACAAAAA 4


RESULT 2759
ABS77577/c
ID   ABS77577 standard; DNA; 22 BP.
XX
AC   ABS77577;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #61.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 20; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         22 AAAAACAAAAAAACAAAAA 4


RESULT 2760
ACD99369/c
ID   ACD99369 standard; DNA; 22 BP.
XX
AC   ACD99369;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #55.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 10; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         22 AAAAACAAAAAAACAAAAA 4


RESULT 2761
ADB36438/c
ID   ADB36438 standard; DNA; 22 BP.
XX
```

```
AC   ADB36438;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #52.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Claim 10; Page 6; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||| |||||
Db         22 AAAAACAAAAAAACAAAAA 4


RESULT 2762
ABV74140/c
ID   ABV74140 standard; DNA; 22 BP.
XX
AC   ABV74140;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of an oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 22;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||||
Db         19 TGTCAAAAAAAAAAAAAAA 1


RESULT 2763
AAA66932
ID   AAA66932 standard; DNA; 22 BP.
XX
AC   AAA66932;
XX
DT   09-OCT-2000  (first entry)
XX
DE   Dog genomic marker oligonucleotide sequence SEQ ID NO:794.
XX
KW   Dog; genome; genomic marker; radiation hybrid map; identification;
KW   chromosome location; gene marker; polymorphic microsatellite marker;
KW   phenotype; behaviour; pedigree; ss.
```

XX
OS Canis familiaris.
XX
PN WO200029615-A2.
XX
PD 25-MAY-2000.
XX
PF 15-NOV-1999; 99WO-IB001907.
XX
PR 13-NOV-1998; 98US-0108193P.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Galibert F, Andre C;
XX
DR WPI; 2000-387821/33.
XX
PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral traits
PT or in genetic diseases and for studying dog pedigrees.
XX
PS Claim 1; Page 87; 87pp; English.
XX
CC The present invention describes a radiation hybrid map of the dog (Canine
CC familiaris) genome comprising the genome location of a marker selected
CC from AAA66139 to AAA66942. The radiation hybrid map is useful for
CC identifying and localising dog genes, since it covers approximately 80 %
CC of the dog genome and provides a dense map integrating different types
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC (or complementary sequences) are especially useful to identify genes
CC responsible for phenotypic and behavioural traits in dogs, to identify
CC morbid genes, to analyse diseases and identify implicated genes in such
CC diseases and their alleles, and to study dog pedigrees. They may also be
CC useful for isolating corresponding human gene sequences e.g. genes
CC involved in genetic diseases
XX
SQ Sequence 22 BP; 4 A; 8 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 777 CTCTGAACCTCCCCTGTCA 795
||||||| ||| |||||||
Db 4 CTCTGAAACTCTCCTGTCA 22

RESULT 2764
ABL35690
ID ABL35690 standard; DNA; 22 BP.
XX
AC ABL35690;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 616.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .22
FT /*tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
PN WO200193902-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018276.
XX
PR 07-JUN-2000; 2000US-0209797P.
XX
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Klinman DM;
XX
DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 63; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 22 BP; 0 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2156 TTTTTTCTCCTTTTTTTTT 2174
||| ||||| |||||||||
Db 4 TTTGTTCTCTTTTTTTTTT 22

RESULT 2765
ABV74138
ID ABV74138 standard; DNA; 23 BP.
XX
AC ABV74138;
XX
DT 23-JAN-2003 (first entry)
XX
DE 5' End of cDNA library clone.
XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; arometic; pesticide; mosquito; ss.
XX
OS Aedes aegypti.
XX
PN WO200277200-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009559.
XX
PR 27-MAR-2001; 2001US-0279168P.
PR 31-JAN-2002; 2002US-0353392P.
XX
PA (INSC-) INSCENT INC.
XX
PI Woods D, Dimitratos S;
XX

```
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of the 5' end of a cDNA clone isolated from
CC   a mosquito antenna cDNA library. The clone was isolated using a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides (see ABV74137) with a 5' polylinker, a
CC   poly-T run capable of binding cDNAs by their poly-A tail and a unique 3'
CC   sequence, which allows an anchored oligonucleotide in each well to
CC   selectively hybridise only to those cDNA clones with a complementary 5'
CC   end. The unique 3' key sequences are designed to give a comprehensive
CC   level of degeneracy since they are diverse and numerous enough to ensure
CC   that every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 23 BP; 16 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||||
Db          5 TGTCAAAAAAAAAAAAAAA 23


RESULT 2766
ABV74139/c
ID   ABV74139 standard; DNA; 23 BP.
XX
AC   ABV74139;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of an oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 23 BP; 2 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ||  ||||||||||||||||
Db         19 TGTCAAAAAAAAAAAAAAA 1


RESULT 2767
AAT60786
ID   AAT60786 standard; DNA; 23 BP.
XX
AC   AAT60786;
XX
DT   28-OCT-1997  (first entry)
XX
DE   Subtelomeric primer XpJCTN for measuring telomere length.
XX
KW   Telomere; hybridisation; cell turnover; tumour; osteoarthritis;
KW   alpha-thalassaemia; liver cirrhosis; muscular dystrophy; atherosclerosis;
KW   Hutchison-Gifford progeria; Down's syndrome; cardiovascular disease;
```

```
KW   HIV infection; fertility; PCR; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9641016-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US010035.
XX
PR   07-JUN-1995;   95US-00479916.
XX
PA   (GERO-) GERON CORP.
XX
PI   Kozlowski MR,  Prowse KR,  Wang S,  Wong S,  Kim NW;
XX
DR   WPI; 1997-108648/10.
XX
PT   Measuring telomere length - by forming primer extension prods.
PT   complementary to telomere, or by hybridisation with complementary
PT   labelled probe.
XX
PS   Disclosure; Page 19; 64pp; English.
XX
CC   A method for measuring telomere length has been produced which involves:
CC   (a) covalently attaching an oligonucleotide linker to a telomere; (b)
CC   contacting a primer comprising a sequence sufficiently complementary to
CC   the linker to hybridise specifically under conditions so that the primer
CC   extends to form a primer extension product complementary to the telomere;
CC   and (c) correlating telomere length with primer extension product size,
CC   to provide a measure of telomere length. The present sequence represents
CC   a subtelomeric primer XpJCTN used in this invention. As telomere length
CC   serves as a biomarker for cell turnover, determination of telomere length
CC   can be used to diagnose and stage diseases and conditions such as
CC   tumours, alpha-thalassaemia, liver cirrhosis, muscular dystrophy,
CC   osteoarthritis, Hutchison-Gifford progeria, Down's syndrome,
CC   atherosclerosis, cardiovascular disease, HIV infection and fertility
CC   problems. The methods can also be used to monitor the effectiveness of
CC   various therapeutics in expanding, and/or reducing the proliferative
CC   lifespan of cells. The methods are conducive to high throughput or
CC   automated processes, provide for intracellular and intracellular telomere
CC   length determination and comparison and for the separation of cells or
CC   chromosomes based on telomere length
XX
SQ   Sequence 23 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTATAAG 1820
              ||||||||||||  |:|| ||
Db          3 CTCTGAAAGTGGACCWATCAG 23


RESULT 2768
AAT60790/c
ID   AAT60790 standard; DNA; 23 BP.
XX
AC   AAT60790;
XX
DT   28-OCT-1997  (first entry)
XX
DE   Subtelomeric primer revXpJCTN for measuring telomere length.
XX
KW   Telomere; hybridisation; cell turnover; tumour; osteoarthritis;
KW   alpha-thalassaemia; liver cirrhosis; muscular dystrophy; atherosclerosis;
KW   Hutchison-Gifford progeria; Down's syndrome; cardiovascular disease;
KW   HIV infection; fertility; PCR; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9641016-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US010035.
XX
PR   07-JUN-1995;   95US-00479916.
XX
PA   (GERO-) GERON CORP.
XX
PI   Kozlowski MR,  Prowse KR,  Wang S,  Wong S,  Kim NW;
XX
DR   WPI; 1997-108648/10.
XX
PT   Measuring telomere length - by forming primer extension prods.
PT   complementary to telomere, or by hybridisation with complementary
PT   labelled probe.
XX
PS   Disclosure; Page 19; 64pp; English.
XX
CC   A method for measuring telomere length has been produced which involves:
CC   (a) covalently attaching an oligonucleotide linker to a telomere; (b)
CC   contacting a primer comprising a sequence sufficiently complementary to
CC   the linker to hybridise specifically under conditions so that the primer
CC   extends to form a primer extension product complementary to the telomere;
CC   and (c) correlating telomere length with primer extension product size,
CC   to provide a measure of telomere length. The present sequence represents
CC   a subtelomeric primer revXpJCTN used in this invention. As telomere
CC   length serves as a biomarker for cell turnover, determination of telomere
CC   length can be used to diagnose and stage diseases and conditions such as
CC   tumours, alpha-thalassaemia, liver cirrhosis, muscular dystrophy,
CC   osteoarthritis, Hutchison-Gifford progeria, Down's syndrome,
CC   atherosclerosis, cardiovascular disease, HIV infection and fertility
CC   problems. The methods can also be used to monitor the effectiveness of
CC   various therapeutics in expanding, and/or reducing the proliferative
CC   lifespan of cells. The methods are conducive to high throughput or
CC   automated processes, provide for intracellular and intracellular telomere
CC   length determination and comparison and for the separation of cells or
CC   chromosomes based on telomere length
XX
SQ   Sequence 23 BP; 4 A; 5 C; 7 G; 6 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTATAAG 1820
              ||||||||||||  |:|| ||
Db          21 CTCTGAAAGTGGACCWATCAG 1


RESULT 2769
AAV62118/c
ID   AAV62118 standard; DNA; 23 BP.
XX
AC   AAV62118;
XX
DT   15-JAN-1999  (first entry)
XX
DE   Telomere length analysis primer #7.
XX
KW   Telomere; primer; cell turnover; proliferative capacity; diagnosis;
KW   prognosis; cancer, cell senescence; disease; liver cirrhosis; modulator;
KW   muscular dystrophy: osteoporosis; wound healing; fertility; treatment;
KW   chemotherapy; ss.
XX
OS   Synthetic.
XX
PN   US5834193-A.
XX
PD   10-NOV-1998.
XX
PF   07-JUN-1996;   96US-00660402.
XX
```

```
PR   07-JUN-1995;   95US-00479916.
XX
PA   (GERO-) GERON CORP.
XX
PI   Kozlowski MR,  Kim NW,  Wang S,  Allsopp R,  Prowse KR,  Wong S;
XX
DR   WPI; 1999-008698/01.
XX
PT   Determining telomere length by hybridisation of chromosomal DNA with
PT   labelled probe - useful for assessing age and proliferative status of
PT   cells, e.g. for diagnosis and prognosis of cancer and in cell senescence.
XX
PS   Disclosure; Col 11; 23pp; English.
XX
CC   AAV62112-V62122 are primers used in a novel method to determine telomere
CC   length. The method involves treating denatured chromosomal DNA, that has
CC   not been fractionated by gel electrophoresis, with a labelled probe
CC   complementary to a telomere repeat sequence. The amount of bound probe
CC   can be correlated with the telomere length, by comparison with results
CC   for a control of known length. Telomere length is a marker of cell
CC   turnover, e.g. the relative age or proliferative capacity, and its
CC   measurement is used in diagnosis, staging and prognosis of cancer, cell
CC   senescence or other diseases (e.g. liver cirrhosis, muscular dystrophy,
CC   osteoporosis, wound healing and fertility problems). Telomere length can
CC   also be used to monitor treatment with compounds that modulate telomere
CC   length, e.g. in cancer chemotherapy. The method can also be used to
CC   identify modulators of telomere length, telomerase activity or the rate
CC   of telomere loss, and to detect telomerase activity. The method is quick,
CC   with better sensitivity, efficiency, reliability and accuracy than known
CC   methods and does not require gels. The method is suitable for automation
CC   and can be applied to single chromosomes (for comparing interchromosome
CC   variations). The method allows separation of cells and/or chromosomes
CC   according to telomere length
XX
SQ   Sequence 23 BP; 4 A; 5 C; 7 G; 6 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTATAAG 1820
             ||||||||||||  |:|| ||
Db         21 CTCTGAAAGTGGACCWATCAG 1

RESULT 2770
AAV62114
ID   AAV62114 standard; DNA; 23 BP.
XX
AC   AAV62114;
XX
DT   15-JAN-1999  (first entry)
XX
DE   Telomere length analysis primer #3.
XX
KW   Telomere; primer; cell turnover; proliferative capacity; diagnosis;
KW   prognosis; cancer, cell senescence; disease; liver cirrhosis; modulator;
KW   muscular dystrophy: osteoporosis; wound healing; fertility; treatment;
KW   chemotherapy; ss.
XX
OS   Synthetic.
XX
PN   US5834193-A.
XX
PD   10-NOV-1998.
XX
PF   07-JUN-1996;   96US-00660402.
XX
PR   07-JUN-1995;   95US-00479916.
XX
PA   (GERO-) GERON CORP.
XX
PI   Kozlowski MR,  Kim NW,  Wang S,  Allsopp R,  Prowse KR,  Wong S;
XX
DR   WPI; 1999-008698/01.
XX
PT   Determining telomere length by hybridisation of chromosomal DNA with
PT   labelled probe - useful for assessing age and proliferative status of
PT   cells, e.g. for diagnosis and prognosis of cancer and in cell senescence.
XX
PS   Disclosure; Col 11; 23pp; English.
XX
CC   AAV62112-V62122 are primers used in a novel method to determine telomere
CC   length. The method involves treating denatured chromosomal DNA, that has
CC   not been fractionated by gel electrophoresis, with a labelled probe
CC   complementary to a telomere repeat sequence. The amount of bound probe
CC   can be correlated with the telomere length, by comparison with results
CC   for a control of known length. Telomere length is a marker of cell
CC   turnover, e.g. the relative age or proliferative capacity, and its
CC   measurement is used in diagnosis, staging and prognosis of cancer, cell
CC   senescence or other diseases (e.g. liver cirrhosis, muscular dystrophy,
CC   osteoporosis, wound healing and fertility problems). Telomere length can
CC   also be used to monitor treatment with compounds that modulate telomere
CC   length, e.g. in cancer chemotherapy. The method can also be used to
CC   identify modulators of telomere length, telomerase activity or the rate
CC   of telomere loss, and to detect telomerase activity. The method is quick,
CC   with better sensitivity, efficiency, reliability and accuracy than known
CC   methods and does not require gels. The method is suitable for automation
CC   and can be applied to single chromosomes (for comparing interchromosome
CC   variations). The method allows separation of cells and/or chromosomes
CC   according to telomere length
XX
SQ   Sequence 23 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 1 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   81.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTATAAG 1820
             ||||||||||||  |:|| ||
Db         3 CTCTGAAAGTGGACCWATCAG 23

RESULT 2771
AAF60331
ID   AAF60331 standard; DNA; 23 BP.
XX
AC   AAF60331;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Human liver RNA reverse transcription primer.
XX
KW   Human; endostatin; antitumour; cytostatic; antiarthritic; antipsoriatic;
KW   antidiabetic; ophthalmological; gene therapy; angiogenic inhibitor;
KW   adenoviral vector; diabetic retinopathy; cardiovascular disease;
KW   arthritis; psoriasis; cerebral oedema; intravascular coagulopathy;
KW   lymphoma; leukaemia; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200112830-A1.
XX
PD   22-FEB-2001.
XX
PF   11-AUG-2000; 2000WO-EP007865.
XX
PR   13-AUG-1999;   99US-00373938.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Hallenbeck PL,  Chen CT;
XX
DR   WPI; 2001-202871/20.
XX
```

```
PT   Adenoviral vector for treating tumors and disorders associated with
PT   angiogenesis, such as cancer, arthritis, and psoriasis, comprises a DNA
PT   sequence encoding an angiogenic inhibitor, particularly endostatin.
XX
PS   Example 4; Page 31; 59pp; English.
XX
CC   The present sequence was used in the construction of an adenoviral vector
CC   which includes a DNA sequence encoding endostatin. The adenoviral vector
CC   is useful for expressing endostatin in a mammalian cell such as an A549
CC   or Hep3B cell. It is useful for treating other diseases and disorders
CC   associated with angiogenesis, such as neovascular diseases of the eye,
CC   including diabetic retinopathy, cardiovascular disease, arthritis,
CC   psoriasis, cerebral oedema and intravascular coagulopathy (Kasabach-
CC   Merritt syndrome). The vector inhibits, prevents or destroys the growth
CC   of tumours by preventing the formation of blood vessels in tumours, such
CC   as lymphoma and leukaemia
XX
SQ   Sequence 23 BP; 5 A; 2 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTTAAGG 1940
              ||||||||||||||| || |
Db          2 TTTTTTTTCAGTGTAAAAG 20


RESULT 2772
ABQ81205
ID   ABQ81205 standard; DNA; 23 BP.
XX
AC   ABQ81205;
XX
DT   05-DEC-2002  (first entry)
XX
DE   Human endostatin cDNA primer.
XX
KW   Endostatin; human; ophthalmological; ocular neovascularisation;
KW   choroidal neovascularisation; gene therapy; adenovirus; vector; primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200267971-A2.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005336.
XX
PR   22-FEB-2001; 2001US-0270787P.
PR   04-APR-2001; 2001US-0281296P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Brazzell RK,  Campochiaro PA,  Dixon KH;
XX
DR   WPI; 2002-698636/75.
XX
PT   Treating or preventing choroidal neovascularization comprises increasing
PT   the amount of endostatin in ocular tissues of afflicted individuals to a
PT   choroidal neovascularization inhibiting level.
XX
PS   Example 6; Page 27; 44pp; English.
XX
CC   The present sequence is a primer that was used in the reverse
CC   transcription of human endostatin mRNA. The resulting cDNA was subjected
CC   to PCR amplification and used to generate a recombinant adenoviral vector
CC   encoding human endostatin. A claimed method for the treatment of ocular,
CC   especially choroidal, neovascularisation involves increasing the level of
CC   endostatin, especially human endostatin (see ABB79901) in ocular tissue.
CC   The increase is effected by administering a viral vector, especially an
CC   adenovirus, adeno-associated virus, a retrovirus or lentivirus vector,
CC   comprising an endostatin-encoding nucleic acid. Cells secreting
CC   endostatin may be encapsulated and implanted within an individual
XX
SQ   Sequence 23 BP; 5 A; 2 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTTAAGG 1940
              ||||||||||||||| || |
Db          2 TTTTTTTTCAGTGTAAAAG 20


RESULT 2773
ABT16546/c
ID   ABT16546 standard; DNA; 23 BP.
XX
AC   ABT16546;
XX
DT   03-APR-2003  (first entry)
XX
DE   Ethylene insensitivity related overlapping oligonucleotide SEQ ID No 20.
XX
KW   Mutant; transformed plant; ethylene-response DNA-binding factor; edf1;
KW   edf2; edf3; edf4; fruit; transgenic plant; floral industry;
KW   fruit processing industry; floral senescence; flower longevity;
KW   decreased floral initiation; post-harvest; transportation; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200289555-A2.
XX
PD   14-NOV-2002.
XX
PF   08-MAY-2002; 2002WO-US014592.
XX
PR   08-MAY-2001; 2001US-0289364P.
PR   08-MAY-2001; 2001US-0289835P.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Stepanova AN,  Ecker JR;
XX
DR   WPI; 2003-120491/11.
XX
PT   Novel mutant or transformed plant comprising mutated forms of edf1, edf2,
PT   edf3 and edf4 genes, and having decreased ethylene sensitivity, such that
PT   its fruit ripens more slowly than wild-type version of the plant.
XX
PS   Disclosure; Page 34; 85pp; English.
XX
CC   The invention relates to a mutant or transformed plant comprising mutated
CC   forms of ethylene-response DNA-binding factors (edf)1, edf2, edf3 and
CC   edf4 genes such that the plant exhibits a decreased response to ethylene,
CC   and comprises fruit which ripens more slowly than a wild-type version of
CC   the plant. The transgenic plants having reduced sensitivity to ethylene
CC   are useful for floral industry and fruit processing industries. Since
CC   ethylene is involved in floral senescence, the modified plants have
CC   longer flower longevity. The modified plants e.g. lettuce, spinach, other
CC   leafy vegetables provide higher yields due to decreased floral
CC   initiation, since the transformed plants do not bolt or flower easily.
CC   The plants provide fruits which ripens more slowly than the wild-type
CC   version of the plant, and thus are advantageous in post-harvest and
CC   transportation conditions. This polynucleotide sequence represents an
CC   overlapping oligonucleotide relating to the ethylene sensitivity
CC   modulation of the invention
XX
SQ   Sequence 23 BP; 5 A; 8 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 2.9e+03;
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```
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        117 GGGGGGATCCTGGATTTAA 135
              ||||||||  |||  ||||||
Db         19 GGGGGGATGCTGAATTTAA 1


RESULT 2774
AAF98935/c
ID   AAF98935 standard; DNA; 24 BP.
XX
AC   AAF98935;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #51.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Disclosure; Page 39; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||  |||||||  |||||
Db         24 AAAAACAAAAAAACAAAAA 6


RESULT 2775
ABS77576/c
ID   ABS77576 standard; DNA; 24 BP.
XX
AC   ABS77576;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #60.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 20; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||  |||||||  |||||
Db         24 AAAAACAAAAAAACAAAAA 6


RESULT 2776
ACD99368/c
ID   ACD99368 standard; DNA; 24 BP.
XX
AC   ACD99368;
XX
DT   25-SEP-2003  (first entry)
XX
```

DE Immunostimulatory nucleic acid #54.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 10; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||| ||||||| |||||
Db 24 AAAAACAAAAAAACAAAAA 6

RESULT 2777
ADB36437/c
ID ADB36437 standard; DNA; 24 BP.
XX
AC ADB36437;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #51.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 6; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||| ||||||| |||||
Db 24 AAAAACAAAAAAACAAAAA 6

RESULT 2778
ABV74853
ID ABV74853 standard; DNA; 24 BP.
XX
AC ABV74853;
XX
DT 05-FEB-2003 (first entry)
XX
DE Protein 16.17 PCR primer #2.
XX
KW Protein 16.17; colipase; cancer; HIV infection; cytostatic; anti-HIV;
KW PCR; primer; ss.
XX
OS Unidentified.
XX
PN CN1351027-A.
XX
PD 29-MAY-2002.
XX
PF 26-OCT-2000; 2000CN-00125840.
XX
PR 26-OCT-2000; 2000CN-00125840.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-619851/67.
XX
PT New polypeptide-protein 16.17 containing colipase characteristics for
PT treating diseases such as cancer and human immunodeficiency virus
PT infection.
XX
PS Example 3; Page 26 (Disclosure); 31pp; Chinese.
XX
CC The present invention relates to protein 16.17 (see ABB98830), which
CC contains colipase characteristics. The protein and its coding sequence
CC are useful for treating diseases such as cancer and HIV infection. The
CC present sequence is a PCR primer, which was used in an example from the
CC invention. Note: The present sequence, SEQ ID 4, shown in the sequence
CC listing differs from the SEQ ID 4 shown in the disclosure (see ABV74866)
XX

```
SQ   Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              | ||||||||||||||| ||
Db          2 TGTTTTTTTTTTTTTTGTA 20


RESULT 2779
AAX75929/c
ID   AAX75929 standard; DNA; 24 BP.
XX
AC   AAX75929;
XX
DT   29-JUL-1999  (first entry)
XX
DE   Human interleukin 1 PCR primer SEQ ID NO:14.
XX
KW   Human; interleukin 1; IL-1B; IL-1A; IL-1RN; diagnosis; detection;
KW   chronic obstructive airway disease; chronic bronchitis; emphysema;
KW   asthma; chronic bronchiolitis; proinflammatory haplotype; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9924615-A2.
XX
PD   20-MAY-1999.
XX
PF   09-NOV-1998;   98WO-US023721.
XX
PR   07-NOV-1997;   97GB-00023553.
PR   12-JAN-1998;   98US-00005923.
XX
PA   (MEDI-) MEDICAL SCI SYSTEMS INC.
XX
PI   Duff GW,  Giovine M,  Barnes PJ,  Lim S;
XX
DR   WPI; 1999-327420/27.
XX
PT   Genotyping nucleic acid samples for interleukin-1 (IL-1) proinflammatory
PT   haplotype alleles, useful for predicting susceptibility to developing
PT   chronic obstructive airway disease.
XX
PS   Disclosure; Page 7; 37pp; English.
XX
CC   The present invention describes genotyping a nucleic acid sample from a
CC   subject to determine at least one allele of an interleukin-1 (IL-1)
CC   proinflammatory haplotype. A method has also bee described for
CC   determining a subject's susceptibility to developing chronic obstructive
CC   airway disease (COAD) or for predicting the rapidity or ultimate
CC   progression of a COAD in the subject by: (a) obtaining a nucleic acid
CC   sample from the subject; and (b) detecting at least one allele of an IL-1
CC   proinflammatory haplotype in the sample, where detection of at least one
CC   of these alleles indicates that the patient has an increased
CC   susceptibility to developing COAD. The method is useful for determining
CC   the susceptibility of subjects to developing chronic obstructive airway
CC   disease or for predicting the rapidity or ultimate progression of chronic
CC   obstructive airway disease (COAD). COAD can be asthma, emphysema, chronic
CC   bronchitis or chronic bronchiolitis. The method provides for early
CC   identification of chronic obstructive airway disease (COAD), facilitating
CC   administration of appropriate treatment at the earliest stage, thereby
CC   increasing the probability of a positive outcome. The present sequence
CC   represents a PCR primer used in the method of the invention
XX
SQ   Sequence 24 BP; 9 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2444 CTTTTTTGAGACATGGGAT 2462
              ||| ||||| |||||||||
Db         19 CTTCTTTGACACATGGGAT 1


RESULT 2780
AAZ24999
ID   AAZ24999 standard; DNA; 24 BP.
XX
AC   AAZ24999;
XX
DT   24-DEC-1999  (first entry)
XX
DE   Sense probe to Fragile X syndrome gene.
XX
KW   Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
KW   in situ hybridisation; detection; expansion; Fragile X syndrome; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5962332-A.
XX
PD   05-OCT-1999.
XX
PF   11-DEC-1995;   95US-00570155.
XX
PR   17-MAR-1994;   94US-00214823.
PR   07-MAR-1995;   95US-00399499.
XX
PA   (UYMA-) UNIV MASSACHUSETTS.
XX
PI   Taneja KL,  Singer RH;
XX
DR   WPI; 1999-579615/49.
XX
PT   Detection of trinucleotide repeats.
XX
PS   Disclosure; Col 20; 18pp; English.
XX
CC   This oligonucleotides is targeted to the CGG trinucleotide repeats found
CC   in the FMR1 gene. Excessive numbers of the trinucleotide repeats in the
CC   FMR1 gene leads to the disease Fragile X syndrome. This sequence is used
CC   as a sense oligonucleotide control probe for the hybridisation reaction.
CC   The invention relates to a method for the detection of trinucleotide
CC   repeat expansion, e.g. in the FMR1 gene or Mt-PK gene (leading to
CC   myotonic dystrophy) by in situ hybridization
XX
SQ   Sequence 24 BP; 0 A; 6 C; 14 G; 2 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          4 GCGGCGGCGGCGGCGGCGG 22


RESULT 2781
AAZ24998/c
ID   AAZ24998 standard; DNA; 24 BP.
XX
AC   AAZ24998;
XX
DT   24-DEC-1999  (first entry)
XX
DE   Antisense probe to Fragile X syndrome gene.
XX
KW   Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
KW   in situ hybridisation; detection; expansion; Fragile X syndrome; ss.
XX
```

OS Synthetic.
OS Homo sapiens.
XX
PN US5962332-A.
XX
PD 05-OCT-1999.
XX
PF 11-DEC-1995; 95US-00570155.
XX
PR 17-MAR-1994; 94US-00214823.
PR 07-MAR-1995; 95US-00399499.
XX
PA (UYMA-) UNIV MASSACHUSETTS.
XX
PI Taneja KL, Singer RH;
XX
DR WPI; 1999-579615/49.
XX
PT Detection of trinucleotide repeats.
XX
PS Disclosure; Col 20; 18pp; English.
XX
CC This oligonucleotides is targeted to the CGG trinucleotide repeats found
CC in the FMR1 gene. Excessive numbers of the trinucleotide repeats in the
CC FMR1 gene leads to the disease Fragile X syndrome. This sequence is used
CC as an antisense oligonucleotide probe for the hybridisation reaction. The
CC invention relates to a method for the detection of trinucleotide repeat
CC expansion, e.g. in the FMR1 gene or Mt-PK gene (leading to myotonic
CC dystrophy) by in situ hybridization
XX
SQ Sequence 24 BP; 0 A; 14 C; 6 G; 2 T; 0 U; 2 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGCAG 69
||||||| ||||||||| |
Db 21 GCGGCGGCGGCGGCGGCGG 3

RESULT 2782
AAZ95163/c
ID AAZ95163 standard; DNA; 24 BP.
XX
AC AAZ95163;
XX
DT 05-JUN-2000 (first entry)
XX
DE Forward primer #9 used to sequence UGT2B7 polymorphic fragments.
XX
KW UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KW drug interaction; detect; human; single nucleotide polymorphism; primer;
KW ss.
XX
OS Synthetic.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US016675.
XX
PR 28-JUL-1998; 98US-0094391P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions.
XX
PS Example 2; Page 22; 72pp; English.
XX
CC This sequence represents a primer used to sequence polymorphic fragments
CC of the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene. UDP-
CC glucuronosyltransferases (UGTs) are a family of enzymes that catalyse the
CC glucuronic acid conjugation of a wide range of endogenous and exogenous
CC substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms
CC in the liver. Alteration of the expression or function of UGTs may effect
CC drug metabolism. The invention relates to non-chromosomal nucleic acid
CC molecules, which comprise human UGT2B sequence polymorphisms (see
CC AAZ95051-Z95110). Probes which detect the UGT2B locus polymorphisms can
CC be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines
XX
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2153 GATTTTTTTCTCCTTTTTT 2171
||||||||| || ||||||
Db 19 GATTTTTTTTTCTTTTTTT 1

RESULT 2783
AAC96274
ID AAC96274 standard; DNA; 24 BP.
XX
AC AAC96274;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #6.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of

```
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 24 BP; 4 A; 3 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTAACTACGA 19


RESULT 2784
AAC61624
ID   AAC61624 standard; DNA; 24 BP.
XX
AC   AAC61624;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Reporter probe for human interleukin 1beta gene allele T.
XX
KW   Human; interleukin 1beta; bioelectronic microchip;
KW   single nucleotide polymorphism; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058522-A1.
XX
PD   05-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-US008617.
XX
PR   30-MAR-1999;   99US-0126865P.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Giles PN,  Dillon PJ,  Wu DJ,  Foster CB,  Chanock SJ;
XX
DR   WPI; 2000-638354/61.
XX
PT   Detecting single nucleotide polymorphism by utilizing a bioelectronic
PT   microchip having several test sites.
XX
PS   Example 2; Page 16; 46pp; English.
XX
CC   Reporter probes AAC61623-26 were used to discriminate between different
CC   alleles of the human interleukin 1beta (IL-1beta) gene. The method of the
CC   invention was used for detecting single nucleotide polymorphisms (SNPs)
CC   in the IL-1beta gene. The method utilises electronic circuitry on silicon
CC   microchips. The method provides accurate discrimination of amplified DNA
CC   samples following electronic transport, concentration, and attachment of
CC   DNA to selected electrodes (test sites). The test sites make up organised
CC   arrays of samples that are distinguished by using internal controls of
CC   dual labelled reporters comprising wild type and mismatched sequences to
CC   validate the SNP genotype. Multiples of SNPs in target nucleic acids from
CC   a patient sample source or a SNP in target nucleic acids of multiple
CC   patient sample sources can also be detected using the electronically
CC   addressable microchip
XX
SQ   Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2444 CTTTTTTGAGACATGGGAT 2462
                 ||| ||||| |||||||||
Db          2 CTTCTTTGACACATGGGAT 20


RESULT 2785
ABA04964
ID   ABA04964 standard; DNA; 24 BP.
XX
AC   ABA04964;
XX
DT   01-MAR-2002  (first entry)
XX
DE   Human FD14 PCR primer #1.
XX
KW   Human; FD14; tumour; embryo maldevelopment; tissue; cytostatic;
KW   immunodeficiency disease; immune disease; immunomodulatory; gene therapy;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1312286-A.
XX
PD   12-SEP-2001.
XX
PF   07-MAR-2000; 2000CN-00111937.
XX
PR   07-MAR-2000; 2000CN-00111937.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-018504/03.
XX
PT   Human FD14 polypeptides and polynucleotides encoding it.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The present invention relates to human FD14 (AAM47799). FD14 and its
CC   coding sequence are useful for treating several diseases, such as
CC   malignant tumours, embryo and tissue maldevelopment, immunodeficiency
CC   diseases, various acquired and hereditary disease and immune disease. The
CC   present sequence is a PCR primer, which was used in an example from the
CC   present invention
XX
SQ   Sequence 24 BP; 0 A; 6 C; 16 G; 2 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||||||||| |
Db          6 GCGGCGGCGGCGGCGGCTG 24


RESULT 2786
AAD46030/c
ID   AAD46030 standard; DNA; 24 BP.
XX
AC   AAD46030;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human UGT2B7 DNA sequencing forward primer #9.
XX
KW   Human; UDP-glucoronosyl transferase; UGT; UGT2B7; toxicity; cancer;
KW   therapy; epirubicin; cytostatic; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200259375-A2.
XX
```

PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002083.
XX
PR 26-JAN-2001; 2001US-0264534P.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Ratain MJ, Innocenti F, Das S, Iyer L, Sawyer M;
XX
DR WPI; 2002-691534/74.
XX
PT Determining the dose of a UGT2B7-glucuronidated drug for treating cancer,
PT comprises determining the level of UGT2B7 activity or expression in a
PT patient.
XX
PS Disclosure; Page 53; 160pp; English.
XX
CC The invention relates to an UDP-glucoronosyl transferase (UGT) enzyme,
CC UGT2B7. The invention also relates to compositions and methods for
CC optimising UGT2B7 substrate dosings and for predicting UGT2B7 substrate
CC toxicity. The method is useful in determining the dose of a UGT2B7-
CC glucuronidated drug that may be used in treating cancer patients. It is
CC also useful in determining persons at risk for epirubicin toxicity, in
CC reducing or eliminating side effects associated with epirubicin
CC treatment, and in ways of increasing the efficacy of dosage regimens. The
CC present sequence is a primer used for sequencing human UGT2B7 DNA
XX
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2153 GATTTTTTTCTCCTTTTTT 2171
||||||||| || ||||||
Db 19 GATTTTTTTTTCTTTTTTT 1

RESULT 2787
ABK53197/c
ID ABK53197 standard; DNA; 24 BP.
XX
AC ABK53197;
XX
DT 12-AUG-2002 (first entry)
XX
DE Bacillus subtilis carboxymethyl cellulase (CMCase) 3' PCR primer.
XX
KW Spore coat protein; spore surface; delivery system; bioconversion;
KW recombinant live vaccine; resistance property; protein microarray;
KW whole cell absorber; secretion signal; target signal; cell membrane;
KW surface display motif; carboxymethyl cellulase; CMCase; PCR; primer; ss.
XX
OS Bacillus subtilis.
XX
PN WO200246388-A1.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-KR002124.
XX
PR 08-DEC-2000; 2000KR-00074835.
XX
PA (GENO-) GENOFOCUS CO LTD.
XX
PI Pan J, Choi S, Jung H;
XX
DR WPI; 2002-463830/49.
XX
PT Displaying a protein of interest on spore surface, by transforming a host
PT cell with a vector comprising a gene encoding a spore coat protein and a
PT gene encoding a protein of interest, useful for preparing protein
PT microarray.
XX
PS Example 4; Page 143; 158pp; English.
XX
CC The present invention relates to a new method for displaying a protein of
CC interest on a spore surface. The method of the invention involves
CC preparing a vector comprising a gene construct containing a gene encoding
CC a spore coat protein and a gene encoding a protein of interest,
CC transforming a host cell with the vector, displaying the protein of
CC interest on a surface of a spore of the host cell, and recovering the
CC spore. The method is useful for producing a delivery system for
CC recombinant live vaccine. The method is also useful for improving a
CC protein of interest using a resistance property of spore, in
CC bioconversion reactions, for preparing protein microarray, for producing
CC an antibody to antigen in vertebrates, and for preparing a whole cell
CC absorber. The spore coat proteins used circumvent a necessity for passage
CC across cell membrane, so that they do not need secretion signal and
CC target signal which are prerequisites of surface display motif, therefore
CC ensuring a surface display of protein, such as beta-galactosidase, in
CC orderly fashion, which is difficult to pass across cell membrane. The
CC present nucleic acid sequence represents a Bacillus subtilis
CC carboxymethyl cellulase (CMCase) PCR primer that was used in the methods
CC of the invention for construction of recombinant vectors
XX
SQ Sequence 24 BP; 12 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1760 ATTCATTAAGCTTTTTTTT 1778
||| ||||||||||||||
Db 22 ATTAGTTAAGCTTTTTTTT 4

RESULT 2788
ABL60935/c
ID ABL60935 standard; DNA; 24 BP.
XX
AC ABL60935;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human nucleotide reducing enzyme 59.62 cDNA isolating primer 2.
XX
KW Nucleotide reducing enzyme 59.62; embryo development; teratogenesis;
KW blood system disease; human; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1333352-A.
XX
PD 30-JAN-2002.
XX
PF 07-JUL-2000; 2000CN-00117037.
XX
PR 07-JUL-2000; 2000CN-00117037.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-305607/35.
XX
PT Human nucleotide reducing enzyme 59.62 polypeptide and its encoding
PT polynucleotide, for treating e.g. embryo development teratogenesis.
XX
PS Example 2; Page 17 (disclosure); 34pp; Chinese.
XX
CC The invention relates to a novel human nucleotide reducing enzyme 59.62
CC polypeptide and encoding polynucleotide. The polynucleotide, polypeptide
CC and its antagonist are useful for treating e.g. embryo development
CC teratogenesis, blood system disease, and growth development disturbance

```
CC   disease. The present sequence represents the human nucleotide reducing
CC   enzyme 59.62 cDNA isolating RT-PCR primer
XX
SQ   Sequence 24 BP; 6 A; 2 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              ||||  ||||||||||||||
Db         21 TTGATTAAAAAAAAAAAAA 3


RESULT 2789
ABQ76045
ID   ABQ76045 standard; DNA; 24 BP.
XX
AC   ABQ76045;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human actin similar protein 56.43 RT-PCR primer #2.
XX
KW   Human; actin similar protein 56.43; palsy; arrhythmia; bronchial asthma;
KW   peptic ulcer; diabetes; tumour; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339501-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119737.
XX
PR   23-AUG-2000; 2000CN-00119737.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-472210/51.
XX
PT   New polypeptide-human actin similar protein 56.43 for treating periodic
PT   palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes, and tumors.
XX
PS   Example 3; Page 20 (Disclosure); 35pp; Chinese.
XX
CC   This invention describes a novel human actin similar protein 56.43,
CC   polynucleotides encoding the polypeptide and a DNA recombination process
CC   to produce the polypeptide. The present invention also discloses the
CC   method of applying the polypeptide in treating various diseases, such as
CC   periodic palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes,
CC   tumours, etc. The present invention also discloses the antagonist
CC   resisting the polypeptide and its treatment effect. This sequence
CC   represents a RT-PCR primer used in the amplification of the human actin
CC   similar protein 56.43 described in the disclosure of the invention
XX
SQ   Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              | ||||||||||||||| ||
Db          2 TGTTTTTTTTTTTTTGAA 20


RESULT 2790
ABQ76045/c
ID   ABQ76045 standard; DNA; 24 BP.
XX
AC   ABQ76045;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human actin similar protein 56.43 RT-PCR primer #2.
XX
KW   Human; actin similar protein 56.43; palsy; arrhythmia; bronchial asthma;
KW   peptic ulcer; diabetes; tumour; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339501-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119737.
XX
PR   23-AUG-2000; 2000CN-00119737.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-472210/51.
XX
PT   New polypeptide-human actin similar protein 56.43 for treating periodic
PT   palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes, and tumors.
XX
PS   Example 3; Page 20 (Disclosure); 35pp; Chinese.
XX
CC   This invention describes a novel human actin similar protein 56.43,
CC   polynucleotides encoding the polypeptide and a DNA recombination process
CC   to produce the polypeptide. The present invention also discloses the
CC   method of applying the polypeptide in treating various diseases, such as
CC   periodic palsy, arrhythmia, bronchial asthma, peptic ulcer, diabetes,
CC   tumours, etc. The present invention also discloses the antagonist
CC   resisting the polypeptide and its treatment effect. This sequence
CC   represents a RT-PCR primer used in the amplification of the human actin
CC   similar protein 56.43 described in the disclosure of the invention
XX
SQ   Sequence 24 BP; 5 A; 0 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 24;
  Best Local Similarity   89.5%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2801
              || ||||||||||||||| |
Db         20 TTCAAAAAAAAAAAAAACA 2


RESULT 2791
ABL45245
ID   ABL45245 standard; DNA; 25 BP.
XX
AC   ABL45245;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:2289.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
```

XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 49; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 25 BP; 18 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 25;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
|||| || ||||||||||||
Db 2 AAAAGAAGAAAAAAAAAAA 20

RESULT 2792
AAC96268/c
ID AAC96268 standard; DNA; 25 BP.
XX
AC AAC96268;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #25.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 0 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 25;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAA 2799
|| | ||||||||||||||||
Db 19 AACTCAAAAAAAAAAAAAA 1

RESULT 2793
AAH38199/c
ID AAH38199 standard; DNA; 25 BP.
XX
AC AAH38199;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 995.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 55; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The

```
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a single nucleotide
CC   primer extension (SNPE) primer specific for a human SNP containing DNA
CC   sequence
XX
SQ   Sequence 25 BP; 1 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||| ||||| ||||
Db         25 AAAAAAAAGAAAAAGAAAA 7


RESULT 2794
AAC95727/c
ID   AAC95727 standard; DNA; 25 BP.
XX
AC   AAC95727;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #24.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 5 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||| || ||||||||||||
Db         19 AGAGTTAAAAAAAAAAAAA 1


RESULT 2795
AAC96129/c
ID   AAC96129 standard; DNA; 25 BP.
XX
AC   AAC96129;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #96.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              | ||| ||||||||||||||
Db         19 AGTTGGAAAAAAAAAAAAA 1


RESULT 2796
AAQ98161/c
ID   AAQ98161 standard; DNA; 25 BP.
XX
AC   AAQ98161;
XX
```

DT 05-FEB-1996 (first entry)
XX
DE Hind III primer/adaptor.
XX
KW Hind III primer/adaptor; random oligonucleotide identification;
KW beta-galactosidase gene; E. coli; infectious diseases;
KW herpes simplex virus; ss.
XX
OS Synthetic.
XX
PN WO9516054-A1.
XX
PD 15-JUN-1995.
XX
PF 02-DEC-1994; 94WO-US013884.
XX
PR 02-DEC-1993; 93US-00161281.
XX
PA (MIRA/) MIRABELLI C K.
PA (ECKE/) ECKER D J.
PA (VICK/) VICKERS T A.
PA (ROBE/) ROBERTSON D L.
XX
PI Mirabelli CK, Ecker DJ, Vickers TA, Robertson DL;
XX
DR WPI; 1995-224334/29.
XX
PT Identification of oligo:nucleotide(s) with a desired activity, e.g.
PT activity against an infectious agent - by cloning vectors contg. randomly
PT sequenced oligo:nucleotide(s) into cells and assaying for the desired
PT phenotype.
XX
PS Claim 25; Page 25; 53pp; English.
XX
CC AAQ98161 is a random oligonucleotide Hind III primer/adaptor used in a
CC new method for the identification of random oligonucleotides which
CC inhibit the expression of a target gene, e.g. the beta-galactosidase gene
CC in E. coli. Such random oligonucleotides may be used in the treatment of
CC infectious diseases, pref. herpes simplex virus infection
XX
SQ Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 25;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||||| ||
Db 25 AAAAAAAAAAAAAAACCAA 7

RESULT 2797
AAC96249/c
ID AAC96249 standard; DNA; 25 BP.
XX
AC AAC96249;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #6.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 25;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAA 2799
| |||| ||||||||||||
Db 19 AGTTGACAAAAAAAAAAAA 1

RESULT 2798
AAC95664/c
ID AAC95664 standard; DNA; 25 BP.
XX
AC AAC95664;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #9.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 37; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and

```
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              | |||| ||||||||||||
Db         19 AGTTGACAAAAAAAAAAAA 1


RESULT 2799
AAC96421
ID   AAC96421 standard; DNA; 25 BP.
XX
AC   AAC96421;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #23.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 5 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCA 1789
              |||||||||||  || ||||
Db          2 TTTTTTTTTTTCAATCCCA 20


RESULT 2800
AAC95706
ID   AAC95706 standard; DNA; 25 BP.
XX
AC   AAC95706;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #3.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 4 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 25;
  Best Local Similarity   89.5%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              ||||||||||||  || |||
Db          1 TTTTTTTTTTTTCAAGTTT 19


RESULT 2801
AAC96550
ID   AAC96550 standard; DNA; 25 BP.
XX
AC   AAC96550;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB345 gene PCR primer #21.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
```

XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 53; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 0 A; 5 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 25;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2184
||||||||||||| | ||
Db 1 TTTTTTTTTTTTTCTCTT 19

RESULT 2802
AAQ47178/c
ID AAQ47178 standard; DNA; 26 BP.
XX
AC AAQ47178;
XX
DT 25-MAR-2003 (revised)
DT 25-JAN-1994 (first entry)
XX
DE MHC DR A intron binding oligomer Tcon.
XX
KW MHC; major histocompatability complex; class II; control oligomers; DR A;
KW transplantation; antigen; autoimmune disease; ss.
XX
OS Synthetic.
XX
PN WO9314769-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000797.
XX
PR 31-JAN-1992; 92US-00830427.
PR 14-SEP-1992; 92US-00944868.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;
XX
DR WPI; 1993-258367/32.
XX
PT Depletion of transplantation antigens in donor cells - using anti-sense
PT or triplex-forming oligonucleotide(s), used for treating auto-immune
PT disease and in transplants.
XX
PS Example; Page 22; 71pp; English.
XX
CC The sequences given in AAQ47176-77 represent triplex forming oligo-
CC nucleotides which bind to the mRNA sequence of the MHC class II locus DR
CC A structural gene at positions 851-876. The sequences given in AAQ47178-
CC 80 represent control oligomers which contain base compositions similar to
CC that around this DR A region but not containing the correct sequences. DR
CC A is a transplantation antigen. Binding of this sequence to the DR A gene
CC inhibits antigen production. This method may be used for treating
CC individuals with autoimmune disease, characterised by dysfunctional
CC expression of a transplantation antigen. It may also be used to produce
CC cells which are more easily transplanted into a recipient. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 4 G; 22 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.8; DB 1; Length 26;
Best Local Similarity 89.5%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||| ||||||| |||
Db 26 AAAAAAACAAAAAAACAAA 8

RESULT 2803
AAF74933
ID AAF74933 standard; DNA; 27 BP.
XX
AC AAF74933;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:30.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention

```
XX
SQ   Sequence 27 BP; 20 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 27;
  Best Local Similarity   89.5%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||  ||
Db          1 AAAAAAAAAAAAAAAACGAA 19


RESULT 2804
AAQ85070/c
ID   AAQ85070 standard; DNA; 29 BP.
XX
AC   AAQ85070;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Oligonucleotide clamp.
XX
KW   Oligonucleotide clamp; diagnosis; therapeutic agents; herpes virus;
KW   cytomegalovirus; human papilloma virus; HIV; oncogenes;
KW   bromoacetylamidated; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "covalently bound cholesterol group"
FT   misc_feature    15. .16
FT                   /*tag=  b
FT                   /note= "linkage or monomer containing a bromoacetylamino
FT                   functionality"
FT   modified_base   29
FT                   /*tag=  c
FT                   /note= "covalently bound cholesterol group"
XX
PN   WO9501456-A1.
XX
PD   12-JAN-1995.
XX
PF   01-JUL-1994;   94WO-US007541.
XX
PR   02-JUL-1993;   93US-00087387.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Lloyd DH;
XX
DR   WPI; 1995-061019/08.
XX
PT   New oligo:nucleotide clamps that stably bind to target polynucleotide(s)
PT   - may be used in diagnosis and therapy to inhibit genes or mRNA of, e.g.,
PT   herpes:virus, HIV, oncogene(s), etc.
XX
PS   Example 10; Page 28; 44pp; English.
XX
CC   The oligonucleotide clamps AAQ85069 and AAQ85070 are specific for a ss,
CC   or ds target nucleotide. When bound to the target sequence the two
CC   oligonucleotides form a stable non-covalent link, clamping the target
CC   sequence. This technique may be used to inhibit the expression, or
CC   function of an exogenous gene in a host (pref. human). The gene may be
CC   from herpes virus, cytomegalovirus, human papilloma virus, HIV or an
CC   oncogene. Therefore the clamps may be used in the treatment and diagnosis
CC   of human viral diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 2 A; 3 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 29;
  Best Local Similarity   89.5%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTGTA 1997
              ||||||| |||||||||  |
Db         29 AAAAAAAAAAAAGTGTGAA 11


RESULT 2805
AAQ83933/c
ID   AAQ83933 standard; DNA; 29 BP.
XX
AC   AAQ83933;
XX
DT   25-MAR-2003  (revised)
DT   04-OCT-1995  (first entry)
XX
DE   Oligonucleotide clamp containing free amines in the hinge region.
XX
KW   HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Modified with cholesterol"
FT   modified_base   15. .16
FT                   /*tag=  b
FT                   /note= "C(pnp)A, pnp = a linkage or monomer containing a
FT                   bromoacetylamino functionality, and p = phosphodiester
FT                   linkage"
FT   modified_base   29
FT                   /*tag=  c
FT                   /note= "Modified with cholesterol"
XX
PN   WO9501365-A1.
XX
PD   12-JAN-1995.
XX
PF   05-JUL-1994;   94WO-US007557.
XX
PR   02-JUL-1993;   93US-00087386.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM;
XX
DR   WPI; 1995-060944/08.
XX
PT   Synthesis of branched polymers and novel branched polymeric structures -
PT   used as molecular probes esp. for detecting poly-nucleotide(s).
XX
PS   Example 5; Page 31; 52pp; English.
XX
CC   This sequence represents an oligonucleotide clamp which was used to bind
CC   a target sequence comprising a segment of the HIV pol and nef genes in
CC   single stranded or double stranded forms. An oligonucleotide clamp is a
CC   compound capable of forming a covalently closed macromolecule or a stable
CC   circular complex after specifically binding to the target polynucleotide.
CC   The hinge region of this molecule comprises free amines. Oligonucleotide
CC   clamps generally comprise one or more oligonucleotide moieties capable of
CC   specific binding to the target molecule and one or more pairs of binding
CC   moieties covalently linked to the oligonucleotide moieties. Upon
CC   annealing of the oligonucleotides moieties to the target polynucleotide,
CC   the binding moieties of a pair are bought into juxtaposition so that they
CC   form a stable covalent or non-covalent linkage or complex. The
CC   interaction of the binding moieties effectively clamps the specifically
CC   annealed oligonucleotide moieties to the target polynucleotide. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 2 A; 3 C; 0 G; 24 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 15.8;  DB 1;  Length 29;
  Best Local Similarity   89.5%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTGTA 1997
              ||||||| ||||||||| |
Db         29 AAAAAAAAAAAAAGTGTGAA 11


RESULT 2806
AAV12929/c
ID   AAV12929 standard; DNA; 34 BP.
XX
AC   AAV12929;
XX
DT   15-MAY-1998  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:38 from US5174320 Example 18.
XX
KW   Synthesis; selection; amplification; circular oligonucleotide;
KW   rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS   Synthetic.
XX
PN   US5714320-A.
XX
PD   03-FEB-1998.
XX
PF   23-FEB-1995;   95US-00393439.
XX
PR   15-APR-1993;   93US-00047860.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-144278/13.
XX
PT   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT   template to produce oligonucleotide multimer for cleavage.
XX
PS   Example 18; Col 57; 38pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example of
CC   the present invention. The present invention describes a method for
CC   synthesising a selected oligonucleotide (I) having well defined ends. The
CC   method comprises: (a) annealing a primer to a single-stranded (ss)
CC   circular template to yield a primed circular template, where the template
CC   comprises: (i) at least one nucleotide sequence complementary to (I); and
CC   (ii) at least one nucleotide effective to produce a cleavage site in the
CC   oligonucleotide multimer; (b) combining the primed circular template with
CC   at least two types of nucleotide triphosphates and a polymerase enzyme
CC   without the addition of auxiliary proteins to yield a ss oligonucleotide
CC   multimer complementary to the circular oligonucleotide template,
CC   comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC   multimer at the cleavage site to produce (I) having well defined ends.
CC   The method is used for the large-scale synthesis of DNA and RNA oligomers
CC   for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ   Sequence 34 BP; 1 A; 7 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 34;
  Best Local Similarity   89.5%;  Pred. No. 4.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||| ||| ||||
Db         34 GAAAAAAAAAGAAAGAAAA 16


RESULT 2807
AAV59243/c
ID   AAV59243 standard; DNA; 34 BP.
XX
AC   AAV59243;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Small synthetic DNA circle sequence ID No.38.
XX
KW   ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1
FT                   /*tag=  a
FT                   /note= "Bound to position 34"
FT   modified_base   4
FT                   /*tag=  c
FT                   /note= "5-methyl-C residue"
FT   modified_base   9
FT                   /*tag=  d
FT                   /note= "5-methyl-C residue"
FT   modified_base   15
FT                   /*tag=  e
FT                   /note= "5-methyl-C residue"
FT   modified_base   20
FT                   /*tag=  f
FT                   /note= "5-methyl-C residue"
FT   modified_base   24
FT                   /*tag=  g
FT                   /note= "5-methyl-C residue"
FT   modified_base   34
FT                   /*tag=  h
FT                   /note= "5-methyl-C residue"
FT   misc_binding    34
FT                   /*tag=  b
FT                   /note= "Bound to position 1"
XX
PN   WO9838300-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US003784.
XX
PR   26-FEB-1997;   97US-00805631.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-481202/41.
XX
PT   Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT   oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
PT   polymerase to form multimer(s) which can be cleaved.
XX
PS   Example 18; Page 59; 100pp; English.
XX
CC   The oligomer sequence ID No.38 was used in an example of the invention
CC   for synthesising an RNA oligonucleotide, comprising combining a single-
CC   stranded circular oligonucleotide template comprising at least one copy
CC   of a nucleotide sequence complementary to the sequence of the desired RNA
CC   oligonucleotide with at least 2 types of ribonucleotide triphosphate and
CC   a polymerase enzyme to yield a single-stranded RNA oligonucleotide
CC   multimer complementary to the circular oligonucleotide template, where
CC   the RNA oligonucleotide multimer comprises multiple copies of the desired
CC   RNA oligonucleotide. The methods can be used for producing RNA
CC   oligonucleotides having a specific sequence and well defined ends. The
CC   RNA oligonucleotides produced can be used as probes, standards and
CC   diagnostic or therapeutic agents. They can be used for modifying the
CC   structure or function of a target molecule. They can also be used to
CC   cleave disease-associated RNA, DNA or protein
XX
```

```
SQ   Sequence 34 BP; 1 A; 7 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.8;  DB 1;  Length 34;
  Best Local Similarity   89.5%;  Pred. No. 4.1e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              |||||||||| ||| ||||
Db         34 GAAAAAAAAAGAAAGAAAA 16


RESULT 2808
AAV19118/c
ID   AAV19118 standard; DNA; 17 BP.
XX
AC   AAV19118;
XX
DT   28-AUG-1998  (first entry)
XX
DE   Anchored oligo(T) primer.
XX
KW   Secreted apoptosis-related protein; SARP; mSARP1; mouse; prostate cancer;
KW   breast cancer; diagnosis; gene therapy; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9813493-A2.
XX
PD   02-APR-1998.
XX
PF   24-SEP-1997;   97WO-US017154.
XX
PR   24-SEP-1996;   96US-0026603P.
PR   11-OCT-1996;   96US-0028363P.
XX
PA   (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI   Umansky S,  Melkonyan H;
XX
DR   WPI; 1998-230704/20.
XX
PT   New secreted apoptosis-related proteins - useful for modulating
PT   apoptosis, particularly for treatment of prostatic or breast cancer, also
PT   for diagnosis and monitoring of disease.
XX
PS   Example 1; Page 30; 101pp; English.
XX
CC   This oligo(T) synthetic oligonucleotide was used for first strand cDNA
CC   synthesis from total RNA isolated from either logarithmically growing or
CC   quiescent 10T1/2 mouse fibroblast cells. It was also used with an
CC   arbitarary d(N10) primer in PCR. The PCR products were used in a
CC   differential display to identify the mSARP1 gene (see AAV19112) that
CC   codes for novel murine secreted apoposis-related protein mSARP1 (see
CC   AAW37814). The invention relates to SARP polynucleotides (see also
CC   AAV19113-15) and polypeptides (see also AAW37815-17), antibodies specific
CC   for SARP, and use of such polynucleotides and antibodies in diagnostic
CC   and therapeutic methods, and methods for treating diseases related to the
CC   regulation of SARP expression in tissue and body fluid samples, including
CC   cancers
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              : |||||||||||||||
Db         17 SNAAAAAAAAAAAAAAA 1


RESULT 2809
AAZ89372
ID   AAZ89372 standard; DNA; 17 BP.
XX
AC   AAZ89372;
XX
DT   15-JUN-2000  (first entry)
XX
DE   RNA detecting primer #2.
XX
KW   Amplification; detection; gene expression; primer; ss.
XX
OS   Unidentified.
XX
PN   DE19840731-A1.
XX
PD   09-MAR-2000.
XX
PF   07-SEP-1998;   98DE-01040731.
XX
PR   07-SEP-1998;   98DE-01040731.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX
DR   WPI; 2000-257789/23.
XX
PT   Analysis of RNA samples, useful for detection of differential gene
PT   expression uses two differently labeled primers.
XX
PS   Disclosure; Page 10; 10pp; German.
XX
CC   This invention describes a novel method for analysis of an RNA sample
CC   which comprises amplifying cDNA with first and second differently labeled
CC   primers and analysis of the amplified labeled cDNA. The method is useful
CC   for analyzing differential gene expression, for identifying and/or
CC   characterizing pharmacological activities or for identifying target
CC   genes. The use of different primer combinations allow more cDNAs to be
CC   amplified. The method also provides a more detailed analysis than prior
CC   art methods. This sequence represents a primer used to illustrate the
CC   method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTM 16


RESULT 2810
AAZ89372/c
ID   AAZ89372 standard; DNA; 17 BP.
XX
AC   AAZ89372;
XX
DT   15-JUN-2000  (first entry)
XX
DE   RNA detecting primer #2.
XX
KW   Amplification; detection; gene expression; primer; ss.
XX
OS   Unidentified.
XX
PN   DE19840731-A1.
XX
PD   09-MAR-2000.
XX
PF   07-SEP-1998;   98DE-01040731.
XX
PR   07-SEP-1998;   98DE-01040731.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
```

XX
DR WPI; 2000-257789/23.
XX
PT Analysis of RNA samples, useful for detection of differential gene
PT expression uses two differently labeled primers.
XX
PS Disclosure; Page 10; 10pp; German.
XX
CC This invention describes a novel method for analysis of an RNA sample
CC which comprises amplifying cDNA with first and second differently labeled
CC primers and analysis of the amplified labeled cDNA. The method is useful
CC for analyzing differential gene expression, for identifying and/or
CC characterizing pharmacological activities or for identifying target
CC genes. The use of different primer combinations allow more cDNAs to be
CC amplified. The method also provides a more detailed analysis than prior
CC art methods. This sequence represents a primer used to illustrate the
CC method of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2800
:||||||||||||||||
Db 16 KAAAAAAAAAAAAAAA 1

RESULT 2811
AAX19021
ID AAX19021 standard; DNA; 22 BP.
XX
AC AAX19021;
XX
DT 13-MAY-1999 (first entry)
XX
DE Calravirus PCR primer 3NTRAP 2.
XX
KW Hop mosaic virus; HMV; infection; immunological method; diagnosis;
KW detection; ELISA; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9905166-A1.
XX
PD 04-FEB-1999.
XX
PF 22-JUL-1998; 98WO-JP003265.
XX
PR 23-JUL-1997; 97JP-00212568.
XX
PA (SAPB) SAPPORO BREWERIES LTD.
XX
PI Suda N, Hataya T;
XX
DR WPI; 1999-142849/12.
XX
PT New nucleic acid comprising hop mosaic virus gene - used in method for
PT detection of hop mosaic virus.
XX
PS Example 3; Page 14; 38pp; English.
XX
CC The present invention describes a hop mosaic virus gene. The present
CC invention also describes a method of assaying for the presence of hop
CC mosaic virus in a hop sample, comprising: (a) treating an isolated and
CC purified nucleic acid (I) comprising the hop mosaic virus gene or a
CC fragment of the gene with a sample containing nucleic acid (II) obtained
CC from hop; and (b) detecting the presence of hybridisation between (I) and
CC (II); or (c) by PCR amplification of (II) with (I), where the fragment
CC comprises at least 15 nucleotides, and detection of the products. Plural
CC detection procedures required in conventional immunological methods are
CC unnecessary using the method of the invention, which allows for quicker
CC detection of hop mosaic virus. The method also allows for the diagnosis
CC of hop mosaic virus infection with a higher accuracy than the
CC conventional ELISA. The present sequence represents a PCR primer used in
CC the present invention to amplify Calravirus which belongs to the same
CC group as hop mosaic virus
XX
SQ Sequence 22 BP; 3 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1282 CCATGGGACCAGCAGGCTCGCC 1303
| |||| ||| |||||| ||||
Db 1 CGATGGTACCTGCAGGCGCGCC 22

RESULT 2812
AAI67259/c
ID AAI67259 standard; DNA; 22 BP.
XX
AC AAI67259;
XX
DT 11-FEB-2002 (first entry)
XX
DE B533S forward primer.
XX
KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
KW cancer; B311D; B533S; B511S; GABApie; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200175171-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US010631.
XX
PR 03-APR-2000; 2000US-0194241P.
PR 20-JUL-2000; 2000US-0219862P.
PR 27-JUL-2000; 2000US-0221300P.
PR 18-DEC-2000; 2000US-0256592P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
XX
DR WPI; 2001-626449/72.
XX
PT Identifying tissue (tumor)-specific polynucleotides overexpressed in
PT tissue of interest as compared to control tissue, for detecting cancer
PT cells in patient, comprises DNA microarray analysis or quantitative
PT polymerase chain reaction.
XX
PS Claim 40; Page 42; 127pp; English.
XX
CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SP1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SP1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. Sequences
CC AAI67256-265 represent primers and probes used in quantitative real-time
CC PCR analysis of breast tumour specific genes
XX
SQ Sequence 22 BP; 4 A; 11 C; 1 G; 6 T; 0 U; 0 Other;

```
  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2671 ACAGTGTGTGTGGGTGAAATGG 2692
              |||||||||| | | |||| ||
Db         22 ACAGTGTGTGGGTGAGAAAGGG 1


RESULT 2813
AAF55172
ID   AAF55172 standard; DNA; 22 BP.
XX
AC   AAF55172;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Probe used to identify human hypocretin (orexin) receptor 1 gene.
XX
KW   Human; hypocretin receptor 1; orexin receptor 1; HCRTR1; chromosome 1;
KW   1p33; central nervous system modulator; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200114555-A1.
XX
PD   01-MAR-2001.
XX
PF   22-AUG-2000; 2000WO-US022986.
XX
PR   23-AUG-1999;   99US-00379083.
PR   07-JAN-2000; 2000US-00479128.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Olafsdottir BR,  Gulcher J;
XX
DR   WPI; 2001-211306/21.
XX
PT   Novel isolated nucleic acid molecule encoding hypocretin (orexin)
PT   receptor 1 useful for treating and diagnosing narcolepsy.
XX
PS   Example 1; Page 20; 44pp; English.
XX
CC   Probes AAF55160-76 were used to identify a human hypocretin (orexin)
CC   receptor 1 (HCRTR1) gene. The HCRTR1 gene is present on chromosome 1,
CC   location 1p33. It is likely that a mutation in the HCRTR1 gene is
CC   associated with narcolepsy. HCRTR1 is a central nervous system modulator.
CC   The HCRTR1 polypeptide and polynucleotide are useful for diagnosing or
CC   treating narcolepsy in an individual. The HCRTR1 polynucleotide is a
CC   source of probes and primers, and is also used to produce the protein
CC   recombinantly
XX
SQ   Sequence 22 BP; 5 A; 0 C; 10 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1006 GAAGTTGGACAAGATCGGGTTG 1027
              ||||||| | | ||| ||||||
Db          1 GAAGTTGTAGATGATGGGGTTG 22


RESULT 2814
AAS21990/c
ID   AAS21990 standard; DNA; 22 BP.
XX
AC   AAS21990;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human COL1A1 PCR primer for Exon 2 #3.
XX
KW   Human; collagen; COL1A1; COL1A2; COL9A1; COL9A2; COL9A3; ss;
KW   osteoporosis; multiple epiphyseal dysplasia; osteogenesis imperfecta;
KW   shortness of stature; low bone density; gene therapy; PCR primer.
XX
OS   Homo sapiens.
XX
PN   US6265157-B1.
XX
PD   24-JUL-2001.
XX
PF   03-OCT-1997;   97US-00943731.
XX
PR   03-DEC-1991;   91US-00803628.
PR   13-MAR-1994;   94US-00212322.
XX
PA   (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA   (UYJE-) UNIV JEFFERSON THOMAS.
PA   (UYOU-) UNIV OULU.
XX
PI   Prockop DJ,  Spotila LD,  Deltas CD,  Sereda L;
PI   Westerhausen Larson A,  Pack M,  Colige A,  Early J,  Koerkkoe J;
PI   Ala-Kokko L,  Annunen S,  Pihlajamaa T,  Vuoristo M,  Paassilta P;
XX
DR   WPI; 2001-432201/46.
XX
PT   Detecting collagen gene alteration, useful for diagnosing osteoporosis,
PT   multiple epiphyseal dysplasia, osteogenesis imperfecta, shortness of
PT   stature and low bone density in humans.
XX
PS   Example 4; Fig 21; 617pp; English.
XX
CC   The invention relates to Detecting a collagen gene alteration associated
CC   with a pathological condition in a human subject by obtaining from the
CC   subject a sample nucleic acid containing a portion of at least 15
CC   consecutive nucleotides of the segment of the COL1A1 gene extending in
CC   the 5' to 3' direction from 78 nucleotides of intron 27 located adjacent
CC   exon 28 through the 3' end of intron 51, where the portion contains an
CC   intronic nucleotide and a first and second site, determining the sequence
CC   of the portion and comparing the sequence of the portion with the
CC   corresponding consensus sequence of the COL1A1 gene where a difference
CC   between the sequence of the portion and the consensus sequence indicates
CC   the presence of the collagen alteration in the subject. The method is
CC   used for detecting abnormalities in a COL1 or COL9 gene is useful for
CC   determining whether a subject is afflicted with pathological conditions
CC   associated with an altered collagen gene such as osteoporosis, multiple
CC   epiphyseal dysplasia, osteogenesis imperfecta, shortness of stature and
CC   low bone density. Identification of an abnormality in a collagen gene is
CC   also useful for designing a therapeutic nucleotide or gene therapy agent
CC   which can be administered to the subject to correct or alleviate the
CC   abnormality. The method is useful for detecting mutations in both the
CC   coding and non-coding sequences of any of the COL1 or COL9 genes.
CC   Therefore the method can be used to detect collagen gene alterations
CC   which affect either the primary sequence of a collagen protein chain,
CC   splicing of the mRNA encoding such chains or regulation of expression of
CC   the genes encoding such chains. The present sequence is a PCR primer
CC   which amplifies a nucleic acid from a collagen gene of the invention
XX
SQ   Sequence 22 BP; 2 A; 7 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 22;
  Best Local Similarity   81.8%;  Pred. No. 2.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        224 GACGGGAGCAGCAATGGGAATC 245
              |||||||||||| | | || |
Db         22 GACGGGAGCAGCATTAGCAAAC 1


RESULT 2815
ADA45284
ID   ADA45284 standard; DNA; 22 BP.
```

XX
AC ADA45284;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MLH1 gene PCR primer #9.
XX
KW Functional allele profile; genetic inheritance; haplotype; population;
KW disease; pharmacogenetic application; selective pressure; human; MSH2;
KW MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003096236-A1.
XX
PD 22-MAY-2003.
XX
PF 08-AUG-2001; 2001US-00923327.
XX
PR 12-FEB-1996; 96US-00598591.
PR 12-FEB-1997; 97US-00798691.
PR 04-AUG-1997; 97US-00905772.
PR 22-MAY-1998; 98US-00084471.
PR 04-AUG-1998; 98US-00129134.
PR 14-MAR-2000; 2000US-00524794.
XX
PA (ONCO-) ONCORMED INC.
XX
PI Murphy PD;
XX
DR WPI; 2003-576875/54.
XX
PT Determining a functional allele profile of a gene in a population by
PT identifying the nucleotide sequence of a gene of genomic DNA from each of
PT the individuals with a family history of functional alleles of the gene
PT of interest.
XX
PS Example 2; Page 10; 28pp; English.
XX
CC The present invention relates to a method for determining a functional
CC allele profile of a gene in a population. The method comprises
CC identifying the nucleotide sequence of a gene of interest out of genomic
CC DNA from each of a population of individuals identified as having a
CC family history which indicates inheritance of functional alleles of the
CC gene of interest, and rank ordering the frequency of occurrence of each
CC haplotype, where the identity of the alleles containing each haplotype
CC and the determination of their relative frequencies constitutes the
CC functional allele profile of the gene of interest in the population. The
CC method is useful for determining functional allele profiles which are
CC useful in the treatment and diagnosis of diseases, for genetic and
CC pharmacogenetic applications, and for evaluating the degree to which the
CC gene(s) are under selective pressure. The present sequence represents a
CC PCR primer used in the method of the invention.
XX
SQ Sequence 22 BP; 1 A; 4 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 91 GATTTTGGATTTACCGCTTGGG 112
||||||| ||| || ||||||
Db 1 GATTTTGTGTTTTCCCCTTGGG 22

RESULT 2816
ADD21919/c
ID ADD21919 standard; DNA; 22 BP.
XX
AC ADD21919;
XX
DT 15-JAN-2004 (first entry)
XX
DE Protein translation efficiency-related DNA sequence #103.
XX
KW nucleotide production; translation efficiency; protein synthesis; ds.
XX
OS Unidentified.
XX
PN WO2003056009-A1.
XX
PD 10-JUL-2003.
XX
PF 27-DEC-2002; 2002WO-JP013756.
XX
PR 27-DEC-2001; 2001JP-00396941.
XX
PA (ENDO/) ENDO Y.
XX
PI Endo Y, Sawasaki T;
XX
DR WPI; 2003-618079/58.
XX
PT Preparing translation controlling nucleotides used for increased
PT efficiency during protein synthesis.
XX
PS Claim 11; Page 68; 87pp; Japanese.
XX
CC The invention comprises a method for preparing nucleotides that control
CC translation efficiency of proteins. The nucleotides of the invention are
CC useful for increasing efficiency during protein synthesis. The present
CC DNA sequence is used in the exemplification of the invnetion.
XX
SQ Sequence 22 BP; 7 A; 8 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2739 GTTGTGTGTATGATACGTGTAT 2760
| |||||||||||||| | | ||
Db 22 GGTGTGTGTATGATAAGAGAAT 1

RESULT 2817
AAT28017
ID AAT28017 standard; DNA; 23 BP.
XX
AC AAT28017;
XX
DT 16-DEC-1996 (first entry)
XX
DE Primer (B5LFr4) for amplifying antibody Fv light chain sequence.
XX
KW Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
KW detection; imaging; immunotoxin; targetting; assay; immunoassay;
KW Lewis(Y) carbohydrate antigen; ss.
XX
OS Synthetic.
XX
PN WO9613594-A1.
XX
PD 09-MAY-1996.
XX
PF 26-OCT-1995; 95WO-US013811.
XX
PR 28-OCT-1994; 94US-00331396.
PR 28-OCT-1994; 94US-00331397.
PR 28-OCT-1994; 94US-00331398.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;
PI Fitzgerald D, Brinkmann U, Pai L;
XX
DR WPI; 1996-251462/25.

XX
PT Single chain fusion proteins and antibodies - useful to diagnose and
PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.
XX
PS Example 1; Page 33; 116pp; English.
XX
CC A novel recombinant DNA molecule which encodes a single chain fusion
CC protein or antibody comprising the Fv region of both the light and heavy
CC chains of an antibody (Ab) fused together, and an effector molecule,
CC where the fusion protein or Ab has the binding specificity of monoclonal
CC Ab (MAb) B1, B3 or B5, can be used for the production of such fusion
CC proteins or antibodies. The fusion proteins can be used in compositions
CC as an immunotoxin to inhibit tumour cell growth. The single chain
CC antibody can be used to detect the presence or absence of cells bearing a
CC Lewis(Y) carbohydrate antigen in a patient. The antibodies are also
CC useful as multiple targetting moieties, providing at least 2 kinds of
CC biological activity. They can also be used in diagnostic assays and for
CC the imaging of tumours when attached to a radiolabel and for the
CC pathological diagnosis of tumours. Humanised antibodies are less
CC immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable
CC for long term treatment. The primers used for amplifying the Fv heavy and
CC light chain sequences of the B1, B3 and B5 MAb's are described in
CC AAT28002-T28017
XX
SQ Sequence 23 BP; 5 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2250 GAAGCTTTATTTGCATATTTAT 2271
|||||||||||| || ||| |
Db 2 GAAGCTTTATTTCCAACTTTGT 23

RESULT 2818
AAT76235/c
ID AAT76235 standard; DNA; 23 BP.
XX
AC AAT76235;
XX
DT 15-SEP-1997 (first entry)
XX
DE Human IL6 antisense oligonucleotide HUMIL6AS2.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US009306.
XX
PR 07-JUN-1995; 95US-00474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW, Metzger WJ;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject.
XX
PS Claim 5; Page 31; 71pp; English.
XX
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide HUMIL6AS2
CC specific for the human IL6. The method can be used to treat airway
CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
CC disease, bronchitis and other airway diseases characterised by an
CC inflammatory response. By eliminating adenosine from the antisense ON,
CC its liberation upon antisense degradation is prevented, thereby
CC preventing adenosine-induced bronchoconstriction in patients with hyper-
CC reactive airways
XX
SQ Sequence 23 BP; 0 A; 4 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 441 AGCCGGCGCCCACAGGCAGCCA 462
||||| | | ||||| ||||||
Db 23 AGCCGCCCCACACAGACAGCCA 2

RESULT 2819
AAX54065/c
ID AAX54065 standard; DNA; 23 BP.
XX
AC AAX54065;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human IL-6 antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 51; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those

```
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 23 BP; 0 A; 4 C; 12 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        441 AGCCGGCGCCCACAGGCAGCCA 462
              ||||| | | ||||| ||||||
Db         23 AGCCGCCCCACACAGACAGCCA 2


RESULT 2820
AAX81611/c
ID   AAX81611 standard; DNA; 23 BP.
XX
AC   AAX81611;
XX
DT   26-AUG-1999  (first entry)
XX
DE   PCR primer used to amplify erythrovirus V9 nucleotide sequences.
XX
KW   Erythrovirus V9; differential diagnosis; parvovirus; infection;
KW   erythrovirus screening; typing; immunoassay; PCR primer; ss.
XX
OS   Synthetic.
OS   Erythrovirus.
XX
PN   FR2771751-A1.
XX
PD   04-JUN-1999.
XX
PF   03-DEC-1997;   97FR-00015197.
XX
PR   03-DEC-1997;   97FR-00015197.
XX
PA   (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX
PI   Nguyen QT,  Garbarg CA,  Auguste V;
XX
DR   WPI; 1999-349543/30.
XX
PT   Erythrovirus V9 and its nucleic acid sequences - can be used in the
PT   diagnosis of its infections.
XX
PS   Claim 3; Page 27; 80pp; French.
XX
CC   AAX81588-X81630 represent PCR primers used to amplify erythrovirus V9
CC   polynucleotide sequences. Probes and primers derived from erythrovirus V9
CC   polynucleotide sequences (AAX81580) can be used for differential
CC   diagnosis of erythrovirus (parvovirus) infections by a combination of
CC   amplification and hybridisation assay. The probes can also be used to
CC   assess susceptibility to erythrovirus infection and for erythrovirus
CC   screening and typing. The antibodies can be used in immunoassays for
CC   diagnosis of erythrovirus V9 infections
XX
SQ   Sequence 23 BP; 16 A; 1 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAA 2188
                ||| |||||| | ||||||||
Db         22 TTTCATTTTTTATATTTTTTAA 1


RESULT 2821
AAA33509/c
ID   AAA33509 standard; DNA; 23 BP.
XX
AC   AAA33509;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1198.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Claim 18; Page 414; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 23 BP; 0 A; 4 C; 12 G; 7 T; 0 U; 0 Other;
```

```
  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        441 AGCCGGCGCCCACAGGCAGCCA 462
              ||||| | | ||||| ||||||
Db         23 AGCCGCCCCACACAGACAGCCA 2


RESULT 2822
AAF19631/c
ID   AAF19631 standard; DNA; 23 BP.
XX
AC   AAF19631;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human IL6 polynucleotide fragment #1198.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 210; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 23 BP; 0 A; 4 C; 12 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        441 AGCCGGCGCCCACAGGCAGCCA 462
              ||||| | | ||||| ||||||
Db         23 AGCCGCCCCACACAGACAGCCA 2


RESULT 2823
ABZ95325/c
ID   ABZ95325 standard; DNA; 23 BP.
XX
AC   ABZ95325;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human IL-6 antisense frgment no.1189.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 10567; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
```

```
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 23 BP; 0 A; 4 C; 12 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 23;
  Best Local Similarity   81.8%;  Pred. No. 3.1e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        441 AGCCGGCGCCCACAGGCAGCCA 462
              ||||| | | ||||| ||||||
Db         23 AGCCGCCCCACACAGACAGCCA 2


RESULT 2824
AAA94317
ID   AAA94317 standard; DNA; 24 BP.
XX
AC   AAA94317;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 25-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 43; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 24 BP; 1 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              | |  ||||| ||||||||||
Db          1 CGCGGTTTTTATTTTTTTTTT 22


RESULT 2825
ABQ77631
ID   ABQ77631 standard; DNA; 24 BP.
XX
AC   ABQ77631;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human Hsmar1 protein 15.95 RT-PCR primer, SEQ ID NO:4.
XX
KW   Human; Hsmar1 protein 15.95; mariner1 transposase;
KW   recombinant production; gene therapy; tumour; cancer;
KW   embryonic development disorder; diabetes; menstrual disorder;
KW   peptic ulcer; arrhythmia; anaemia; cytostatic; cardiant;
KW   reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1341642-A.
XX
PD   27-MAR-2002.
XX
PF   05-SEP-2000; 2000CN-00125027.
XX
PR   05-SEP-2000; 2000CN-00125027.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-520718/56.
XX
PT   A human Hsmar1 polypeptide 15.95, useful for curing e.g. tumors and
PT   diabetes.
XX
PS   Example 3; Page 19 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to human mariner1 transposase (Hsmar1) protein
CC   15.95 (ABB09530) and nucleic acids encoding it (ABQ77629). The protein
CC   has a molecular weight of 15.95 kD and has 84% identity and 91% homology
CC   over a 145 amino acid stretch with human mariner1 transposase given in
CC   GenBank accession number U52077. The invention also relates to a method
CC   for the recombinant production of the protein, an antagonist of the
CC   protein, and the use of the protein, gene and antagonist in therapeutic
CC   applications. Hsmar1 protein 15.95 can be used in the treatment of a
CC   variety of diseases such as embryonic development disorders, tumours,
CC   diabetes, menstrual disorders, peptic ulcers, arrhythmia, anaemia and
CC   epilepsy. The present sequence represents cDNA encoding human Hsmar1
CC   protein 15.95. Sequences ABQ77630-ABQ77631 represent reverse
CC   transcription-PCR (RT-PCR) primers used in an exemplification of the
CC   invention to isolate human Hsmar1 protein 15.95 cDNA
XX
```

```
SQ   Sequence 24 BP; 3 A; 3 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAAC 2189
              | ||||||||||||||    |||
Db          2 TGTTTTTTTTTTTTTTGCCAAC 23


RESULT 2826
ABL58652
ID   ABL58652 standard; DNA; 24 BP.
XX
AC   ABL58652;
XX
DT   17-JUL-2002  (first entry)
XX
DE   Human development regulator GTP-binding protein 1 (DRG1) primer 1.
XX
KW   Human; GTP-binding; GTP-binding protein 1 (DRG1) 9.35; cancer;
KW   embryo development disorder; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1331209-A.
XX
PD   16-JAN-2002.
XX
PF   30-JUN-2000; 2000CN-00116923.
XX
PR   30-JUN-2000; 2000CN-00116923.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305503/35.
XX
PT   Human development regulator GTP-binding protein 1 (DRG1) 9.35 polypeptide
PT   and its encoding polynucleotide, for treating e.g. cancer.
XX
PS   Example 2; Page 18 (disclosure); 33pp; Chinese.
XX
CC   The invention relates to human development regulator GTP-binding protein
CC   1 (DRG1) 9.35 polypeptide and its encoding nucleic acid. The
CC   polynucleotide, polypeptide and its antagonist are useful for treating
CC   e.g. embryo development disorder and cancer. The current sequence
CC   represents a human development regulator GTP-binding protein 1 (DRG1)
CC   9.35 related primer
XX
SQ   Sequence 24 BP; 4 A; 2 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||  | ||| |||
Db          1 TTTTTTTTTTTTCCATTGGAAG 22


RESULT 2827
AAT39969
ID   AAT39969 standard; DNA; 24 BP.
XX
AC   AAT39969;
XX
DT   24-JUN-1997  (first entry)
XX
DE   Minimal motif coding sequence ZGE1/ZGE2.
XX
KW   Epstein-Barr virus; EBV; nuclear antigen; EBVNA1; antigenic protein;
KW   Glycine-rich repeat sequence; immune system; regulatory protein; enzyme;
KW   cytokine; lymphokine; cell adhesion molecule; costimulatory molecule;
KW   drug resistance; tumour suppressant; genetic disease; viral disease;
KW   enzyme disorder; Gaucher's disease; cancer; immune system disorder; GRRS;
KW   gene therapy; minimal motif; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  a
FT                   /note= "5' overhang"
FT   misc_feature    complement(24)
FT                   /*tag=  b
FT                   /note= "5' overhang of CTCC"
XX
PN   WO9632483-A1.
XX
PD   17-OCT-1996.
XX
PF   10-APR-1996;   96WO-GB000876.
XX
PR   10-APR-1995;   95SE-00001324.
PR   01-SEP-1995;   95US-00522995.
PR   15-SEP-1995;   95US-00529190.
XX
PA   (MASU/) MASUCCI M.
XX
PI   Masucci M;
XX
DR   WPI; 1996-477134/47.
DR   P-PSDB; AAW05708.
XX
PT   New proteins containing GRRS which are invisible to the immune system -
PT   used for treating cancer, immune system disorders, viral diseases, etc.
XX
PS   Example 1; Page 43; 61pp; English.
XX
CC   AAT39966-T39973 represent double stranded coding sequences for minimal
CC   motifs of glycine-rich repeat sequences (GRRS). Full length GRRS
CC   sequences, such as the Epstein-Barr virus strain B95.8 nuclear antigen
CC   (EBNA1) represented by AAW05704, can be used in the method of the
CC   invention. The method of the invention is for making an antigenic protein
CC   invisible to the immune system, and consists of inserting a GRRS into the
CC   antigenic protein. The method can be used to insert a GRRS into
CC   therapeutic proteins, marker genes, regulatory proteins of viral vectors,
CC   or vaccine components. The therapeutic proteins include enzymes,
CC   cytokines, lymphokines, cell adhesion molecules, costimulatory molecules,
CC   or protein products of drug resistant genes or tumour suppressor genes.
CC   The antigenic proteins or corresponding nucleic acids are used to treat
CC   genetic and viral diseases, especially enzyme disorders such as Gaucher's
CC   disease, cancer, immune system disorders and other diseases treatable by
CC   gene therapy
XX
SQ   Sequence 24 BP; 5 A; 3 C; 13 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        795 AGAAGGAGCTGGTGGGGGCCGT 816
              |||||||||||| || | | ||
Db          3 AGAAGGAGCTGGAGGTGCCGGT 24


RESULT 2828
AAD12863/c
ID   AAD12863 standard; DNA; 24 BP.
XX
AC   AAD12863;
XX
DT   16-OCT-2001  (first entry)
```

```
XX
DE   Human CASB765 cDNA amplifying primer #2.
XX
KW   Human; CASB765; tumour; immunogen; cancer; colorectal; lung;
KW   preneoplastic lesion; colon; autoimmune disease; cytostatic; vaccine;
KW   gene therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157077-A1.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-GB000372.
XX
PR   02-FEB-2000; 2000GB-00002402.
XX
PA   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Gaulis SRJ,  Larminie CGC,  Vinals Y De BassolsC;
XX
DR   WPI; 2001-488867/53.
XX
PT   Novel CASB765 polypeptide, used to treat or diagnose colorectal or lung
PT   cancer, or preneoplastic lesions of lung or colon.
XX
PS   Example 9; Page 65; 88pp; English.
XX
CC   The invention relates to human CASB765 protein which is specifically
CC   expressed or over-expressed in tumours. The CASB765 polypeptide serves as
CC   immunogen for tumours. The CASB765 polynucleotide and polypeptide are
CC   used for diagnosis, in vaccine composition for prophylactic and
CC   therapeutic treatment of cancers, especially colorectal and lung cancer,
CC   preneoplastic lesions of lung and colon, and autoimmune diseases. The
CC   present sequence is a PCR primer used for amplification of human CASB765
CC   cDNA
XX
SQ   Sequence 24 BP; 7 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1394 TCTGCCCTGCAGAACTACATCA 1415
              |||||| || | | ||||||||
Db         22 TCTGCCTTGGACACCTACATCA 1


RESULT 2829
AAC91733
ID   AAC91733 standard; DNA; 24 BP.
XX
AC   AAC91733;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 787 RACE PCR primer, SEQ ID NO:17.
XX
KW   Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW   reduced expression; detection; diagnosis; drug screening;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073440-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003192.
XX
PR   27-MAY-1999;   99JP-00148785.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-032159/04.
XX
PT   Pollinosis-associated gene 787 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 12; Page 26-27; 54pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 787 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   after the pollen-scattering season, relative to expression levels in T-
CC   cells before the pollen-scattering season. The gene was isolated from T-
CC   cells from individuals allergic to pollen using the differential display
CC   method. The invention also relates to pollinosis-associated gene 787
CC   primers and probes; methods of detection of pollinosis-associated gene
CC   787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC   detection of pollinosis-associated gene 787 nucleic acids. The invention
CC   additionally encompasses a method of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis- associated gene 787
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 787 cDNA
XX
SQ   Sequence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        773 AACCCTCTGAACCTCCCCTGTC 794
              | ||||||||| |||| || ||
Db          1 AGCCCTCTGAATCTCCACTCTC 22


RESULT 2830
AAC91993
ID   AAC91993 standard; DNA; 24 BP.
XX
AC   AAC91993;
XX
DT   20-MAR-2001  (first entry)
XX
DE   T-box binding site in human IL-2 promoter.
XX
KW   T-bet; T box expressed in T cells protein; autoimmune disease; human;
KW   Th2-type dysfunction; T-box binding site; IL-2 promoter; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073453-A1.
XX
PD   07-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US015345.
XX
PR   02-JUN-1999;   99US-0137085P.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Glimcher LH,  Szabo SJ;
XX
DR   WPI; 2001-061537/07.
```

```
XX
PT   Novel protein, T-bet, a new member of T-box family of transcription
PT   factors is useful for identifying modulators of T-bet activity which
PT   treat allergies, cancers, autoimmune and infectious diseases.
XX
PS   Example 13; Page 82; 126pp; English.
XX
CC   The present invention relates to human anmd murine T box expressed in T
CC   cells (T-bet) protein and coding sequences (see AAC91988-C91989 and
CC   AAB51013-B51014). T-bet can be used in the treatment of autoimmune
CC   diseases associated with a Th2-type dysfunction e.g. diabetes mellitus,
CC   arthritis, multiple sclerosis, autoimmune thyroiditis, psoriasis,
CC   keratoconjunctivitis, alopecia areata, allergic responses due to
CC   arthropod bite reactions, Crohn's disease, aphthous ulcer, iritis,
CC   conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma,
CC   allergic asthma, cutaneous lupus, erythematosus, scleroderma, vaginitis,
CC   proctitis, and drug eruptions. The present sequence is a T-box binding
CC   site from human IL-2 promoter
XX
SQ   Sequence 24 BP; 6 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1705 GAGCTATCTCCTAACTTTGGAC 1726
              |||||||| ||||| | ||| |
Db          1 GAGCTATCACCTAAGTGTGGGC 22


RESULT 2831
ABL40063
ID   ABL40063 standard; DNA; 24 BP.
XX
AC   ABL40063;
XX
DT   15-MAY-2002  (first entry)
XX
DE   DNA-cysteine methyltransferase methylation protein 10 PCR primer #2.
XX
KW   Human; DNA-cysteine methyltransferase methylation protein 10; enzyme;
KW   cytostatic; antihormone; gene therapy; malignant tumour;
KW   embryonic development disorder; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200827-A2.
XX
PD   03-JAN-2002.
XX
PF   11-JUN-2001; 2001WO-CN000943.
XX
PR   12-JUN-2000; 2000CN-00116428.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-075671/10.
XX
PT   DNA-cysteine methytransferase methylation protein 10 and encoding
PT   polynucleotide, used in diagnosis and treatment of malignant tumors, and
PT   embryonic development disorders.
XX
PS   Disclosure; Page 29; 31pp; Chinese.
XX
CC   The present invention describes human DNA-cysteine methyltransferase
CC   methylation protein 10 (I). (I) has cytostatic and antihormone
CC   activities. The polynucleotide (II) encoding (I) can be used in gene
CC   therapy. (I) and (II) can be used in the diagnosis and treatment of
CC   malignant tumour, and embryonic development disorders. The present
CC   sequence represents a PCR primer which is given in the present invention.
CC   N.B. The present sequence is designated as SEQ ID NO:4 in the Sequence
CC   Listing, but does not correspond with the SEQ ID NO:4 sequence given in
CC   Example 3
XX
SQ   Sequence 24 BP; 6 A; 1 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1762 TCATTAAGCTTTTTTTTTTGA 1783
              | || |||||||| ||| |||
Db          2 TTATGAAGCTTTTTATTTGTGA 23


RESULT 2832
ABK13945
ID   ABK13945 standard; DNA; 24 BP.
XX
AC   ABK13945;
XX
DT   21-MAY-2002  (first entry)
XX
DE   RT-PCR primer #2 for cDNA encoding human uridylic acid kinase 11.
XX
KW   Human; uridylic acid kinase 11; sterility; pregnant pathological disease;
KW   embryonic development disturbance; dysgenesis; tumour; inherited disease;
KW   reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1321759-A.
XX
PD   14-NOV-2001.
XX
PF   29-APR-2000; 2000CN-00115574.
XX
PR   29-APR-2000; 2000CN-00115574.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-140659/19.
XX
PT   Novel polypeptide-human uridylic acid kinase 11 and polynucleotide for
PT   coding for polypeptide.
XX
PS   Example 2; Page 17 (disclosure); 32pp; Chinese.
XX
CC   The present invention relates to the isolation of human uridylic acid
CC   kinase 11, and the polynucleotide encoding it. Also described is the
CC   process for preparing the polypeptide by DNA recombination and the
CC   application of the polypeptide and polynucleotide in treating diseases,
CC   such as sterility, pregnant pathological disease, embryonic development
CC   disturbance, dysgenesis, some tumours and some inherited diseases.
CC   Antagonists against the polypeptide can also be used in treating such
CC   diseases. The present sequence for reverse transcriptase (RT)-PCR primer
CC   #2 is used with RT-PCR primer #1 (ABK13944) for isolating cDNA encoding
CC   human uridylic acid kinase 11
XX
SQ   Sequence 24 BP; 8 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2390 TTTTATTTATGCGTAATTTAAT 2411
              ||||| ||||| | ||||| ||
Db          1 TTTTAATTATGTGCAATTTTAT 22


RESULT 2833
ABQ78172/c
```

```
ID   ABQ78172 standard; DNA; 24 BP.
XX
AC   ABQ78172;
XX
DT   27-NOV-2002  (first entry)
XX
DE   Plant related PCR primer 3.
XX
KW   DNA integration; transformation; cereal; plant; transgenic; PCR; primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   DE10061634-A1.
XX
PD   20-JUN-2002.
XX
PF   11-DEC-2000; 2000DE-01061634.
XX
PR   11-DEC-2000; 2000DE-01061634.
XX
PA   (WEIS-) WEISSHEIMER MALZFABRIK FRIEDRICH.
XX
PI   Stahl R;
XX
DR   WPI; 2002-530152/57.
XX
PT   Determining unknown genomic sequence segments, useful e.g. for
PT   identifying integration sites in transgenic plants, that border a known
PT   sequence.
XX
PS   Example 4; Page 6; 32pp; German.
XX
CC   The invention relates to determining, even in a very complex genome,
CC   unknown sequence segments that flank a known segment. The 5' end of the
CC   unknown sequence is determined by: (a) cleaving genomic DNA with a
CC   restriction enzyme; (b) hybridising cleavage products with a labelled
CC   probe, optionally also an unlabelled bridging probe; (c) purifying the
CC   single-stranded product that has hybridised; (d) attaching a double-
CC   stranded adapter to one end of the single stranded product, optionally
CC   also attaching labelled probe to the other end; (e) preparing and
CC   amplifying the double stranded DNA; and (f) sequence analysis of the
CC   amplicon. The 3' end of the unknown sequence is determined similarly. The
CC   method is used to determine the integration site of a foreign or natural
CC   DNA (introduced by transformation or crossing) in the genome and to
CC   identify promoters, terminators or unknown genes, particularly in animal
CC   or especially cereal plant genomes. The present sequence is that of a PCR
CC   primer useful in examples of the invention analysing barley DNA for
CC   agrobacterium transformation
XX
SQ   Sequence 24 BP; 3 A; 5 C; 12 G; 4 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGCCCCACGC 624
              || | |||||||||| ||| ||
Db         23 CCCAGCTGCTGCTGCACCAAGC 2


RESULT 2834
AAD35583
ID   AAD35583 standard; DNA; 24 BP.
XX
AC   AAD35583;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Human hSCD5 cDNA amplifying PCR primer, hSCD5pcDNA3.1F.
XX
KW   Human; stearoyl-CoA desaturase; hSCD5; enzyme; lipidaemia; skin disease;
KW   delta-9 desaturase; cholesterol disorder; cardiovascular disease; cancer;
KW   diabetes; baldness; multiple sclerosis; anorectic; cytostatic; cosmetic;
KW   obesity; gene therapy; vaccine; protein therapy; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226944-A2.
XX
PD   04-APR-2002.
XX
PF   26-SEP-2001; 2001WO-CA001354.
XX
PR   26-SEP-2000; 2000US-0235640P.
XX
PA   (XENO-) XENON GENETICS INC.
XX
PI   Brownlie A;
XX
DR   WPI; 2002-372121/40.
XX
PT   Isolated polynucleotides encoding human stearoyl-CoA desaturase with
PT   delta-9 desaturase activity, useful for preventing diagnosing and
PT   treating e.g. cardiovascular disease, baldness and skin diseases.
XX
PS   Example 2; Page 32; 53pp; English.
XX
CC   The invention relates to isolated polynucleotides encoding human stearoyl
CC   -CoA desaturase (hSCD5) with Delta-9 desaturase activity. HSCD5 may be
CC   used in the prevention, diagnosis and treatment of diseases associated
CC   with inappropriate hSCD5 expression and used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of hSCD5 by expressing
CC   inactive proteins or to supplement the patients own production of hSCD5.
CC   Disorders that may be prevented and/or treated using the modulators
CC   including, for example cholesterol disorders, lipidaemias, cardiovascular
CC   disease, diabetes, obesity, baldness, skin diseases, cancer and multiple
CC   sclerosis. Human SCD5 is used in gene therapy and protein therapy and
CC   also used as vaccine. The present sequence is human SCD5 cDNA amplifying
CC   PCR primer
XX
SQ   Sequence 24 BP; 5 A; 12 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        464 CAGCAGGCCTGGCCCGGCCGCC 485
              || || ||| |||||||||| ||
Db          1 CACCATGCCAGGCCCGGCCACC 22


RESULT 2835
ABV74368
ID   ABV74368 standard; DNA; 24 BP.
XX
AC   ABV74368;
XX
DT   31-JAN-2003  (first entry)
XX
DE   Ubiquitin specific proteinase 23.10 PCR primer SEQ ID NO 4.
XX
KW   Ubiquitin specific proteinase 23.10; enzyme; tumour; diabetes;
KW   menstrual disorder; peptic ulcer; arrhythmia; anaemia; epilepsy;
KW   cytostatic; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1345976-A.
XX
PD   24-APR-2002.
XX
PF   29-SEP-2000; 2000CN-00125542.
XX
PR   29-SEP-2000; 2000CN-00125542.
```

XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-575979/62.
XX
PT Novel ubiquitin specific proteinase 23.10 polypeptide and polynucleotide
PT for encoding the polypeptide, useful for curing several diseases, such as
PT tumor, diabetes, menstrual disorder, peptic ulcer, arrhythmic, anemia and
PT epilepsy.
XX
PS Example 3; Page 17 (Disclosure); 31pp; Chinese.
XX
CC The invention relates to ubiquitin specific proteinase 23.10 and the
CC polynucleotide encoding it. The polypeptide is useful for curing several
CC diseases, such as tumour, diabetes, menstrual disorder, peptic ulcer,
CC arrhythmia, anaemia and epilepsy. The present sequence is that of a
CC ubiquitin specific proteinase 23.10 PCR primer, useful in examples of the
CC invention
XX
SQ Sequence 24 BP; 4 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1757 TTTATTCATTAAGCTTTTTTTT 1778
||||||||| | | ||||||
Db 2 TTTATTCATTTATTTATTTTTT 23

RESULT 2836
AAD38971
ID AAD38971 standard; DNA; 24 BP.
XX
AC AAD38971;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human GDD DNA amplifying forward RT-PCR primer, GDDpr-11f.
XX
KW Human; dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
KW autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
KW graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
KW antiviral; enzyme; reverse transcription; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200234900-A1.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-AU001388.
XX
PR 27-OCT-2000; 2000AU-00001078.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Abbott CA, Gorrell MD;
XX
DR WPI; 2002-454646/48.
XX
PT New dipeptidyl peptidase (DPP) peptides, useful for screening inhibitors
PT of DPP catalytic activity, which may be employed to treat e.g. neoplasia,
PT type II diabetes, cirrhosis, autoimmunity, graft rejection and HIV
PT infection.
XX
PS Example; Page 32; 91pp; English.
XX
CC The present invention relates to dipeptidyl peptidase (DPP) proteins and
CC polynucleotides encoding such proteins. The DPP peptides are useful for
CC screening inhibitors of DPP catalytic activity. The inhibitors are useful
CC for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
CC rejection and HIV (human immuno deficiency virus) infection. The present
CC DNA sequence is a reverse transcription (RT)-PCR primer which is used for
CC amplifying human GDD DNA. This sequence is used in the exemplification of
CC the invention
XX
SQ Sequence 24 BP; 5 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 795 AGAAGGAGCTGGTGGGGGCCGT 816
|||||||||||||| | || |
Db 2 AGAAGGAGCTGGTGCAGCCCTT 23

RESULT 2837
ABS62457
ID ABS62457 standard; DNA; 24 BP.
XX
AC ABS62457;
XX
DT 05-NOV-2002 (first entry)
XX
DE Analyte sorting tag sequence #929.
XX
KW Analyte sorting oligonucleotide tag; ss.
XX
OS Synthetic.
XX
PN WO200259355-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-CA000089.
XX
PR 25-JAN-2001; 2001US-0263710P.
PR 10-JUL-2001; 2001US-0303799P.
XX
PA (TMBI-) TM BIOSCIENCE CORP.
XX
PI Kobler D, Fieldhouse D;
XX
DR WPI; 2002-619176/66.
XX
PT Polynucleotides comprising minimally cross-hybridizing nucleotide
PT sequences, useful as tags or tag complements for use in a wide variety of
PT research, medical or industrial applications, e.g. in diagnostic assays
PT or DNA sequencing.
XX
PS Example 2; Page 74; 120pp; English.
XX
CC The invention relates to a composition, which comprises molecules for use
CC as tags or tag complements. Each molecule comprises an oligonucleotide
CC selected from a set of oligonucleotides based on numeric identifiers
CC (numerals 1-3) corresponding to the pattern of nucleotide bases present
CC in 1168 nucleotide sequences fully defined in the specification. These
CC oligonucleotides were found to be non-cross hybridising. The composition
CC is useful as a tag or tag complement, in analysing a biological sample
CC for the presence of a mutation or polymorphism at a locus in a nucleic
CC acid, and in determining the presence of a target suspected of being
CC contained in a mixture. Also for use in a wide variety of research,
CC medical, or industrial applications, e.g. identification of disease-
CC related polynucleotides in diagnostic assays, screening for clones of
CC novel target polynucleotides, identification of specific polynucleotide
CC in blots of mixtures of polynucleotides, therapeutic blocking of
CC inappropriately expressed genes or DNA sequencing. The polynucleotides of
CC the composition are particularly useful in methods involving highly
CC parallel processing of analytes. The use of the polynucleotides provides
CC minimal cross-hybridisation or cross-talk during the sorting process.
CC Thus, any sequence within the family of sequences will not significantly
CC cross-hybridise with any other sequence derived from that family, making

```
CC   it suitable for highly parallel processing of analytes. ABS61529-ABS62696
CC   represent oligonucleotide tags of the invention
XX
SQ   Sequence 24 BP; 11 A; 0 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2751 ATACGTGTATAATAAAAGTATT 2772
              ||| |||||||| | |||| ||
Db          1 ATAAGTGTATAAGAGAAGTGTT 22


RESULT 2838
ABS61625
ID   ABS61625 standard; DNA; 24 BP.
XX
AC   ABS61625;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Analyte sorting tag sequence #97.
XX
KW   Analyte sorting oligonucleotide tag; ss.
XX
OS   Synthetic.
XX
PN   WO200259355-A2.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-CA000089.
XX
PR   25-JAN-2001; 2001US-0263710P.
PR   10-JUL-2001; 2001US-0303799P.
XX
PA   (TMBI-) TM BIOSCIENCE CORP.
XX
PI   Kobler D,  Fieldhouse D;
XX
DR   WPI; 2002-619176/66.
XX
PT   Polynucleotides comprising minimally cross-hybridizing nucleotide
PT   sequences, useful as tags or tag complements for use in a wide variety of
PT   research, medical or industrial applications, e.g. in diagnostic assays
PT   or DNA sequencing.
XX
PS   Example 2; Page 59; 120pp; English.
XX
CC   The invention relates to a composition, which comprises molecules for use
CC   as tags or tag complements. Each molecule comprises an oligonucleotide
CC   selected from a set of oligonucleotides based on numeric identifiers
CC   (numerals 1-3) corresponding to the pattern of nucleotide bases present
CC   in 1168 nucleotide sequences fully defined in the specification. These
CC   oligonucleotides were found to be non-cross hybridising. The composition
CC   is useful as a tag or tag complement, in analysing a biological sample
CC   for the presence of a mutation or polymorphism at a locus in a nucleic
CC   acid, and in determining the presence of a target suspected of being
CC   contained in a mixture. Also for use in a wide variety of research,
CC   medical, or industrial applications, e.g. identification of disease-
CC   related polynucleotides in diagnostic assays, screening for clones of
CC   novel target polynucleotides, identification of specific polynucleotide
CC   in blots of mixtures of polynucleotides, therapeutic blocking of
CC   inappropriately expressed genes or DNA sequencing. The polynucleotides of
CC   the composition are particularly useful in methods involving highly
CC   parallel processing of analytes. The use of the polynucleotides provides
CC   minimal cross-hybridisation or cross-talk during the sorting process.
CC   Thus, any sequence within the family of sequences will not significantly
CC   cross-hybridise with any other sequence derived from that family, making
CC   it suitable for highly parallel processing of analytes. ABS61529-ABS62696
CC   represent oligonucleotide tags of the invention
XX
SQ   Sequence 24 BP; 10 A; 0 C; 6 G; 8 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2685 TGAAATGGAGATTTGGAATTGA 2706
              ||||   |||||||| ||||||
Db          3 TGAAGAAGAGATTTGAAATTGA 24


RESULT 2839
ABI89286
ID   ABI89286 standard; DNA; 24 BP.
XX
AC   ABI89286;
XX
DT   15-FEB-2002  (first entry)
XX
DE   Capture oligonucleotide Zip ID#3445 oligo #1.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW   oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US010958.
XX
PR   14-APR-2000; 2000US-0197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch.
XX
PS   Example 5; Fig 25; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention
XX
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```
SQ   Sequence 24 BP; 3 A; 9 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        717 ACCTGTTGCTGCACGATCAGAC 738
              ||| ||| ||||||| || |||
Db          2 ACCCGTTTCTGCACGGTCTGAC 23


RESULT 2840
ABI89287/c
ID   ABI89287 standard; DNA; 24 BP.
XX
AC   ABI89287;
XX
DT   15-FEB-2002  (first entry)
XX
DE   Capture oligonucleotide Zip ID#3445 oligo #2.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW   oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US010958.
XX
PR   14-APR-2000; 2000US-0197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch.
XX
PS   Example 5; Fig 25; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention
XX
SQ   Sequence 24 BP; 6 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        717 ACCTGTTGCTGCACGATCAGAC 738
              ||| ||| ||||||| || |||
Db         23 ACCCGTTTCTGCACGGTCTGAC 2


RESULT 2841
ABA97546
ID   ABA97546 standard; DNA; 24 BP.
XX
AC   ABA97546;
XX
DT   05-APR-2002  (first entry)
XX
DE   Cancer cell discrimination method PCR primer SEQ ID NO: 13.
XX
KW   Telomerase; enzyme; cancer cell discrimination; reverse transcriptase;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2001309791-A.
XX
PD   06-NOV-2001.
XX
PF   02-MAY-2000; 2000JP-00138250.
XX
PR   02-MAY-2000; 2000JP-00138250.
XX
PA   (KANE/) KANEUCHI H.
PA   (KAMI/) KAMIMORI M.
XX
DR   WPI; 2002-134853/18.
XX
PT   Discrimination of a cancer cell in a sample tissue, comprises determining
PT   the expression level of a reverse transcriptase component of telomerase
PT   using a hybridization assay.
XX
PS   Example; Page 6; 16pp; Japanese.
XX
CC   The present invention relates to a method for the discrimination of a
CC   cancer cell in a sample tissue, which involves determining the expression
CC   level of a reverse transcriptase component of telomerase in a cell
CC   constituting the sample tissue by an in situ hybridization of the mRNA of
CC   the enzyme, and judging a cell showing a higher expression level than
CC   that of the reverse transcriptase component of telomerase in a normal
CC   cell to be a cancer cell. The present sequence is a PCR primer used in
CC   the exemplification of the invention
XX
SQ   Sequence 24 BP; 3 A; 7 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2566 CTCTGTTCTTGGCTTGGAAGAT 2587
              |||||| || ||| |||| |||
Db          2 CTCTGTGCTGGGCCTGGACGAT 23


RESULT 2842
ABS55785
ID   ABS55785 standard; DNA; 24 BP.
XX
AC   ABS55785;
XX
DT   03-JAN-2003  (first entry)
XX
```

DE Human Sailor transposase 12.87 RT PCR primer #2.
XX
KW Human; ss; sailor transposase 12.87; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; immunological disease; HIV;
KW inflammation; PCR; primer; reverse transcriptase PCR.
XX
OS Homo sapiens.
XX
PN CN1352243-A.
XX
PD 05-JUN-2002.
XX
PF 02-NOV-2000; 2000CN-00127156.
XX
PR 02-NOV-2000; 2000CN-00127156.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-714441/78.
XX
PT New human sailor transposase 12.87 polypeptide for treating malignant
PT tumors, hemopathy, human immunodeficiency virus infection, immunological
PT diseases, and various inflammations.
XX
PS Example 2; Page 17 (disclosure); 33pp; Chinese.
XX
CC The present invention discloses a new kind of polypeptide, human sailor
CC transposase 12.87, polynucleotides encoding the polypeptide and a DNA
CC recombination process to produce the polypeptide. The present invention
CC also discloses applying the polypeptide in treating various diseases,
CC such as malignant tumours, haemopathy, human immunodeficiency virus (HIV)
CC infection, immunological diseases, and various inflammations. The present
CC invention also discloses the antagonist resisting the polypeptide and its
CC treatment effect. The present invention also discloses application of the
CC polynucleotides encoding human sailor transposase 12.87. The present
CC sequence is a reverse transcriptase (RT)-PCR primer used to isolate
CC nucleic acids encoding sailor transposase 12.87
XX
SQ Sequence 24 BP; 4 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1772 TTTTTTTTTTGAACCCCATTCT 1793
||||||||||| | | || |||
Db 1 TTTTTTTTTTGGAACACAGTCT 22

RESULT 2843
ABV93494
ID ABV93494 standard; DNA; 24 BP.
XX
AC ABV93494;
XX
DT 08-JAN-2003 (first entry)
XX
DE Bacillus thuringiensis toxin Cry mutant oligonucleotide #18.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS; ss.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN FR2822157-A1.
XX
PD 20-SEP-2002.
XX
PF 19-MAR-2001; 2001FR-00003691.
XX
PR 19-MAR-2001; 2001FR-00003691.
XX
PA (AVET) AVENTIS CROPSCIENCE SA.
XX
PI Freyssinet G, Rang C, Frutos R;
XX
DR WPI; 2003-002439/01.
XX
PT New modified Cry protein, useful as insecticide, comprises at least one
PT additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS Example 3; Page 26; 134pp; French.
XX
CC The present invention describes a modified Cry protein (I) that is
CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 15.6; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 3.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTTTTTT 2186
|||||||| || || ||||| |
Db 1 CTTTTTTTATTATTATTTTTAT 22

RESULT 2844
ABV93779
ID ABV93779 standard; DNA; 24 BP.
XX
AC ABV93779;
XX
DT 08-JAN-2003 (first entry)
XX
DE B. thuringiensis toxin Cry oligonucleotide mutant #18 SEQ ID NO:30.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS; ss.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN FR2822157-A1.
XX
PD 20-SEP-2002.
XX
PF 19-MAR-2001; 2001FR-00003691.
XX
PR 19-MAR-2001; 2001FR-00003691.
XX
PA (AVET) AVENTIS CROPSCIENCE SA.
XX
PI Freyssinet G, Rang C, Frutos R;
XX
DR WPI; 2003-002439/01.
XX
PT New modified Cry protein, useful as insecticide, comprises at least one

```
PT   additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS   Disclosure; Page 105; 134pp; French.
XX
CC   The present invention describes a modified Cry protein (I) that is
CC   sensitive to pepsin and comprises at least one additional pepsin cleavage
CC   site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC   proteins by incorporating at least one extra PCS; (b) polynucleotides
CC   (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC   (II) and terminator; (d) expression or transformation vector (III) that
CC   contains CG; (e) host organism (IV) transformed with (III), also, where
CC   the organism is a plant, its parts and seeds; (f) production of (I) by
CC   growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC   against (I). (I) has insecticide activity. (I) can be used as
CC   insecticides, particularly where expressed in transgenic plants. (I) are
CC   sensitive to enzymes in the digestive tract of mammals, so do not persist
CC   in the tract (lack of persistence is required by regulatory authorities
CC   for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC   increase degradation in the digestive tract of insects, so have no effect
CC   on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 3.3e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2186
              |||||||| || || ||||| |
Db          1 CTTTTTTTATTATTATTTTTAT 22


RESULT 2845
AAC96427
ID   AAC96427 standard; DNA; 25 BP.
XX
AC   AAC96427;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #29.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 3.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||||||  |  |||
Db          1 TTTTTTTTTTTTTTCCTCCCTT 22


RESULT 2846
AAC95726
ID   AAC95726 standard; DNA; 25 BP.
XX
AC   AAC95726;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #23.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 3.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||||||  |  |||
Db          1 TTTTTTTTTTTTTTCCTCCCTT 22


RESULT 2847
```

```
AAC96039/c
ID   AAC96039 standard; DNA; 25 BP.
XX
AC   AAC96039;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #6.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 44; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 3.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              ||   || ||||||||||||||
Db         22 AGGGGTGCAAAAAAAAAAAAAA 1


RESULT 2848
AAC96245
ID   AAC96245 standard; DNA; 25 BP.
XX
AC   AAC96245;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPA1 gene PCR primer #2.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 1 A; 2 C; 3 G; 19 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 25;
  Best Local Similarity   81.8%;  Pred. No. 3.5e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||| | || || ||
Db          2 TTTTTTTTTTCTGTTGTTCTA 23


RESULT 2849
AAZ59153
ID   AAZ59153 standard; DNA; 26 BP.
XX
AC   AAZ59153;
XX
DT   17-APR-2000  (first entry)
XX
DE   Oligonucleotide #10 for DNA determination method.
XX
KW   Oligonucleotide; restriction enzyme; PCR primer; amplification; template;
KW   vector; ss.
XX
OS   Synthetic.
XX
PN   JP11341986-A.
XX
PD   14-DEC-1999.
XX
PF   02-JUN-1998;   98JP-00152598.
XX
PR   02-JUN-1998;   98JP-00152598.
XX
PA   (HITA ) HITACHI LTD.
PA   (AMSH ) NYCOMED AMERSHAM PLC.
XX
DR   WPI; 2000-101695/09.
XX
PT   A process for preparation of a DNA sample - and a reagent for the
PT   preparation.
XX
PS   Example 1; Page 11; 16pp; Japanese.
XX
CC   This sequence represents an oligonucleotide used in a novel method for
CC   the direct and complete determination of long DNA sequences of
```

```
CC   restriction enzymes from PCR products. The method allows independent
CC   recognition of amplified DNA fragments at both ends and removal of one
CC   primer binding site can be carried out and leads to the following steps:
CC   (1) the resultant cleaved PCR fragment having the one primer binding site
CC   is used as a template for the simultaneous determination of the PCR
CC   fragment and the downstream fragment; (2) the fragments can be used for
CC   the determination of long DNA sequences; (3) the PCR amplification of 2
CC   primers provide replacements of the both ends with different restriction
CC   enzyme fragments; and (4) the above mentioned steps may give polarity of
CC   the fragment at both ends for integration in vectors and may be applied
CC   for preparation of samples
XX
SQ   Sequence 26 BP; 1 A; 1 C; 4 G; 18 T; 0 U; 2 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 26;
  Best Local Similarity   81.8%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
                | |  |||||||||||||| |
Db          1 TGTGGTTTTTTTTTTTTTTCA 22


RESULT 2850
AAH40741
ID   AAH40741 standard; DNA; 26 BP.
XX
AC   AAH40741;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific upper PCR primer SEQ ID 3537.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW   Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW   polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW   inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200129262-A2.
XX
PD   26-APR-2001.
XX
PF   13-OCT-2000; 2000WO-US028436.
XX
PR   15-OCT-1999;   99US-0160096P.
XX
PA   (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI   Picoult-Newburg L,  Pohl M;
XX
DR   WPI; 2001-290930/30.
XX
PT   New genotyping oligonucleotide, useful for detecting the presence,
PT   absence or identity of single polynucleotide polymorphism in a nucleic
PT   acid sample.
XX
PS   Claim 1; Page 68; 83pp; English.
XX
CC   Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC   primer extension (SNPE) primers, and the sequences of regions flanking
CC   sites of single nucleotide polymorphisms SNPs. The present invention
CC   includes kits for determining the presence or absence of a SNP, using the
CC   oligonucleotides of the invention. The PCR primers are used to amplify a
CC   SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC   The oligonucleotides are useful for genotyping a nucleic acid sample by
CC   performing a single-nucleotide primer extension reaction. The
CC   oligonucleotides are useful for determining the presence, absence or
CC   identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC   assess by association analysis the genotype of an individual or group of
CC   individuals, having a pathological phenotypic trait suspected of being
CC   caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC   agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC   osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC   traits also include symptoms of or susceptibility to multifactorial
CC   disease of which a component is or may be genetic such as autoimmune
CC   diseases, including, rheumatoid arthritis, multiple sclerosis,
CC   inflammation, cancer, nervous system diseases and infection by pathogenic
CC   microorganism. The method is also useful in forensic investigations and
CC   paternity analysis. The present sequence represents a PCR primer specific
CC   for a human SNP containing DNA sequence
XX
SQ   Sequence 26 BP; 16 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.6%;  Score 15.6;  DB 1;  Length 26;
  Best Local Similarity   81.8%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
                ||||||  |||  |||| |||||
Db          3 TTGAAACAAATCAAAACAAAAA 24


RESULT 2851
AAX18370/c
ID   AAX18370 standard; DNA; 17 BP.
XX
AC   AAX18370;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 11.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 11; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || ||||||||||||||
Db         17 TTAAAAAAAAAAAAAAA 1
```

RESULT 2852
AAX18371/c
ID AAX18371 standard; DNA; 17 BP.
XX
AC AAX18371;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 12.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 11; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         17 ATAAAAAAAAAAAAAAA 1
```

RESULT 2853
ADB04270/c
ID ADB04270 standard; DNA; 17 BP.
XX
AC ADB04270;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5256.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5256; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              ||||||||||||||| |
Db         17 AAAAAAAAAAAAAAAGA 1
```

RESULT 2854
AAX69798
ID AAX69798 standard; RNA; 17 BP.
XX
AC AAX69798;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1093.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX

```
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   5.9%;  Pred. No. 1.8e+03;
  Matches    1;  Conservative   15;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
              : |:::::::::::::::
Db          1 UACUUUUUUUUUUUUUU 17


RESULT 2855
AAX69804/c
ID   AAX69804 standard; RNA; 17 BP.
XX
AC   AAX69804;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              ||| ||||||||||||||
Db         17 TTGGAAAAAAAAAAAAA 1


RESULT 2856
AAX69803/c
ID   AAX69803 standard; RNA; 17 BP.
XX
AC   AAX69803;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
```

```
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              | ||||||||||||||||
Db         17 TGGAAAAAAAAAAAAAA 1


RESULT 2857
AAX69796
ID   AAX69796 standard; RNA; 17 BP.
XX
AC   AAX69796;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1091.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   11.8%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative   14;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTT 2177
              :|: |:::::::::::::
Db          1 UCUACUUUUUUUUUUUU 17


RESULT 2858
AAX69797
ID   AAX69797 standard; RNA; 17 BP.
XX
AC   AAX69797;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1092.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   11.8%;  Pred. No. 1.8e+03;
  Matches    2;  Conservative   14;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2178
              |: |:::::::::::::
Db          1 CUACUUUUUUUUUUUU 17


RESULT 2859
AAA25453
```

```
ID   AAA25453 standard; DNA; 17 BP.
XX
AC   AAA25453;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTGTA 17


RESULT 2860
AAA25452
ID   AAA25452 standard; DNA; 17 BP.
XX
AC   AAA25452;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||||||  |
Db          1 TTTTTTTTTTTTTTGT 17


RESULT 2861
AAA25452/c
ID   AAA25452 standard; DNA; 17 BP.
XX
AC   AAA25452;
XX
```

```
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         17 ACAAAAAAAAAAAAAAA 1


RESULT 2862
ABA91530
ID   ABA91530 standard; DNA; 17 BP.
XX
AC   ABA91530;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.
XX
KW   DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        8
FT                   /*tag=  a
FT                   /label= RNA
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 4; Page 49; 72pp; English.
XX
CC   The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC   AGT02014. This is one of a set of oligonucleotides (see ABA91527-30) used
CC   to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC   oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC   the set had a different number of ribonucleotides, 1 in the present case.
CC   The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC   (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC   minutes. The results showed that 4 ribonucleotides were the minimum
CC   number for RNA cleavage. The invention provides probes for nucleic acid
CC   hybridisation. The probes form a hairpin structure comprising a double-
CC   stranded stem and a single-stranded loop, and are capable of both
CC   intramolecular and intermolecular hybridisation. The double-stranded stem
CC   may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC   RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC   strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC   can be removed. Arrays and methods for nucleic acid hybridisation using
CC   the probes are provided
XX
SQ   Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||| |||||||||
Db          1 TTTTTTATTTTTTTTT 17


RESULT 2863
ABA91530/c
ID   ABA91530 standard; DNA; 17 BP.
XX
AC   ABA91530;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.
XX
KW   DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
```

```
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        8
FT                   /*tag=  a
FT                   /label= RNA
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 4; Page 49; 72pp; English.
XX
CC   The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC   AGT02014. This is one of a set of oligonucleotides (see ABA91527-30) used
CC   to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC   oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC   the set had a different number of ribonucleotides, 1 in the present case.
CC   The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC   (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC   minutes. The results showed that 4 ribonucleotides were the minimum
CC   number for RNA cleavage. The invention provides probes for nucleic acid
CC   hybridisation. The probes form a hairpin structure comprising a double-
CC   stranded stem and a single-stranded loop, and are capable of both
CC   intramolecular and intermolecular hybridisation. The double-stranded stem
CC   may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC   RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC   strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC   can be removed. Arrays and methods for nucleic acid hybridisation using
CC   the probes are provided
XX
SQ   Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
                ||||||||| |||||||
Db         17 AAAAAAAAATAAAAAAA 1


RESULT 2864
AAD44151
ID   AAD44151 standard; DNA; 17 BP.
XX
AC   AAD44151;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-AT PCR primer #2 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1D; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo AT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

  Query Match              0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
                | ||||||||||||||||
Db          1 TVTTTTTTTTTTTTTTT 17


RESULT 2865
AAD44151/c
ID   AAD44151 standard; DNA; 17 BP.
XX
AC   AAD44151;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-AT PCR primer #2 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
```

PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Fig 1D; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo AT
CC PCR primer used to illustrate the method of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2802
||||||||||||||| |
Db 17 AAAAAAAAAAAAAAABA 1

RESULT 2866
ABT38816
ID ABT38816 standard; DNA; 17 BP.
XX
AC ABT38816;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4453.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 554; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 1 A; 4 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2153 GATTTTTTTCTCCTTTT 2169
||| ||||||||||||
Db 1 GATCTTTTTCTCCTTTT 17

RESULT 2867
ABT34888
ID ABT34888 standard; DNA; 17 BP.
XX
AC ABT34888;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 525.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 95; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral

```
CC   diseases that are characterised by development of tumours or cell
CC   degeneration, specifically cancer but also Alzheimer's disease and
CC   schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC   patient samples is useful for diagnosis and/or prognosis of these
CC   diseases. The polypeptides can also be used to generate antibodies, and
CC   both the polypeptide and antibodies are useful as components of protein
CC   chips. The nucleic acid sequences of the invention can be used in gene
CC   therapy. This polynucleotide sequence represents a tumour suppression
CC   related human fukutin oligonucleotide of the invention
XX
SQ   Sequence 17 BP; 4 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2013 GATCAAGTCCTCTGGTA 2029
                ||||||||| |||||||
Db          1 GATCAAGTCTTCTGGTA 17


RESULT 2868
ADB04269
ID   ADB04269 standard; DNA; 17 BP.
XX
AC   ADB04269;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5255.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5255; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
                | ||||||||||||||||
Db          1 TTCTTTTTTTTTTTTTT 17


RESULT 2869
ADB04269/c
ID   ADB04269 standard; DNA; 17 BP.
XX
AC   ADB04269;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5255.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5255; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||||||| ||
Db         17 AAAAAAAAAAAAAAGAA 1


RESULT 2870
ADB04273
ID   ADB04273 standard; DNA; 17 BP.
XX
AC   ADB04273;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5259.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5259; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              |||||||||||||| |
Db          1 TTTTTTTTTTTTTTGA 17


RESULT 2871
ADB04273/c
ID   ADB04273 standard; DNA; 17 BP.
XX
AC   ADB04273;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5259.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5259; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db         17 TCAAAAAAAAAAAAAA 1


RESULT 2872
ADB43022
ID   ADB43022 standard; DNA; 17 BP.
XX
AC   ADB43022;
XX
DT   18-DEC-2003  (revised)
DT   04-DEC-2003  (first entry)
XX
DE   Tumour suppression/reversion associated nucleotide #3345.
XX
```

```
KW   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW   primer; probe; tumour suppression; tumour reversion; apoptosis;
KW   virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2003040369-A2.
XX
PD   15-MAY-2003.
XX
PF   17-SEP-2002; 2002WO-IB004219.
XX
PR   17-SEP-2001; 2001FR-00011981.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-441574/41.
XX
PT   New nucleic acid encoding human prostate membrane-specific antigen,
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 423; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 17;
  Best Local Similarity   94.1%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              ||||| ||||||||||
Db          1 GATCCCATTTTAATATT 17


RESULT 2873
AAV54164/c
ID   AAV54164 standard; cDNA; 18 BP.
XX
AC   AAV54164;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 1.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 47; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAA 2799
              || |||||||||||||||
Db         18 TTAAAAAAAAAAAAAAA 2


RESULT 2874
AAV54166
ID   AAV54166 standard; cDNA; 18 BP.
XX
AC   AAV54166;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 3.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
```

```
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCA 18


RESULT 2875
AAZ90648
ID   AAZ90648 standard; DNA; 18 BP.
XX
AC   AAZ90648;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #9.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCA 18


RESULT 2876
AAZ90646/c
ID   AAZ90646 standard; DNA; 18 BP.
XX
AC   AAZ90646;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #7.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              || |||||||||||||
Db         18 TTAAAAAAAAAAAAAA 2


RESULT 2877
AAQ20109
ID   AAQ20109 standard; DNA; 18 BP.
XX
AC   AAQ20109;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 943 to target human TNF Receptor mRNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW   cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
```

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XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 27; 42pp; English.
XX
CC   The oligomer was designed to target human TNF receptor mRNA beginning at
CC   nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC   ethanocytosine group. See also AAQ20108
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||| ||||||||||||
Db          1 TTTTATTTTTTTTTTT 17


RESULT 2878
AAQ20108
ID   AAQ20108 standard; DNA; 18 BP.
XX
AC   AAQ20108;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 942 to target human TNF Receptor mRNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW   cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/03.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 27; 42pp; English.
XX
CC   The oligomer was designed to target human TNF receptor mRNA beginning at
CC   nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC   ethanocytosine group. See also AAQ20109
XX
SQ   Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||| ||||||||||||
Db          1 TTTTCTTTTTTTTTTT 17


RESULT 2879
AAQ30446/c
ID   AAQ30446 standard; DNA; 18 BP.
XX
AC   AAQ30446;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR941 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   5
FT                   /*tag=  a
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
```

```
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||||||||||| ||||
Db         17 AAAAAAAAAAAAGAAAA 1


RESULT 2880
AAQ25501
ID   AAQ25501 standard; DNA; 18 BP.
XX
AC   AAQ25501;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Purine rich HUMNFR target duplex sequence.
XX
KW   Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV;
KW   hepatitis; malignancy; inflammation; ds.
XX
OS   Synthetic.
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 11; Page 64; 77pp; English.
XX
CC   The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
CC   sequence beginning at nucleotide 2354. The sequence is a viral duplex
CC   sequence contg. a purine-rich region concentrated on one chain of the
CC   duplex. The sequence may be prepd. by standard DNA synthesis. The HUMNFR
CC   duplex sequence is used as a target for novel oligomers which are capable
CC   of forming a triplex at physiological pH by coupling into the major
CC   groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of
CC   forming a triplex with this sequence. The oligomers are used in the
CC   treatment of inflammation. Similar oligomers may be used to target viral
CC   DNA duplexes specific for HIV, herpes and other viruses. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. The oligomer is able to
CC   inhibit gene expression, as verified by in vitro systems. See also
CC   AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 18 BP; 16 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              |||| ||||||||||||
Db          1 AAAAGAAAAAAAAAAA 17


RESULT 2881
AAQ30448
ID   AAQ30448 standard; DNA; 18 BP.
XX
AC   AAQ30448;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    5
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "N6 methyl-8-oxo-2' deoxyadenine"
FT   modified_base    18
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
```

```
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||| ||||||||||||
Db          1 TTTTATTTTTTTTTTT 17


RESULT 2882
AAQ30447
ID   AAQ30447 standard; DNA; 18 BP.
XX
AC   AAQ30447;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
XX
KW   Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW   HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    5
FT                    /*tag=  a
FT                    /mod_base= m5c
FT   modified_base    18
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 72; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC   a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC   and others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||| ||||||||||||
Db          1 TTTTCTTTTTTTTTTT 17


RESULT 2883
AAV54173/c
ID   AAV54173 standard; cDNA; 18 BP.
XX
AC   AAV54173;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 10.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
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```
Db         18 GTAAAAAAAAAAAAAA 2


RESULT 2884
AAV54169
ID   AAV54169 standard; cDNA; 18 BP.
XX
AC   AAV54169;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 6.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTCT 18


RESULT 2885
AAV54167/c
ID   AAV54167 standard; cDNA; 18 BP.
XX
AC   AAV54167;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 4.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         18 ATAAAAAAAAAAAAAA 2


RESULT 2886
AAZ90649/c
ID   AAZ90649 standard; DNA; 18 BP.
XX
AC   AAZ90649;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #10.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
```

```
SQ   Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         18 GTAAAAAAAAAAAAAA 2


RESULT 2887
AAZ90645
ID   AAZ90645 standard; DNA; 18 BP.
XX
AC   AAZ90645;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #6.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              |||||||||||||||  |
Db          2 TTTTTTTTTTTTTTCT 18


RESULT 2888
AAZ90643/c
ID   AAZ90643 standard; DNA; 18 BP.
XX
AC   AAZ90643;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #4.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         18 ATAAAAAAAAAAAAAA 2


RESULT 2889
AAV54168
ID   AAV54168 standard; cDNA; 18 BP.
XX
AC   AAV54168;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 5.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
```

```
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTGT 18


RESULT 2890
AAV54168/c
ID   AAV54168 standard; cDNA; 18 BP.
XX
AC   AAV54168;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 5.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 48; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         18 ACAAAAAAAAAAAAAAA 2


RESULT 2891
AAV54174/c
ID   AAV54174 standard; cDNA; 18 BP.
XX
AC   AAV54174;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 11.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         18 GCAAAAAAAAAAAAAAA 2


RESULT 2892
AAV54165
ID   AAV54165 standard; cDNA; 18 BP.
XX
AC   AAV54165;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 2.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
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PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 47; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTGA 18


RESULT 2893
AAV54165/c
ID   AAV54165 standard; cDNA; 18 BP.
XX
AC   AAV54165;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 2.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 47; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2800
              | ||||||||||||||
Db         18 TCAAAAAAAAAAAAAA 2


RESULT 2894
AAV16014
ID   AAV16014 standard; DNA; 18 BP.
XX
AC   AAV16014;
XX
DT   21-MAY-1998  (first entry)
XX
DE   PCR primer G-R used to identify Sox-3 gene mutations in mice.
XX
KW   Mutation; Sox-3; ENU mutagenesis; mutational screening; recessive;
KW   single strand conformation polymorphism; SSCP; phenotypic alteration;
KW   PCR primer; amplify; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO9744485-A1.
XX
PD   27-NOV-1997.
XX
PF   16-MAY-1997;   97WO-GB001354.
XX
PR   17-MAY-1996;   96GB-00010355.
XX
PA   (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX
PI   Goodfellow PN;
XX
DR   WPI; 1998-018536/02.
XX
PT   Identification of mutation(s) in genes of interest - without prior
PT   observation of phenotypic alteration in the mutated organism or cell.
XX
PS   Example 4; Page 41; 66pp; English.
XX
CC   PCR primers AAV16001-18 were used to identify mutations in Sox-3 using
CC   the method of the invention. The primers are located throughout the gene
CC   and are unique to Sox-3. The method comprises testing a nucleic acid
CC   sample from a mutated organism for a mutation in a gene of interest
CC   without the prior observation of a phenotypic alteration in the mutated
CC   organism resulting from the mutation. Sox-3 is a member of the Sox gene
CC   family, a family of about 20 genes which all encode a "HMG" box, which is
CC   a DNA-binding domain. Mice were mutagenised using ENU mutagenesis. The
CC   mutagenised mice were tested by PCR with each primer set and fluorescent
CC   single strand conformation polymorphism (SSCP), which identifies mice
CC   carrying mutations in Sox-3. The method provides mutational screening
CC   based on genomic and genetic techniques rather than on phenotypic
CC   observation. The method identifies and characterises genes via
CC   mutagenesis to identify genes encoding products which may have
CC   therapeutic benefit. The method also identifies the presence of mutations
CC   in a gene which do not rely solely upon prior matching of a gene with a
CC   disease. Heterozygotic organisms can also be screened to identify those
CC   carrying a mutation in a copy of a gene of interest even though the gene
CC   may be recessive and therefore causes no phenotypic alteration
XX
SQ   Sequence 18 BP; 0 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              ||||||| |||||||||
Db          1 GCGGCGGCGGCGGCGGC 17
```

```
RESULT 2895
AAZ90644
ID   AAZ90644 standard; DNA; 18 BP.
XX
AC   AAZ90644;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #5.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
                ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTGT 18


RESULT 2896
AAZ90644/c
ID   AAZ90644 standard; DNA; 18 BP.
XX
AC   AAZ90644;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #5.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
                | ||||||||||||||
Db         18 ACAAAAAAAAAAAAAA 2


RESULT 2897
AAZ90650/c
ID   AAZ90650 standard; DNA; 18 BP.
XX
AC   AAZ90650;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #11.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
```

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                  | ||||||||||||||||
Db          18 GCAAAAAAAAAAAAAAA 2


RESULT 2898
AAZ90647
ID   AAZ90647 standard; DNA; 18 BP.
XX
AC   AAZ90647;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #8.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
                ||||||||||||||| |
Db          2 TTTTTTTTTTTTTTGA 18


RESULT 2899
AAZ90647/c
ID   AAZ90647 standard; DNA; 18 BP.
XX
AC   AAZ90647;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #8.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
                | ||||||||||||||||
Db          18 TCAAAAAAAAAAAAAAA 2


RESULT 2900
AAZ43273
ID   AAZ43273 standard; DNA; 18 BP.
XX
AC   AAZ43273;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Murine Sox3 gene PCR primer 14.
XX
KW   Screening; mutation; treatment; disease; drug discovery; PCR primer; ss.
XX
OS   Mus musculus.
XX
PN   US5994075-A.
XX
PD   30-NOV-1999.
XX
PF   16-MAY-1997;   97US-00857946.
XX
PR   17-MAY-1996;   96US-0017824P.
XX
PA   (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX
PI   Goodfellow PN;
XX
DR   WPI; 2000-038255/03.
XX
PT   Identifying a mutation in a gene of interest in an organism useful for
PT   identifying genes encoding products which may have therapeutic benefits.
XX
PS   Example 5; Col 65-66; 70pp; English.
XX
CC   This invention describes a novel mutational screening method based on
CC   genomic and genetic techniques to identify and characterize a mutation in
CC   a gene of interest without first selecting a phenotypic characteristic.
CC   The screening methods are useful for identifying genes encoding products
CC   which may have therapeutic benefit for treating human or animal diseases.
CC   The method can be used for the DNA mutation screening of a class or a
CC   family of genes providing a rapid assay for identifying mutant genes. The
CC   methods produce organisms which can be used for drug discovery e.g.
CC   providing a model for the study and treatment of a disease state, allow
```

CC in vitro assessment of drug activity and interbreeding of mutants which
CC allow investigation of gene interactions in the overall phenotype. A
CC range of phenotypes associated with different mutations, and specified
CC mutations in a gene of interest can be determined. The method can be
CC adapted to screen for a mutation in two or more genes of interest in an
CC organism. The methods allow mutations in a gene of interest to be
CC identified without having to rely on matching a gene with a disease.
CC AAZ43260-Z43421 represent PCR primers used in the method of the invention
XX
SQ Sequence 18 BP; 0 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGC 67
||||||| |||||||||
Db 1 GCGGCGGCGGCGGCGGC 17

RESULT 2901
AAA05258
ID AAA05258 standard; DNA; 18 BP.
XX
AC AAA05258;
XX
DT 19-MAY-2000 (first entry)
XX
DE PCR primer G-R used in Sox-3 amplimer generation.
XX
KW PCR primer; Sox-2; Sox-3; T gene; Tyrosinase; MGF; Sry; c-kit; Tryp-1;
KW Pax-6; mutation detection; therapeutic target identification; mouse;
KW mast cell growth factor; ss.
XX
OS Mus sp.
XX
PN US6015670-A.
XX
PD 18-JAN-2000.
XX
PF 14-NOV-1997; 97US-00970740.
XX
PR 17-MAY-1996; 96US-0017824P.
PR 16-MAY-1997; 97US-00857946.
XX
PA (HEXA-) HEXAGEN TECHNOLOGY LTD.
XX
PI Goodfellow PN;
XX
DR WPI; 2000-181139/16.
XX
PT Detecting mutations in selected genes, useful e.g. for identifying
PT therapeutic targets or products, by analyzing DNA in mutated embryonic
PT stem cells without phenotypic characterization.
XX
PS Example 5; Col 31; 66pp; English.
XX
CC PCR primers AAA05245-A05406 are used to generate amplimers from the mouse
CC Sox-3 gene, Sox-2 gene, T gene, tyrosinase gene, Tryp-1 gene, Sry gene,
CC MGF (mast cell growth factor) gene, c-kit gene, and the Pax-6 gene. The
CC primers are used in a method for the identification of a mutation in a
CC selected gene in a tissue without the prior observation of a phenotypic
CC alteration in the mutated organism or cell. The method is used to
CC identify mutations in a selected gene that encode products of potential
CC therapeutic activity or that are potential targets, particularly where
CC the gene of interest has been identified as a candidate gene by
CC positional cloning. Other applications are determining functions of genes
CC ; detecting the range of phenotypes associated with different mutations
CC in a particular gene and identification of particular mutations. Animals
CC containing an identified mutation are used as models for studying
CC diseases or their treatment, and cells from them for in vitro assessment
CC of drug action. Interbreeding of mutant mice is used to investigate
CC genetic interaction in the overall phenotype
XX
SQ Sequence 18 BP; 0 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGGC 67
||||||| |||||||||
Db 1 GCGGCGGCGGCGGCGGC 17

RESULT 2902
AAF56305/c
ID AAF56305 standard; DNA; 18 BP.
XX
AC AAF56305;
XX
DT 19-APR-2001 (first entry)
XX
DE Human mGluR1alpha GB-PR1:HSU31215 antisense oligonucleotide #6.
XX
KW Antisense; metabotropic glutamate receptor type 1; mGluR1; pain;
KW inflammation; arthritis; opioid analgesic; glutamate; neurotoxicity;
KW tumour; human; ss.
XX
OS Homo sapiens.
XX
PN WO200105963-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-CA000824.
XX
PR 15-JUL-1999; 99US-0144004P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Fundytus ME, Coderre TJ, Cohen SR, Henry JL, Vainio A;
XX
DR WPI; 2001-159534/16.
XX
PT New antisense oligonucleotides to metabotropic glutamate receptor type 1
PT gene, which specifically hybridize to mRNA expressed from the gene useful
PT for treating disorders related to elevated glutamate level such as pain.
XX
PS Claim 2; Page 18; 97pp; English.
XX
CC The present invention relates to an antisense oligonucleotide derived
CC from the sequence of metabotropic glutamate receptor type 1 (mGluR1)
CC gene. The antisense oligonucleotide binds to a portion of mRNA expressed
CC from the gene or its splice variant. The binding of the oligonucleotide
CC to the mRNA is effective in decreasing the translation of the mRNA in a
CC host cell expressing the gene. The oligonucleotides are useful for
CC treating chronic pain caused by injury or inflammation of a nerve caused
CC by arthritis. The oligonucleotides may be used with an opioid analgesic.
CC They are also useful for minimizing glutamate neurotoxicity and/or
CC excitotoxicity associated with stroke, ischemia, CNS trauma,
CC neurodegenerative disorders, gastrointestinal disorders or to inhibit
CC tumour formation
XX
SQ Sequence 18 BP; 13 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2162 CTCCTTTTTTTTTTTTT 2178
|||||||| ||||||||
Db 18 CTCCTTTTGTTTTTTTT 2

RESULT 2903

```
ACF36862
ID   ACF36862 standard; DNA; 18 BP.
XX
AC   ACF36862;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human lactoferrin gene exon 12 PCR primer #30.
XX
KW   Human; lactoferrin; Lf; chromosome 3q21-23; lactoprotein regulation;
KW   genetic diagnosis; disease resistance; transgenic animal; gene therapy;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1373215-A.
XX
PD   09-OCT-2002.
XX
PF   28-FEB-2001; 2001CN-00109073.
XX
PR   28-FEB-2001; 2001CN-00109073.
XX
PA   (LINN/) LI N.
XX
PI   Li N,  Liu Z,  Wu C;
XX
DR   WPI; 2003-141474/14.
XX
PT   Complete sequence of human lectoferritin gene and its regulatory element.
XX
PS   Example 2; Page 18 (Disclosure); 0pp; Chinese.
XX
CC   The invention relates to the complete sequence of the human lactoferrin
CC   (Lf) gene (ACF36873), comprising a part of the regulatory region and all
CC   exons and introns. The lactoferrin gene is located on chromosome 3q21-23.
CC   The lactoferrin gene can be used in the recombinant preparation of human
CC   lactoferrin by a eukaryotic expression system, and in the regulation of
CC   expression of the lactoprotein gene. It may also be used in screening for
CC   genetic markers associated with resistance to disease, and is useful in
CC   the generation of a transgenic animal, and in gene therapy. Sequences
CC   ACF36833-ACF36872 represent PCR primers used in an example from the
CC   invention to amplify the human lactoferrin gene
XX
SQ   Sequence 18 BP; 1 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2630 TCTCGTTCCTGTTGGGC 2646
                ||||||| |||||||||
Db          1 TCTCGTTGCTGTTGGGC 17


RESULT 2904
ADA27361
ID   ADA27361 standard; DNA; 18 BP.
XX
AC   ADA27361;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human microsatellite repeat M2_3_8.
XX
KW   ds; HLA-related research; HLA class II-associated disease;
KW   transplantation matching; recombination hot spot identification;
KW   linkage disequilibrium study; human; microsatellite.
XX
OS   Homo sapiens.
XX
PN   US2003108940-A1.
XX
PD   12-JUN-2003.
XX
PF   06-DEC-2002; 2002US-00314405.
XX
PR   15-NOV-2000; 2000US-00713616.
XX
PA   (INOK/) INOKO H.
XX
PI   Inoko H,  Tamiya G,  Matsuzaka Y;
XX
DR   WPI; 2003-616782/58.
XX
PT   New oligonucleotide primer capable of specifically hybridizing to a DNA
PT   having the sequence of the flanking regions of a microsatellite (e.g.
PT   M249), useful for HLA-related research, e.g. transplantation matching.
XX
PS   Example 2; Page 5; 20pp; English.
XX
CC   The invention relates to an oligonucleotide primer capable of
CC   specifically hybridising to a DNA having the sequence of the flanking
CC   regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-
CC   11, M2-2-20, M2-2-21, M2-2-22, M2-2-23, M2-2-24, M2-4-25, M2-4-26, M2-2-
CC   29, M2-2-32, M2-4-32, M2-4-33, M2-4-37, M2-3-22, M2-2-36, M2-5-11, M2-2-
CC   46, and M2-2-48. The primer is useful for determining the number of
CC   repeat units of the microsatellite cited above. The primer is useful in
CC   HLA-related research, such as genetic mapping of HLA class II-associated
CC   diseases, transplantation matching, population genetics, and
CC   identification of recombination hot spots as well as linkage
CC   disequilibrium studies. The present sequence represents the human
CC   microsatellite repeat M2_3_8.
XX
SQ   Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGC 67
              ||||||| |||||||||
Db          1 GCGGCGGCGGCGGCGGC 17


RESULT 2905
ADD20088/c
ID   ADD20088 standard; DNA; 18 BP.
XX
AC   ADD20088;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Oreochromis niloticus microsatellite primer  SEQ ID NO:723.
XX
KW   single nucleotide polymorphism; SNP; fish; Salmo salar;
KW   Orechromis niloticus; Atlantic halibut; microsatellite; cod;
KW   polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW   detection; primer; ss.
XX
OS   Synthetic.
OS   Oreochromis niloticus.
XX
PN   WO2003060160-A2.
XX
PD   24-JUL-2003.
XX
PF   17-JAN-2003; 2003WO-IB000112.
XX
PR   18-JAN-2002; 2002US-0349950P.
PR   16-AUG-2002; 2002US-0404200P.
XX
PA   (GENO-) GENOMAR ASA.
XX
PI   Lie O,  Slettan A,  Hoyum M,  Lingaas F;
XX
```

DR WPI; 2003-627388/59.
XX
PT Novel isolated nucleic acid molecule comprising single nucleotide
PT polymorphism associated with fish, useful for forming PCR primers which
PT are used for detecting single nucleotide polymorphisms in fish nucleic
PT acids.
XX
PS Claim 18; SEQ ID NO 723; 233pp; English.
XX
CC The present invention describes an isolated nucleic acid (I) comprising a
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC (i), or its complement under highly stringent hybridisation conditions.
CC Also described: (1) an isolated oligonucleotide (II) comprising at least
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites, or their complement; (2)
CC a primer pair (III) suitable for use in PCR, comprising two (II) capable
CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC origin of fish sample comprising providing a parentage genotype database
CC comprising a collection of candidate parent genotypes, where each of the
CC candidate parent genotype represents a distinct origin, and comparing a
CC sample genotype to the parentage genotype database, where a match between
CC the sample genotype and one of the candidate parent genotype identifies
CC to the origin of the sample. (M1) is useful for determining the origin of
CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC detecting nucleic acid molecule comprising SNP in a sample, which
CC involves contacting the sample containing nucleic acids with one or more
CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC useful for detecting nucleic acid molecule comprising a polymorphic
CC sequence in a sample, comprising contacting the sample containing nucleic
CC acids with one or more (II) which is derived from O. niloticus
CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC sites or seabass polymorphic sites, and identifying a nucleic acid that
CC hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC comprising a microsatellite sequence in sample. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 18 BP; 2 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.4;  DB 1;  Length 18;
  Best Local Similarity   94.1%;  Pred. No. 2e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        815 GTAATGAACCCCACTGA 831
              | ||||||||||||||||
Db         18 GAAATGAACCCCACTGA 2
```

RESULT 2906
AAV44628
ID AAV44628 standard; DNA; 19 BP.
XX
AC AAV44628;
XX
DT 24-NOV-1998 (first entry)
XX
DE Human uncoupling protein-2 UCP2 gene primer hUCP2.CDSR5.
XX
KW Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
KW obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
KW hypothermia; wasting; cachexia; anorexia; inflammation; fever;
KW hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9831396-A1.
XX
PD 23-JUL-1998.
XX
PF 22-APR-1997; 97WO-US006864.
XX
PR 15-JAN-1997; 97US-0034960P.
XX
PA (UYDU-) UNIV DUKE.
PA (REGC) UNIV CALIFORNIA.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Surwit RS, Collins SA, Warden CH, Seldin MF, Ricquier D;
PI Bouillaud F;
XX
DR WPI; 1998-413823/35.
XX
PT Method for treating disease associated with altered UCP-2 expression - by
PT administering agent which enhances or inhibits UCP-2 activity,
PT effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT etc.
XX
PS Disclosure; Fig 1F; 98pp; English.
XX
CC Primer hUCP2.CDSR5 is used with forward primer hUCP2.CDSF5 (see AAV44627)
CC in the PCR amplification of a 1125 bp region of the human uncoupling
CC protein-2 (UCP2) gene coding sequence (see also AAV44595). The invention
CC relates to a method for treating diseases associated with altered UCP2
CC expression, such as obesity, diabetes, syndrome X, hypothermia,
CC hyperinsulinaemia, glucose intolerance, wasting, anorexia, inflammation,
CC cachexia, fever or hyperthermia
XX
SQ Sequence 19 BP; 8 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.4;  DB 1;  Length 19;
  Best Local Similarity   94.1%;  Pred. No. 2.3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGA 1556
              ||||||| |||||||||
Db          1 AGGAGAGAAGGGAAGGA 17
```

RESULT 2907
ABZ85436/c
ID ABZ85436 standard; DNA; 20 BP.
XX
AC ABZ85436;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

```
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 678; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              || |||||||||||||
Db         17 TTCAAAAAAAAAAAAA 1


RESULT 2908
AAT73291/c
ID   AAT73291 standard; DNA; 20 BP.
XX
AC   AAT73291;
XX
DT   12-DEC-1997  (first entry)
XX
DE   Primer 1 for pUC19 DNA amplification.
XX
KW   primer; PCR; polymerase chain reaction; sequencing; walking;
KW   complementary extension reaction; low redundancy; universal primer; ss.
XX
OS   Synthetic.
XX
PN   EP767240-A2.
XX
PD   09-APR-1997.
XX
PF   17-SEP-1996;   96EP-00114907.
XX
PR   18-SEP-1995;   95JP-00238141.
PR   30-JAN-1996;   96JP-00013634.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K;
XX
DR   WPI; 1997-205424/19.
XX
PT   Efficient sequencing of long DNA by fragment walking - with simultaneous
PT   sequencing of restriction enzyme fragment and adjacent region of intact
PT   DNA, avoids the need for cloning and requires fewer primers.
XX
PS   Example 1; Page 11; 50pp; English.
XX
CC   A method for DNA analysis based on a complementary extension reaction
CC   using a DNA polymerase, comprises a combination of fragment walking and
CC   DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC   restriction enzyme and the targeted DNA sequence can be determined
CC   directly from the digested DNA fragments. By exploring the overlapping
CC   sequence of the determined base sequence, the overall base sequence of a
CC   lengthy DNA can be determined with low redundancy without cloning or
CC   subcloning. In addition, the method can be done with commercially
CC   available universal primers or with fewer primers than required in
CC   existing methods. AAT73291-92 are primers used in determination of the
CC   pUC19 sequence. Primer extension was carried out using 16 primers
CC   AAT73293
XX
SQ   Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2800
              || |||||||||||||
Db         17 TGCAAAAAAAAAAAAA 1


RESULT 2909
AAT73292/c
ID   AAT73292 standard; DNA; 20 BP.
XX
AC   AAT73292;
XX
DT   12-DEC-1997  (first entry)
XX
DE   Primer 2 for pUC19 DNA amplification.
XX
KW   primer; PCR; polymerase chain reaction; sequencing; walking;
KW   complementary extension reaction; low redundancy; universal primer; ss.
XX
OS   Synthetic.
XX
PN   EP767240-A2.
XX
PD   09-APR-1997.
XX
PF   17-SEP-1996;   96EP-00114907.
XX
PR   18-SEP-1995;   95JP-00238141.
PR   30-JAN-1996;   96JP-00013634.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K;
XX
DR   WPI; 1997-205424/19.
XX
PT   Efficient sequencing of long DNA by fragment walking - with simultaneous
PT   sequencing of restriction enzyme fragment and adjacent region of intact
PT   DNA, avoids the need for cloning and requires fewer primers.
XX
PS   Example 1; Page 11; 50pp; English.
XX
CC   A method for DNA analysis based on a complementary extension reaction
CC   using a DNA polymerase, comprises a combination of fragment walking and
CC   DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC   restriction enzyme and the targeted DNA sequence can be determined
CC   directly from the digested DNA fragments. By exploring the overlapping
CC   sequence of the determined base sequence, the overall base sequence of a
CC   lengthy DNA can be determined with low redundancy without cloning or
CC   subcloning. In addition, the method can be done with commercially
```

```
CC   available universal primers or with fewer primers than required in
CC   existing methods. AAT73291-92 are primers used in determination of the
CC   pUC19 sequence. Primer extension was carried out using 16 primers
CC   AAT73293
XX
SQ   Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              || |||||||||||||||
Db         17 TGCAAAAAAAAAAAAAA 1


RESULT 2910
AAT76100/c
ID   AAT76100 standard; DNA; 20 BP.
XX
AC   AAT76100;
XX
DT   12-SEP-1997  (first entry)
XX
DE   Human histidine decarboxylase antisense oligonucleotide HUMHDCAS4.
XX
KW   Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW   chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS   Synthetic.
XX
PN   WO9640162-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009306.
XX
PR   07-JUN-1995;   95US-00474497.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW,  Metzger WJ;
XX
DR   WPI; 1997-051871/05.
XX
PT   Treatment of airway diseases such as asthma - by topically applying
PT   adenosine-free antisense oligo:nucleotide to airway epithelium of
PT   subject.
XX
PS   Claim 5; Page 26; 71pp; English.
XX
CC   A method for treating airway disease in a subject has been produced,
CC   which involves the topical administration of an essentially adenosine
CC   free antisense oligonucleotide (ON) to the airway epithelium of the
CC   subject. The present sequence is an antisense oligonucleotide HUMHDCAS4
CC   specific for the human histidine decarboxylase. The method can be used to
CC   treat airway diseases such as cystic fibrosis, asthma, chronic
CC   obstructive pulmonary disease, bronchitis and other airway diseases
CC   characterised by an inflammatory response. By eliminating adenosine from
CC   the antisense ON, its liberation upon antisense degradation is prevented,
CC   thereby preventing adenosine- induced bronchoconstriction in patients
CC   with hyper-reactive airways
XX
SQ   Sequence 20 BP; 0 A; 6 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1201 GGCAGCTAGGAAGAACA 1217
              |||||| ||||||||||
Db         20 GGCAGCAAGGAAGAACA 4


RESULT 2911
AAV44626
ID   AAV44626 standard; DNA; 20 BP.
XX
AC   AAV44626;
XX
DT   24-NOV-1998  (first entry)
XX
DE   Human uncoupling protein-2 UCP2 gene primer hUCP2.CDSR4.
XX
KW   Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
KW   obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
KW   hypothermia; wasting; cachexia; anorexia; inflammation; fever;
KW   hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9831396-A1.
XX
PD   23-JUL-1998.
XX
PF   22-APR-1997;   97WO-US006864.
XX
PR   15-JAN-1997;   97US-0034960P.
XX
PA   (UYDU-) UNIV DUKE.
PA   (REGC ) UNIV CALIFORNIA.
PA   (CNRS ) CENT NAT RECH SCI.
XX
PI   Surwit RS,  Collins SA,  Warden CH,  Seldin MF,  Ricquier D;
PI   Bouillaud F;
XX
DR   WPI; 1998-413823/35.
XX
PT   Method for treating disease associated with altered UCP-2 expression - by
PT   administering agent which enhances or inhibits UCP-2 activity,
PT   effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT   etc.
XX
PS   Disclosure; Fig 1F; 98pp; English.
XX
CC   Primer hUCP2.CDSR4 is used with forward primer hUCP2.CDSF4 (see AAV44625)
CC   in the PCR amplification of a 1100 bp region of the human uncoupling
CC   protein-2 (UCP2) gene coding sequence (see also AAV44595). The invention
CC   relates to a method for treating diseases associated with altered UCP2
CC   expression, such as obesity, diabetes, syndrome X, hypothermia,
CC   hyperinsulinaemia, glucose intolerance, wasting, anorexia, inflammation,
CC   cachexia, fever or hyperthermia
XX
SQ   Sequence 20 BP; 9 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGA 1556
              ||||||| |||||||||
Db          2 AGGAGAGAAGGGAAGGA 18


RESULT 2912
AAX53905/c
ID   AAX53905 standard; DNA; 20 BP.
XX
AC   AAX53905;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Histidine decarboxylase receptor antisense oligonucleotide.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
```

```
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 45; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 20 BP; 0 A; 6 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1201 GGCAGCTAGGAAGAACA 1217
              |||||| ||||||||||
Db         20 GGCAGCAAGGAAGAACA 4


RESULT 2913
AAA33348/c
ID   AAA33348 standard; DNA; 20 BP.
XX
AC   AAA33348;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1037.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Claim 18; Page 395; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 20 BP; 0 A; 6 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1201 GGCAGCTAGGAAGAACA 1217
              |||||| ||||||||||
Db         20 GGCAGCAAGGAAGAACA 4


RESULT 2914
AAF19470/c
ID   AAF19470 standard; DNA; 20 BP.
```

```
XX
AC   AAF19470;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human histidine decarboxylase polynucleotide fragment #1037.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 141; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 20 BP; 0 A; 6 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1201 GGCAGCTAGGAAGAACA 1217
                ||||||  ||||||||||
Db         20 GGCAGCAAGGAAGAACA 4


RESULT 2915
AAF99302
ID   AAF99302 standard; DNA; 20 BP.
XX
AC   AAF99302;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #418.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 46; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
                ||  |||||||||||||||
Db          4 TCGTTTTTTTTTTTTTT 20
```

```
RESULT 2916
AAL40102
ID   AAL40102 standard; RNA; 20 BP.
XX
AC   AAL40102;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Pathogenic microorganism detecting PCR primer SEQ ID No 28.
XX
KW   Tuberculosis; Mycobacterium; bovis; BCG; africanum; microti; canotti;
KW   monitoring therapy; pathogenic microorganism; PCR; primer; ss.
XX
OS   Neisseria gonorrhoeae.
OS   Unidentified.
OS   Chimeric.
XX
PN   WO200252043-A1.
XX
PD   04-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-JP011422.
XX
PR   26-DEC-2000; 2000JP-00396222.
PR   26-DEC-2000; 2000JP-00396321.
PR   29-JUN-2001; 2001JP-00199552.
PR   13-SEP-2001; 2001JP-00278920.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
PI   Shimada M,  Hino F,  Kato I;
XX
DR   WPI; 2002-500769/53.
XX
PT   Detecting pathogenic microorganisms with oligonucleotide probes and
PT   primers, useful in disease diagnosis and monitoring therapy.
XX
PS   Claim 35; Page 91; 106pp; Japanese.
XX
CC   The invention relates to a probe containing a 410 or 20 base pair
CC   sequence, given in the specification. It is capable of detecting the
CC   tuberculosis bacterial group including Mycobacterium tuberculosis,
CC   Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti
CC   and/or Mycobacterium canotti. The method is useful in disease diagnosis
CC   and monitoring therapy. This polynucleotide sequence represents a PCR
CC   primer relating to the detection of pathogenic microorganisms of the
CC   invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 7 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.6e+03;
  Matches   14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              ||||| |||||||||::
Db          4 TGCTTCAATGCCTCGUU 20


RESULT 2917
ABS77947
ID   ABS77947 standard; DNA; 20 BP.
XX
AC   ABS77947;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #431.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 27; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2179
              || |||||||||||||||
Db          4 TCGTTTTTTTTTTTTTT 20


RESULT 2918
ABL39308
ID   ABL39308 standard; DNA; 20 BP.
XX
AC   ABL39308;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 737.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
```

XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 283; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2163 TCCTTTTTTTTTTTTT 2179
              || |||||||||||||
Db          4 TCGTTTTTTTTTTTTT 20
```

RESULT 2919
ABK99977/c
ID ABK99977 standard; DNA; 20 BP.
XX
AC ABK99977;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CADPKL DNA PCR primer #1.
XX
KW Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ss;
KW PCR; neuropsychiatric disorder; attention deficit disorder; ADD; primer;
KW schizoaffective disorder; bipolar disorder; unipolar affective disorder;
KW schizophrenia; adolescent conduct disorder; pharmacogenomics;
KW fingerprinting; paternity testing; antidepressant; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200254939-A2.
XX
PD 18-JUL-2002.
XX
PF 07-JAN-2002; 2002WO-US000367.
XX
PR 09-JAN-2001; 2001US-00757300.
XX
PR 23-AUG-2001; 2001US-00935464.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyer JM, Barrington-Martin R, Parker A;
XX
DR WPI; 2002-590643/63.
XX
PT New variants of calcium/calmodulin-dependent protein kinase-like nucleic
PT acids and polypeptides, useful for diagnosing and treating
PT neuropsychiatric disorders, e.g. schizophrenia, schizoaffective disorder,
PT and bipolar disorder.
XX
PS Claim 17; Page 98; 223pp; English.
XX
CC The invention relates to a nucleic acid comprising a polymorphic region
CC of a Calcium/Calmodulin-dependent protein kinase-like gene (CADPKL)
CC allelic variant, and the polypeptide it encodes. CADPKL allelic variants
CC are useful in determining whether a subject has or is at risk of
CC developing a neuropsychiatric disorder, such as schizophrenia, attention
CC deficit disorder (ADD), schizoaffective disorder, bipolar disorder,
CC unipolar affective disorder and adolescent conduct disorder. The
CC polypeptides, polynucleotides, antibodies and modulators of the CADPKL
CC allelic variants are useful for diagnosing or treating these
CC neuropsychiatric disorders. The polypeptides may be used to raise
CC antibodies to a CADPKL polypeptide. The nucleic acids may be used as
CC probes or primers, in pharmacogenomics for designing therapies for the
CC disorders, and in fingerprinting for detection of different individuals
CC with the same species (e.g. paternity testing). This sequence represents
CC a PCR primer used to amplify human CADPKL DNA of the invention
XX
SQ Sequence 20 BP; 8 A; 0 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1785 CCCCATTCTTTCCTTCT 1801
              |||||||||| ||||||
Db         17 CCCCATTCTTCCCTTCT 1
```

RESULT 2920
ABA05915/c
ID ABA05915 standard; DNA; 20 BP.
XX
AC ABA05915;
XX
DT 05-MAR-2002 (first entry)
XX
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 5.
XX
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW PCR primer; ss.
XX
OS Hepatitis B virus.
XX
PN EP1152063-A1.
XX
PD 07-NOV-2001.
XX
PF 03-MAY-2000; 2000EP-00109436.
XX
PR 03-MAY-2000; 2000EP-00109436.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Schroeder KH, Koike K;
XX
DR WPI; 2002-068256/10.
XX
PT Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT risk for hepatocellular carcinoma, comprises identifying full length HBV

PT transcripts and truncated HBV transcripts in a serum sample.
XX
PS Example 1; Page 6; 25pp; English.
XX
CC The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC stages comprising identification of full length HBV transcripts (I) and
CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC is indicative of a particular infection stage. The method is useful for
CC diagnosing HBV infection stages and determining the risk for developing
CC hepatocellular carcinoma. The present sequence is that of a HBV
CC diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAA 2801
| ||||||||||||||||
Db 17 GCAAAAAAAAAAAAAA 1

RESULT 2921
ABI94179/c
ID ABI94179 standard; DNA; 20 BP.
XX
AC ABI94179;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleptide Zip ID#1266 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2642 TGGGCTGAACCCTAAGG 2658
|||||||||| ||||||
Db 19 TGGGCTGAACGCTAAGG 3

RESULT 2922
ABT23594
ID ABT23594 standard; DNA; 20 BP.
XX
AC ABT23594;
XX
DT 22-MAY-2003 (first entry)
XX
DE Stabilising reagent method related oligo SEQ ID No 46.
XX
KW Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
KW specific amplification; pathogenic microorganism; chimeric;
KW genetic engineering; clinical medicine; ss.
XX
OS Unidentified.
XX
PN WO2002101042-A1.
XX
PD 19-DEC-2002.
XX
PF 12-JUN-2002; 2002WO-JP005832.
XX
PR 12-JUN-2001; 2001JP-00177737.
PR 20-AUG-2001; 2001JP-00249689.
XX
PA (TAKI) TAKARA BIO INC.
XX
PI Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
PI Enoki T, Asada K, Kato I;
XX
DR WPI; 2003-148805/14.
XX
PT Method for stabilizing and storing reaction reagents for specific
PT amplification and detection of nucleic acids particularly in e.g.
PT identifying pathogenic microorganisms or viruses in sample.
XX
PS Example 15; Page 121; 177pp; Japanese.
XX
CC The invention relates to a novel stabilising reaction reagent for use in
CC the amplification and/or detection of a target nucleic acid comprising:
CC preparing a reaction mixture with e.g. a nucleic acid as template, at
CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC defined period of time to form a reaction product during the
CC amplification of such target nucleic acid. The method is useful for
CC stabilising and long-term storage of reaction reagents for highly
CC sensitive and specific amplification and detection of nucleic acids
CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent

```
CC   method of the invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 7 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.6e+03;
  Matches   14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              ||||| |||||||||::
Db          4 TGCTTCAATGCCTCGUU 20


RESULT 2923
ABZ89676
ID   ABZ89676 standard; DNA; 20 BP.
XX
AC   ABZ89676;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4918; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db          4 TCAAAAAAAAAAAAAAA 20


RESULT 2924
ABZ89676/c
ID   ABZ89676 standard; DNA; 20 BP.
XX
AC   ABZ89676;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4918; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
```

```
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTA 2187
              ||||||||||||||| |
Db         20 TTTTTTTTTTTTTTGA 4


RESULT 2925
ABZ89720/c
ID   ABZ89720 standard; DNA; 20 BP.
XX
AC   ABZ89720;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4962; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
```

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CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 2 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2799
              ||| ||||||||||||
Db         17 TTGGAAAAAAAAAAAA 1


RESULT 2926
ABZ89440/c
ID   ABZ89440 standard; DNA; 20 BP.
XX
AC   ABZ89440;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4682; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
```

```
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAAC 2189
                ||||||||||||||| ||
Db         20 TTTTTTTTTTTTTGAC 4


RESULT 2927
ABZ89119
ID   ABZ89119 standard; DNA; 20 BP.
XX
AC   ABZ89119;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4361; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
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CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2800
                || ||||||||||||||
Db          4 TGTAAAAAAAAAAAAAA 20


RESULT 2928
ABZ95164/c
ID   ABZ95164 standard; DNA; 20 BP.
XX
AC   ABZ95164;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human histidine decarboxylase antisense fragment no.1027.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 10406; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
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CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 6 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1201 GGCAGCTAGGAAGAACA 1217
              ||||||  ||||||||||
Db         20 GGCAGCAAGGAAGAACA 4


RESULT 2929
ABZ90649/c
ID   ABZ90649 standard; DNA; 20 BP.
XX
AC   ABZ90649;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5891; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 14 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||||  ||
Db         20 TTTTTTTTTTTTTTGAC 4


RESULT 2930
ACC47638
ID   ACC47638 standard; DNA; 20 BP.
XX
AC   ACC47638;
XX
DT   16-SEP-2003  (first entry)
XX
DE   Human IGFBP5 phosphorothioate antisense oligonucleotide, SEQ ID NO:14.
XX
KW   Human; insulin-like growth factor binding protein 5; IGFBP5; IBP5;
KW   chromosome 2q33-34; IGF signal transduction; IGF regulation; apoptosis;
KW   bone growth stimulator; hyperproliferative disorder; cancer; tumour;
KW   breast; prostate; pancreas; neuroendocrine; inflammatory disorder;
KW   colitis; developmental disorder; growth disorder;
KW   Duchenne muscular dystrophy; metabolic disorder; diabetes; osteoporosis;
KW   osteopetrosis; cytostatic; antiinflammatory; expression inhibition;
KW   phosphorothioate; antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "This oligonucleotide has a phosphorothioate
FT                    backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                    and 3' ends, which are 5 nucleotides in length. Also all
FT                    cytosine residues are 5-methylcytosines"
XX
PN   WO2003030826-A2.
XX
PD   17-APR-2003.
XX
PF   07-OCT-2002; 2002WO-US032060.
XX
PR   09-OCT-2001; 2001US-00975123.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Freier SM;
XX
DR   WPI; 2003-381673/36.
XX
PT   New antisense oligonucleotides for modulating insulin-like growth factor
PT   binding protein 5 gene expression, useful for preventing or treating
PT   cancers, inflammatory disorders, developmental disorders or metabolic
PT   disorders.
XX
PS   Claim 3; Page 75; 105pp; English.
XX
CC   Sequences ACC47637-ACC47667 represent phosphorothioate antisense
CC   oligonucleotides targeted to the human insulin-like growth factor binding
CC   protein 5 (IGFBP5) gene, which inhibit its expression. The antisense
CC   oligonucleotides were designed to target different regions of human
CC   IGFBP5 RNA, and were analysed for their effect on IGFBP5 expression by
CC   quantitative real-time PCR. IGFBP5 (also known as IBP5) is a member of
CC   the insulin-like growth factor superfamily, which are involved in the
CC   regulation of IGF action and bioavailablity, and which also mediate IGF-
CC   independent actions, including inhibition or enhancement of apoptosis.
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CC   IGFBP5 is a key component of the IGF system in bone, having a high
CC   specific binding affinity for hydroxyapatite and extracellular matrix
CC   proteins, and appears to act as a growth factor, stimulating bone
CC   formation via an IGF-independent mechanism. IGFBP5 is also expressed in
CC   other tissues, such as kidney, liver, gut endothelium, lung tubules and
CC   mesenchyme, meninges, notochord, muscle and tongue. Its levels are also
CC   increased in inflamed colon smooth muscle cells in an experimental model
CC   of colitis. It is also thought to play a role in prostate cancer
CC   progression, is expressed with high frequency in neuroendocrine tumours,
CC   and has been shown to be induced in breast cancer cells upon treatment
CC   with antioestrogens used to abolish tamoxifen resistant proliferation.
CC   The oligonucleotides of the invention are useful for diagnosis,
CC   prevention and treatment of IGFBP5-related disorders, such as
CC   hyperproliferative disorders (particularly cancers of the breast,
CC   prostate, pancreas or neuroendocrine system), inflammatory disorders
CC   (e.g., colitis), developmental or growth disorders (e.g., Duchenne
CC   muscular dystrophy), or metabolic disorders (e.g., diabetes,
CC   osteoporosis, or osteopetrosis)
XX
SQ   Sequence 20 BP; 5 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCAGG 470
              |||| ||||||||||||
Db          2 AGGCGGCCAGCAGCAGG 18


RESULT 2931
ACD99727
ID   ACD99727 standard; DNA; 20 BP.
XX
AC   ACD99727;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #413.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 20; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
              || |||||||||||||
Db          4 TCGTTTTTTTTTTTTT 20


RESULT 2932
ADB36804
ID   ADB36804 standard; DNA; 20 BP.
XX
AC   ADB36804;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #418.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 11; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTT 2179
              || |||||||||||||
Db          4 TCGTTTTTTTTTTTTT 20


RESULT 2933
ABK99283
ID   ABK99283 standard; RNA; 21 BP.
XX
```

```
AC   ABK99283;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #13.
XX
KW   Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS   Synthetic.
XX
PN   US2002064771-A1.
XX
PD   30-MAY-2002.
XX
PF   06-APR-2001; 2001US-00828034.
XX
PR   07-APR-2000; 2000US-0195852P.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (FERR/) FERRARI E.
XX
PI   Zhong W,  Hong Z,  Ferrari E;
XX
DR   WPI; 2002-582330/62.
XX
PT   Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT   nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT   and template and primer which do not form a stable duplex in the absence
PT   of HCV NS5B.
XX
PS   Example; Page 6; 17pp; English.
XX
CC   The invention relates to a replicase complex comprising a hepatitis C
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 21 BP; 16 A; 3 C; 1 G; 0 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||| |
Db          1 AAAAAAAAAAAAAAACA 17


RESULT 2934
AAQ71626/c
ID   AAQ71626 standard; DNA; 21 BP.
XX
AC   AAQ71626;
XX
DT   25-MAR-2003  (revised)
DT   29-MAR-1995  (first entry)
XX
DE   Primer to amplify streptococcal pyrogenic exotoxin C (speC).
XX
KW   mitogenic factor; microdetection; group A streptococci; spe;
KW   erythrogenic toxin; streptococcal pyrogenic exotoxin; blastogens;
KW   scarlet fever toxin; erythematous skin reaction; infectious disease;
KW   delayed hypersensitivity; primer; PCR; polymerase chain reaction;
KW   streptolysin O; slo; speA; speB; speC; ss.
XX
OS   Synthetic.
XX
PN   EP613947-A2.
XX
PD   07-SEP-1994.
XX
PF   31-JAN-1994;   94EP-00101386.
XX
PR   01-FEB-1993;   93JP-00037383.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
PI   Yutsudo T,  Okumura K,  Iwasaki M,  Hara A,  Kishishita M,  Takeda Y;
PI   Igarashi H,  Hinuma Y;
XX
DR   WPI; 1994-272994/34.
XX
PT   New mitogenic factor gene from Streptococcus pyogenes - used to develop
PT   prods. for the early diagnosis of infectious disease caused by gp A
PT   streptococci.
XX
PS   Example 3; Page 10; 20pp; English.
XX
CC   The primers AAQ71619-26 were used to compare the methods of
CC   microdetection of group A streptococci, the distribution of the genes
CC   encoding other erythrogenic toxins produced by S. pyrogenes was studied.
CC   Unlike the streptolysin O (slo) and streptococcal pyrogenic exotoxin
CC   (spe) genes, the distribution of the mitogenic factor is limited to group
CC   A Streptococci. (See also AAQ71613-18). (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 21 BP; 9 A; 2 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1967 ATATTTACCTTGAAAAA 1983
              ||||||| |||||||||
Db         17 ATATTTATCTTGAAAAA 1


RESULT 2935
AAZ26573
ID   AAZ26573 standard; DNA; 21 BP.
XX
AC   AAZ26573;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 762.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
```

XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 14 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAA 2798
||||| |||||||||
Db 5 ATTGAATAAAAAAAAAA 21

RESULT 2936
AAZ26500
ID AAZ26500 standard; DNA; 21 BP.
XX
AC AAZ26500;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 689.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAA 2799
|| |||||||||||||
Db 5 TTCAAAAAAAAAAAAA 21

RESULT 2937
AAZ26500/c
ID AAZ26500 standard; DNA; 21 BP.
XX
AC AAZ26500;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 689.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;

```
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAA 2188
                ||||||||||||||  ||
Db         21 TTTTTTTTTTTTTTGAA 5


RESULT 2938
AAZ57386/c
ID   AAZ57386 standard; DNA; 21 BP.
XX
AC   AAZ57386;
XX
DT   05-APR-2000  (first entry)
XX
DE   Factor VII mutagenic primer SEQ ID NO:3.
XX
KW   Factor VII; catalytic active site; blood coagulation; plasma; Factor X;
KW   Factor IX; vasotropic; antiischaemic; anticoagulant; myocardial injury;
KW   post-ischaemic reperfusion; platelet deposition; thrombus formation;
KW   vascular potency; mutagenesis; primer; ss.
XX
OS   Synthetic.
XX
PN   US5997864-A.
XX
PD   07-DEC-1999.
XX
PF   06-JUN-1997;   97US-00871003.
XX
PR   28-FEB-1991;   91US-00662920.
PR   21-MAY-1993;   93US-00065725.
PR   23-MAY-1994;   94WO-US005779.
PR   24-OCT-1994;   94US-00327690.
PR   07-JUN-1995;   95US-00475845.
PR   07-JUN-1996;   96US-00660289.
XX
PA   (NOVO ) NOVO-NORDISK AS.
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Hart CE,  Petersen LC,  Hedner U,  Rasmussen ME;
XX
DR   WPI; 2000-104599/09.
XX
PT   Inhibition or minimization of myocardial injury associated with post-
PT   ischemic reperfusion.
XX
PS   Example 1; Col 17; 34pp; English.
XX
CC   The present invention describes a method for the inhibition or
CC   minimisation of myocardial injury associated with post-ischaemic
CC   reperfusion by administering factor VII, which has at least 1
CC   modification in its catalytic triad (therefore inhibiting the ability of
CC   factor VII to activate plasma factor X or IX). The method can be used for
CC   inhibiting or minimising myocardial injury and for imparting regional
CC   myocardial blood flow associated with post-ischaemic reperfusion. It can
CC   also be used for inhibiting blood coagulation, platelet deposition,
CC   thrombus formation and maintaining or improving vascular potency. Factor
CC   VII can be administered at relatively low doses and does not produce
CC   undesirable side effects. Further it acts specifically at sites of
CC   injury. The present sequence represents a primer used in the mutagenesis
CC   of Factor VII
XX
SQ   Sequence 21 BP; 0 A; 10 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
                ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 2939
AAC59861
ID   AAC59861 standard; DNA; 21 BP.
XX
AC   AAC59861;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Oligonucleotide probe for human DNA clone vb27 1.
XX
KW   Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW   systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW   haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW   Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW   contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW   psoriasis; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055375-A1.
XX
PD   21-SEP-2000.
XX
PF   17-MAR-2000; 2000WO-US007285.
XX
PR   17-MAR-1999;   99US-0124808P.
PR   17-MAR-1999;   99US-0124916P.
PR   17-AUG-1999;   99US-0149639P.
PR   01-OCT-1999;   99US-0157247P.
PR   29-NOV-1999;   99US-0167824P.
PR   15-FEB-2000; 2000US-0182711P.
XX
PA   (ALPH-) ALPHAGENE INC.
XX
PI   Valenzuela D,  Yuan O,  Hoffman H,  Hall J,  Rapiejko P;
XX
DR   WPI; 2000-638211/61.
XX
PT   Novel proteins and polypeptides useful for the treatment of e.g multiple
PT   sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer,
```

```
PT   Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
XX
PS   Disclosure; Page 467; 493pp; English.
XX
CC   This invention relates to 59 human secreted proteins and the nucleotide
CC   sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
CC   represent the proteins and their encoding nucleotide sequences, and
CC   sequences AAB34746-B34771 represent fragments of the proteins. Probes for
CC   the DNA sequences are represented by sequences AAC59847-C59596. The
CC   proteins exhibit neuroprotective, dermatological, immunosuppressive,
CC   antiinflammatory, antianaemic, nootropic, antiparkinsonian,
CC   cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,
CC   antibacterial, virucide, and fungicide activity. The proteins and
CC   nucleotide sequences are useful as nutritional sources or supplements and
CC   in research. The proteins are useful for treating immune deficiency and
CC   disorders, which may be genetic or resulting from infections, autoimmune
CC   disorders such as multiple sclerosis, systemic lupus erythmatosus,
CC   rheumatoid arthritis, and for treating myeloid or lymphoid cell
CC   deficiencies such as anaemias by regulating haematopoiesis. The proteins
CC   are also useful in compositions for bone, cartilage, tendon, ligament
CC   and/or nerve tissue growth or regeneration, for wound healing, tissue
CC   repair and replacement and in the treatment of wounds, incisions and
CC   ulcers. Other uses include in the treatment of central and peripheral
CC   nervous system and neuropathies such as Alzheimer's and Parkinson's
CC   diseases and Shy-Drager syndrome, and mechanical and traumatic disorders,
CC   such as spinal cord disorders, head trauma and stroke. The proteins may
CC   also be used as a contraceptive, and for treating coagulation disorders
CC   such as haemophilias. The protein and nucleotide sequences with cadherin
CC   activity are useful for treating cancer. Other uses for the protein
CC   include for inhibiting the growth, infection or function of, or killing,
CC   infectious agents such as bacteria, virus, fungi and other parasites, for
CC   effecting bodily characteristics such as height, weight, hair colour,
CC   effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,
CC   catabolism, anabolism, processing, utilization, storage or elimination of
CC   dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
CC   effecting behavioural characteristics, providing analgesic effects and
CC   for treating hyperproliferative disorders such as psoriasis
XX
SQ   Sequence 21 BP; 6 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCTG 1848
              |||||| ||||||||||
Db          1 TTTAAACACATTCCCTG 17


RESULT 2940
AAC80381/c
ID   AAC80381 standard; DNA; 21 BP.
XX
AC   AAC80381;
XX
DT   03-MAY-2001  (first entry)
XX
DE   Forward primer #150 used for amplification of HLA-C exon 4.
XX
KW   HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200061795-A2.
XX
PD   19-OCT-2000.
XX
PF   05-APR-2000; 2000WO-EP002998.
XX
PR   09-APR-1999;   99EP-00870068.
PR   11-JUN-1999;   99US-0138614P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   De Canck I,  Rombout A,  Rossau R;
XX
DR   WPI; 2000-647426/62.
XX
PT   Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT   of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
PT   primer sets, useful for subtyping or typing of HLA Class I alleles.
XX
PS   Claim 4; Page 47; 128pp; English.
XX
CC   The present invention relates to a method for the locus-specific,
CC   separate amplification of exon 2, exon 3, and/or exon 4 of human
CC   leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC   for subtyping or typing of HLA class 1 alleles. The present sequence is
CC   an amplification primer used in the method
XX
SQ   Sequence 21 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGACA 1075
              |: |||||||: |||||| |
Db         21 GSCCATGTGACYATCCTGAGA 1


RESULT 2941
AAF57100/c
ID   AAF57100 standard; DNA; 21 BP.
XX
AC   AAF57100;
XX
DT   14-MAY-2001  (first entry)
XX
DE   Human Factor VII mutagenic oligo ZC1656.
XX
KW   Factor VIIa; thrombus; vascular patency; blood coagulation; Factor X;
KW   plasma factor; Factor IX; myocardial injury; human; Factor VII;
KW   mutagenesis; ss.
XX
OS   Homo sapiens.
XX
PN   US6183743-B1.
XX
PD   06-FEB-2001.
XX
PF   20-AUG-1999;   99US-00378907.
XX
PR   28-FEB-1991;   91US-00662920.
PR   28-FEB-1992;   92WO-US001636.
PR   21-MAY-1993;   93US-00065725.
PR   23-MAY-1994;   94WO-US005779.
PR   24-OCT-1994;   94US-00327690.
PR   07-JUN-1995;   95US-00475845.
PR   07-JUN-1996;   96US-00660289.
PR   06-JUN-1997;   97US-00871003.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Hart CE,  Petersen LC,  Hedner U,  Rasmussen ME;
XX
DR   WPI; 2001-201993/20.
XX
PT   Use of modified human factor VIIa with a covalent modification in its
PT   catalytic center, to inhibit thrombus formation or to maintain vascular
PT   patency.
XX
PS   Example 1; Col 17; 34pp; English.
XX
```

```
CC   The invention relates to the use of modified human Factor VIIa for
CC   inhibiting thrombus formation, or maintaining or improving vascular
CC   patency in a patient. The modified factor VIIa comprises a covalent
CC   modification in its catalytic center which effectively interrupts the
CC   blood coagulation cascade. The modifications render Factor VIIa
CC   substantially unable to activate plasma factor IX or X. The modified
CC   Factor VIIa can be used for preventing or treating myocardial injury
CC   associated with post-ischemic reperfusion, for improving regional
CC   myocardial blood flow during reperfusion and maintaining or improving
CC   vascular patency in a patient. The present sequence represents a
CC   mutagenic oligo used for generating a Ser344Ala Factor VII active site
CC   mutant
XX
SQ   Sequence 21 BP; 0 A; 10 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        150 GGGGGACGCCGGACGCC 166
              ||||||||||||| |||
Db         19 GGGGGACGCCGGAGGCC 3


RESULT 2942
ABS97681/c
ID   ABS97681 standard; DNA; 21 BP.
XX
AC   ABS97681;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Histamine N-methyl transferase (HNMT) sequencing Primer #4.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; sequencing.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 13; Page 124; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   sequencing primer used to sequence the polymorphic genes of the invention
XX
SQ   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db         19 CATTTTTTTTTTTTTTT 3


RESULT 2943
ABS97669/c
ID   ABS97669 standard; DNA; 21 BP.
XX
AC   ABS97669;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Histamine N-methyl transferase (HNMT) PCR Primer #4.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
```

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 13; Page 123; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention
XX
SQ Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              | ||||||||||||||
```

Db 19 CATTTTTTTTTTTTTT 3

RESULT 2944
ABT06086
ID ABT06086 standard; DNA; 21 BP.
XX
AC ABT06086;
XX
DT 28-OCT-2002 (first entry)
XX
DE Human IgM heavy chain gene related oligo SEQ ID No 100.
XX
KW Single Primer Amplification; nested oligonucleotide extension reaction;
KW hairpin; SPA; library; ds.
XX
OS Homo sapiens.
XX
PN WO200248401-A2.
XX
PD 20-JUN-2002.
XX
PF 10-DEC-2001; 2001WO-US047727.
XX
PR 11-DEC-2000; 2000US-0254669P.
PR 19-SEP-2001; 2001US-0323400P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Barbas-Frederickson S, Lin Y, Mcwhirter J, Maruyama T;
XX
DR WPI; 2002-500537/53.
XX
PT Amplifying nucleic acid by synthesizing template nucleic acid containing
PT a predetermined sequence and hairpin structure and using the template for
PT target amplification by Single Primer Amplification.
XX
PS Example 4; Page 27; 54pp; English.
XX
CC The invention relates to a method for amplifying a nucleic acid using
CC Single Primer Amplification (SPA). The method comprises synthesising a
CC template nucleic acid containing a predetermined sequence and hairpin
CC structure with the nested oligonucleotide extension reaction. The method
CC is useful for amplifying a nucleic acid, preferably for amplifying a
CC family of related nucleic acid sequences to build a complex library of
CC polypeptides encoded by the sequences. The engineered nucleic acid strand
CC is useful for amplifying a nucleic acid strand by providing a nucleic
CC acid with a predetermined sequence engineered onto its first end, a
CC sequence complementary to the predetermined sequence and a hairpin
CC structure between them and contacting the engineered nucleic acid strand
CC with a primer containing at least a portion of the predetermined
CC sequence. This process is done in the presence of a polymerase and
CC nucleotides under conditions suitable for polymerisation to produce a
CC complementary nucleic acid strand. The method of the invention is useful
CC for producing large amounts of a target nucleic acid sequence and for
CC amplifying simultaneously more than one different target nucleic acid
CC sequence located on the same or different nucleic acid molecules. This
CC polynucleotide sequence represents an oligonucleotide relating to the
CC invention
XX
SQ Sequence 21 BP; 5 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1271 GACCGGACACCCCATGG 1287
              ||| ||||||||||||||
Db          5 GACAGGACACCCCATGG 21
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RESULT 2945
ABT23595

```
ID   ABT23595 standard; DNA; 21 BP.
XX
AC   ABT23595;
XX
DT   22-MAY-2003  (first entry)
XX
DE   Stabilising reagent method related oligo SEQ ID No 47.
XX
KW   Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
KW   specific amplification; pathogenic microorganism; chimeric;
KW   genetic engineering; clinical medicine; ss.
XX
OS   Unidentified.
XX
PN   WO2002101042-A1.
XX
PD   19-DEC-2002.
XX
PF   12-JUN-2002; 2002WO-JP005832.
XX
PR   12-JUN-2001; 2001JP-00177737.
PR   20-AUG-2001; 2001JP-00249689.
XX
PA   (TAKI ) TAKARA BIO INC.
XX
PI   Sagawa H,  Uemori T,  Mukai H,  Yamamoto J,  Tomono J,  Kobayashi E;
PI   Enoki T,  Asada K,  Kato I;
XX
DR   WPI; 2003-148805/14.
XX
PT   Method for stabilizing and storing reaction reagents for specific
PT   amplification and detection of nucleic acids particularly in e.g.
PT   identifying pathogenic microorganisms or viruses in sample.
XX
PS   Example 15; Page 121; 177pp; Japanese.
XX
CC   The invention relates to a novel stabilising reaction reagent for use in
CC   the amplification and/or detection of a target nucleic acid comprising:
CC   preparing a reaction mixture with e.g. a nucleic acid as template, at
CC   least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC   defined period of time to form a reaction product during the
CC   amplification of such target nucleic acid. The method is useful for
CC   stabilising and long-term storage of reaction reagents for highly
CC   sensitive and specific amplification and detection of nucleic acids
CC   particularly in identifying pathogenic microorganisms or viruses in a
CC   sample using chimeric oligonucleotide primers, which is useful in genetic
CC   engineering and clinical medicine. This polynucleotide sequence
CC   represents an oligo relating to the novel stabilising reaction reagent
CC   method of the invention
XX
SQ   Sequence 21 BP; 2 A; 6 C; 4 G; 7 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 2.8e+03;
  Matches   14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        932 TGCTTAAATGCCTCGTT 948
              ||||| |||||||||::
Db          4 TGCTTCAATGCCTCGUU 20


RESULT 2946
AAT28050
ID   AAT28050 standard; DNA; 22 BP.
XX
AC   AAT28050;
XX
DT   31-DEC-1996  (first entry)
XX
DE   3'-primer G for human fibroblasts.
XX
KW   Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW   enhanced differential display; EDD; mRNA preparation; senescent cell;
KW   quiescent cell; dividing cell; senescence-related gene; gene expression;
KW   non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW   donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS   Synthetic.
XX
PN   WO9613610-A2.
XX
PD   09-MAY-1996.
XX
PF   24-AUG-1995;   95WO-US011230.
XX
PR   31-OCT-1994;   94US-00332420.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Hirsch KS,  Villeponteau B,  Feng J,  Funk W,  West MD;
XX
DR   WPI; 1996-251464/25.
XX
PT   Identifying, isolating and regulating senescence-related genes - useful
PT   to ameliorate problems associated with accumulation of senescent cells,
PT   e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS   Claim 6; Page 25; 135pp; English.
XX
CC   AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC   differential display (EDD), which is used in conjuncture with the method
CC   of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC   represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC   5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC   complementary to the poly-A tail of the mRNA. In the method of the
CC   invention, mRNA is isolated from a senescent cell, and a young quiescent
CC   cell, and the mRNAs are amplified in separate reaction mixtures. The
CC   amplified sequences are then separated by size or charge, and the
CC   products are analysed to identify a gene from young quiescent cells and
CC   dividing cells, that is present at a different level from senescent
CC   cells. The method can be used for the rapid and efficient identification
CC   and isolation of senescence-related genes and gene products, and to
CC   detect and distinguish between senescent and non-senescent cells. It can
CC   also be used to destroy cells expressing senescence specific (or related)
CC   gene products, and to screen for compounds capable of altering gene
CC   expression in senescent cells. The method can also be used to ameliorate
CC   problems associated with the accumulation of senescent cells such as age-
CC   related lipofuscin accumulation in the retina, and in the treatment of
CC   AIDS. Also, the method can be used to distinguish young cells from
CC   senescent cells in donor tissue, which is useful in removing senescent
CC   melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC   spots
XX
SQ   Sequence 22 BP; 3 A; 3 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2947
AAT28051
ID   AAT28051 standard; DNA; 22 BP.
XX
AC   AAT28051;
XX
DT   31-DEC-1996  (first entry)
XX
DE   3'-primer H for human fibroblasts.
XX
KW   Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW   enhanced differential display; EDD; mRNA preparation; senescent cell;
```

KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent
CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTGA 1783
||||||||||||||| |
Db 5 AAGCTTTTTTTTTTTA 21

RESULT 2948
AAT28052
ID AAT28052 standard; DNA; 22 BP.
XX
AC AAT28052;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer J for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;

KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent
CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTTGA 1783
||||||||||||||| |
Db 5 AAGCTTTTTTTTTTTA 21

RESULT 2949
AAT58492
ID AAT58492 standard; DNA; 22 BP.
XX
AC AAT58492;
XX
DT 24-MAR-1997 (first entry)
XX
DE First primer #9 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;

```
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 15; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2950
AAT58490
ID   AAT58490 standard; DNA; 22 BP.
XX
AC   AAT58490;
XX
DT   24-MAR-1997  (first entry)
XX
DE   First primer #7 for use in enhanced differential display method.
XX
KW   Differential Display; Enhanced Differential Display; EDD; screening;
KW   gene expression; cell type; different; cell development; gene typing;
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 15; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 3 A; 3 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2951
AAT58491
ID   AAT58491 standard; DNA; 22 BP.
XX
AC   AAT58491;
XX
DT   24-MAR-1997  (first entry)
XX
DE   First primer #8 for use in enhanced differential display method.
XX
KW   Differential Display; Enhanced Differential Display; EDD; screening;
KW   gene expression; cell type; different; cell development; gene typing;
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
```

```
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 15; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2952
AAZ47348
ID   AAZ47348 standard; DNA; 22 BP.
XX
AC   AAZ47348;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer G used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 3 A; 3 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTTA 21


RESULT 2953
AAZ47349
ID   AAZ47349 standard; DNA; 22 BP.
XX
AC   AAZ47349;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer H used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
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CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTA 21


RESULT 2954
AAZ47350
ID   AAZ47350 standard; DNA; 22 BP.
XX
AC   AAZ47350;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer I used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTA 21


RESULT 2955
AAA90070/c
ID   AAA90070 standard; DNA; 22 BP.
XX
AC   AAA90070;
XX
DT   21-DEC-2000  (first entry)
XX
DE   Bovine lysosomal traffic regulator gene (lyst) PCR primer LYST15R.
XX
KW   Bovine; cow; Chediak-Higashi syndrome; CH-S; Lyst; detection; PCR primer;
KW   lysosomal traffic regulator; ss.
XX
OS   Bos sp.
XX
PN   JP2000189176-A.
XX
PD   11-JUL-2000.
XX
PF   25-DEC-1998;   99JP-00294619.
XX
PR   25-DEC-1998;   98JP-00368649.
XX
PA   (KAGO-) KAGOSHIMA KEN.
PA   (CHIK-) CHIKUSAN GIJUTSU KYOKAI SH.
XX
DR   WPI; 2000-551638/51.
XX
PT   Gene diagnosis of bovine Chediak-Higashi syndrome.
XX
PS   Example 1; Page 8; 21pp; Japanese.
XX
CC   This invention relates to a reagent used in a method for the genetic
CC   diagnosis of bovine Chediak-Higashi syndrome (CH-S). The reagent contains
CC   a restriction enzyme Fok I or its isoschizomer and is used for the
CC   detection of the presence or absence of a mutation site in the bovine
CC   Lyst gene. The Lyst gene encodes a lysosomal traffic regulator protein.
CC   The invention includes a kit for the detection of bovine CH-S and a
CC   method for the genetic diagnosis of CH-S. The method is used for the
CC   rapid detection of bovine CH-S and its carrier. The present sequence
CC   represents a bovine Lyst gene PCR primer used in the method of the
CC   invention
XX
SQ   Sequence 22 BP; 1 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        964 CAGAAGAGCCAAATCGA 980
              |||||| ||||||||||
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Db         18 CAGAAGGGCCAAATCGA 2


RESULT 2956
AAA88330/c
ID   AAA88330 standard; DNA; 22 BP.
XX
AC   AAA88330;
XX
DT   21-DEC-2000  (first entry)
XX
DE   Bovine lysosomal traffic regulator gene PCR primer SEQ ID NO:25.
XX
KW   Bovine; Chediak-Higashi syndrome; CH-S; diagnosis; detection; Lyst;
KW   lysosomal traffic regulator; PCR primer; ss.
XX
OS   Bos taurus.
XX
PN   JP2000189165-A.
XX
PD   11-JUL-2000.
XX
PF   25-DEC-1998;   98JP-00368649.
XX
PR   25-DEC-1998;   98JP-00368649.
XX
PA   (KAGO-) KAGOSHIMA KEN.
PA   (CHIK-) CHIKUSAN GIJUTSU KYOKAI SH.
XX
DR   WPI; 2000-551636/51.
XX
PT   Genetic diagnosis of bovine Chediak-Higashi syndrome.
XX
PS   Example 1; Page 7; 23pp; Japanese.
XX
CC   The present invention describes a method for the genetic diagnosis of
CC   bovine Chediak-Higashi syndrome (CH-S). The method comprises getting a
CC   bovine nucleic acid sample, subjecting it to a gene amplifying reaction
CC   and examining the mutation on the nucleic acid fragment. The method can
CC   be used for an easy rapid detection of bovine CH-S and its carrier. The
CC   present sequence represents a PCR primer for the bovine lysosomal traffic
CC   regulator (Lyst) gene nucleotide sequence, which is related to CH-S
XX
SQ   Sequence 22 BP; 1 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        964 CAGAAGAGCCAAATCGA 980
              |||||| ||||||||||
Db         18 CAGAAGGGCCAAATCGA 2


RESULT 2957
AAC80382/c
ID   AAC80382 standard; DNA; 22 BP.
XX
AC   AAC80382;
XX
DT   03-MAY-2001  (first entry)
XX
DE   Forward primer #151 used for amplification of HLA-C exon 4.
XX
KW   HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200061795-A2.
XX
PD   19-OCT-2000.
XX
PF   05-APR-2000; 2000WO-EP002998.
XX
PR   09-APR-1999;   99EP-00870068.
PR   11-JUN-1999;   99US-0138614P.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   De Canck I,  Rombout A,  Rossau R;
XX
DR   WPI; 2000-647426/62.
XX
PT   Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT   of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
PT   primer sets, useful for subtyping or typing of HLA Class I alleles.
XX
PS   Claim 4; Page 47; 128pp; English.
XX
CC   The present invention relates to a method for the locus-specific,
CC   separate amplification of exon 2, exon 3, and/or exon 4 of human
CC   leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC   for subtyping or typing of HLA class 1 alleles. The present sequence is
CC   an amplification primer used in the method
XX
SQ   Sequence 22 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   76.2%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGACA 1075
              |: |||||||: |||||| |
Db         22 GSCCATGTGACYATCCTGAGA 2


RESULT 2958
AAH22191
ID   AAH22191 standard; DNA; 22 BP.
XX
AC   AAH22191;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer G.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
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CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 3 A; 3 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTA 21


RESULT 2959
AAH22192
ID   AAH22192 standard; DNA; 22 BP.
XX
AC   AAH22192;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer H.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTA 21


RESULT 2960
AAH22193
ID   AAH22193 standard; DNA; 22 BP.
XX
AC   AAH22193;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer I.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 22;
  Best Local Similarity   94.1%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTGA 1783
              ||||||||||||||| |
Db          5 AAGCTTTTTTTTTTTA 21


RESULT 2961
ADC10242/c
ID   ADC10242 standard; DNA; 22 BP.
XX
AC   ADC10242;
```

XX
DT 18-DEC-2003 (first entry)
XX
DE Human NOVX polypeptide gene reverse primer SEQ ID NO: 264.
XX
KW ss; primer; cytostatic; antidiabetic; anorectic; cerebroprotective;
KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;
KW thyromimetic; NOVX; pathology; cancer; diabetes; obesity;
KW endocrine disorder; CNS disorder; inflammatory disorder;
KW chromosome mapping; tissue typing; predictive medicine.
XX
OS Homo sapiens.
XX
PN WO2003000842-A2.
XX
PD 03-JAN-2003.
XX
PF 04-JUN-2002; 2002WO-US017443.
XX
PR 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295661P.
PR 06-JUN-2001; 2001US-0296404P.
PR 06-JUN-2001; 2001US-0296418P.
PR 07-JUN-2001; 2001US-0296575P.
PR 11-JUN-2001; 2001US-0297414P.
PR 12-JUN-2001; 2001US-0295573P.
PR 12-JUN-2001; 2001US-0297567P.
PR 14-JUN-2001; 2001US-0298285P.
PR 15-JUN-2001; 2001US-0298528P.
PR 18-JUN-2001; 2001US-0299133P.
PR 19-JUN-2001; 2001US-0299230P.
PR 21-JUN-2001; 2001US-0299949P.
PR 22-JUN-2001; 2001US-0300177P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324669P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358656P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359964P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
DR WPI; 2003-210149/20.
XX
PT New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
PS Example B; SEQ ID NO 264; 772pp; English.
XX
CC The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to a primer used to
CC amplify and isolate the coding sequence for one of the polypeptides of
CC the invention.
XX
SQ Sequence 22 BP; 7 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1256 GAACTTCTCAGCCAAGA 1272
|||||||||||||||||
Db 21 GAATTTCTCAGCCAAGA 5

RESULT 2962
AAC80383/c
ID AAC80383 standard; DNA; 23 BP.
XX
AC AAC80383;
XX
DT 03-MAY-2001 (first entry)
XX
DE Forward primer #152 used for amplification of HLA-C exon 4.
XX
KW HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200061795-A2.
XX
PD 19-OCT-2000.
XX
PF 05-APR-2000; 2000WO-EP002998.
XX
PR 09-APR-1999; 99EP-00870068.
PR 11-JUN-1999; 99US-0138614P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Canck I, Rombout A, Rossau R;
XX
DR WPI; 2000-647426/62.
XX
PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
PT primer sets, useful for subtyping or typing of HLA Class I alleles.
XX
PS Claim 4; Page 47; 128pp; English.
XX
CC The present invention relates to a method for the locus-specific,
CC separate amplification of exon 2, exon 3, and/or exon 4 of human
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC for subtyping or typing of HLA class 1 alleles. The present sequence is
CC an amplification primer used in the method
XX
SQ Sequence 23 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 3 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 23;
Best Local Similarity 76.2%; Pred. No. 3.3e+03;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1055 GCTCATGTGACTCTCCTGACA 1075
              |: ||||||||: |||||| |
Db         23 GSCCATGTGACYATCCTGAGA 3
```

RESULT 2963
ABL51554
ID ABL51554 standard; DNA; 23 BP.
XX
AC ABL51554;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human NSAID regulated gene INDO29 antisense PCR primer SEQ ID NO:5.
XX
KW Human; NAG-1; NSAID associated gene; nonsteroidal anti-inflammatory drug;
KW promoter; MIC-1; macrophage inhibitory cytokine-1; cytostatic; cancer;
KW anticancer; NSAID regulated gene; INDO29; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200220759-A2.
XX
PD 14-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-US027544.
XX
PR 08-SEP-2000; 2000US-0231246P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Eling TE, Baek SJ;
XX
DR WPI; 2002-362249/39.
XX
PT New non-steroidal anti-inflammatory drug activated gene with anti-
PT tumorigenic properties, useful in drug screening, particularly for
PT identifying and characterizing agents or compounds having anti-cancer
PT properties.
XX
PS Example 1; Page 34; 67pp; English.
XX
CC The present invention describes an isolated and purified non-steroidal
CC anti-inflammatory drug activated gene (NSAID associated gene, also
CC designated NAG-1), which comprises a 8902 base pair sequence (I). (I) has
CC cytostatic activity. (I) is useful in drug screening, particularly for
CC identifying and characterising agents that are agonistic or antagonistic
CC to the activation of the promoter region of the NAG-1 gene, the
CC activation of which is correlated with the apoptotic elimination of
CC certain cancers. In particular, the DNA is useful for identifying
CC compounds having anti-cancer properties. NAG-1 peptides encoded by (I)
CC are useful for treating cancer. The NAG-1 gene given in the present
CC invention, having Genbank accession number AF019770, is designated as
CC human macrophage inhibitory cytokine-1 (MIC-1). The present sequence
CC represents a PCR primer for a human NSAID regulated gene designated
CC INDO29, which is used in an example from the present invention
XX
SQ Sequence 23 BP; 6 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 23;
Best Local Similarity 94.1%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1550 GGAAGGAACAGGACTGC 1566
              ||||||| |||||||||
Db          5 GGAAGGACCAGGACTGC 21
```

RESULT 2964
ADC66134
ID ADC66134 standard; DNA; 23 BP.
XX
AC ADC66134;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human CFTR exon 21 PCR primer #1.
XX
KW typing; variable site; cystic fibrosis; human;
KW cystic fibrosis transmembrane conductance regulator; CFTR; PCR primer;
KW ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003074737-A1.
XX
PD 12-SEP-2003.
XX
PF 07-MAR-2003; 2003WO-SE000394.
XX
PR 07-MAR-2002; 2002SE-00000695.
XX
PA (PYRO-) PYROSEQUENCING AB.
XX
PI Schiller A, Dunker J;
XX
DR WPI; 2003-731684/69.
XX
PT Typing at least two variable sites of at least one nucleic acid molecule
PT related to cystic fibrosis by simultaneously or sequentially performing
PT primer extension reactions and determining the pattern of nucleotide
PT incorporation.
XX
PS Example 2; Page 29; 69pp; English.
XX
CC The present invention describes a method for typing at least two variable
CC sites of at least one nucleic acid molecule related to cystic fibrosis.
CC The method comprises: (a) providing at least one nucleic acid molecule of
CC a gene related to cystic fibrosis; (b) providing at least one extension
CC primer, which binds to different predetermined sites in the nucleic acid
CC molecules, where at least one extension primer is designed to extend over
CC at least two potential variable sites in the nucleic acid molecule, and
CC nucleotide; (c) simultaneously or sequentially performing primer
CC extension reactions; and (d) determining the pattern of nucleotide
CC incorporation to obtain a test pattern; optionally (e) comparing the test
CC pattern of step (c) with one or more reference patterns, in order to type
CC the variable sites of the nucleic acid molecules. Also described: (1)
CC diagnosing the genetic predisposition of states, diseases and drug
CC response related to the human cystic fibrosis transmembrane conductance
CC regulator (CFTR) gene; and (2) a kit for use in the method for typing
CC comprising at least one extension primer. The method is useful for typing
CC at least two variable sites of at least one nucleic acid molecule related
CC to cystic fibrosis. The present sequence represents a PCR primer for
CC human CFTR, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 23 BP; 0 A; 5 C; 1 G; 16 T; 0 U; 1 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 23;
Best Local Similarity 81.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2156 TTTTTTCTCCTTTTTTTTTT 2176
              :|| |||| ||||| ||||||
Db          1 BTTCTTCTTCTTTTCTTTTT 21
```

RESULT 2965
ABL57074
ID ABL57074 standard; DNA; 24 BP.
XX
AC ABL57074;
XX
DT 22-JUL-2002 (first entry)

```
XX
DE   Molecular beacon oligonucleotide probe.
XX
KW   Molecular beacon; probe; fluorophore; nanoparticle;
KW   nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .20
FT                   /*tag=  d
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-20 of
FT                   sequence in ABL57070"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "disulfide or primary amine joined via a linker to
FT                   the 5' phosphate"
FT   stem_loop       2. .24
FT                   /*tag=  a
FT   modified_base   24
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' linker joined to an amine-reactive
FT                   fluorophore"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 5; Page 33; 62pp; English.
XX
CC   The present sequence is an oligonucleotide probe that was used in a
CC   molecular beacon in an example from the invention. The probe forms a
CC   hairpin structure in the native state. The 5' end of the probe is
CC   covalently joined via a linker to a disulfide or primary amine. The 3'
CC   end of the probe is covalently joined to an amine-reactive fluorescent
CC   dye such as fluorescein. A gold surface or other metal film surface is
CC   attached to the disulfide or amine group to form the molecular beacon. In
CC   the native state with hybridised termini, the proximity of the
CC   fluorophore and quencher (gold surface) in the molecular beacon is such
CC   that little or no fluorescence is detectable. Upon hybridisation of the
CC   central complementary stretch of the probe to a target sequence (e.g. the
CC   sequence in ABL57070), the hairpin undergoes a conformational change
CC   resulting in an increase in fluorescence, the extent of which is
CC   proportional to the amount of binding partner present. The invention
CC   relates generally to the use of metal surface quenchers such as particles
CC   or films for high sensitivity applications in, for example, detection and
CC   diagnostic systems
XX
SQ   Sequence 24 BP; 1 A; 3 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
                ||||||||||||||| |
Db          6 TTTTTTTTTTTTTTCT 22


RESULT 2966
ADC51227/c
ID   ADC51227 standard; DNA; 24 BP.
XX
AC   ADC51227;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Brassica defensin gene PCR primer #2.
XX
KW   antimicrobial protein; defensin; transgenic plant;
KW   composite disease resistance; pathogenic bacteria;
KW   rice white leaf blight; brown-stripe disease; glume blight;
KW   seedling damping-off disease; filamentous fungi; rice blight;
KW   sheath blight disease; leaf blight; gene; ss; PCR.
XX
OS   Unidentified.
OS   Brassica sp.
XX
PN   JP2003088379-A.
XX
PD   25-MAR-2003.
XX
PF   18-SEP-2001; 2001JP-00283117.
XX
PR   18-SEP-2001; 2001JP-00283117.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-621123/59.
XX
PT   Novel protein from Brassica campestris, useful as antimicrobial against
PT   plant pathogenic filamentous fungi or pathogenic bacteria, especially for
PT   treating e.g. rice white leaf blight and sheath blight disease.
XX
PS   Example 1; SEQ ID NO 7; 34pp; Japanese.
XX
CC   The invention comprises the amino acid and coding sequences of
CC   antimicrobial (defensin) proteins from Brassica. The DNA and protein
CC   sequences of the invention are useful for producing transformed plants
CC   with composite disease resistance, especially resistant to diseases
CC   caused by pathogenic bacteria, such as: rice white leaf blight, brown-
CC   stripe disease, glume blight, and seedling damping-off disease. As well
CC   as diseases caused by filamentous fungi, such as: rice blight, sheath
CC   blight disease, and leaf blight. The present DNA sequence represents a
CC   PCR primer that was used in the exemplification of the invention.
XX
SQ   Sequence 24 BP; 1 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
                ||||||||||||||| |
Db         24 AAAAAAAAAAAAAAAGA 8


RESULT 2967
AAH44680/c
ID   AAH44680 standard; DNA; 24 BP.
XX
AC   AAH44680;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human Kazal type inhibitory factor 35 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; Kazal type inhibitory factor 35; malignant tumour; haemopathy;
```

KW human immunodeficiency virus; HIV infection; immunological disease;
KW inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1301765-A.
XX
PD 04-JUL-2001.
XX
PF 29-DEC-1999; 99CN-00127224.
XX
PR 29-DEC-1999; 99CN-00127224.
XX
PA (UYFU-) UNIV FUDAN.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-550471/62.
XX
PT New polypeptide-human kazal type inhibitory factor 35 for treating
PT malignant tumor, hemopathy, human immunodeficiency virus infection,
PT immunological diseases and various inflammations.
XX
PS Example 3; Page 17 (Disclosure); 31pp; Chinese.
XX
CC The present invention discloses a new kind of polypeptide designated
CC human Kazal type inhibitory factor 35. Also described are polynucleotides
CC encoding this polypeptide, and a DNA recombination process to produce the
CC polypeptide. The present invention also describes a method of applying
CC the polypeptide to treat various diseases, such as malignant tumour,
CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
CC diseases and various inflammations. The present sequence represents a PCR
CC primer used in the isolation of human Kazal type inhibitory factor 35,
CC which is used in an example from the present invention
XX
SQ Sequence 24 BP; 1 A; 0 C; 4 G; 19 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 24;
Best Local Similarity 94.1%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2802
|| ||||||||||||||
Db 24 AATAAAAAAAAAAAAA 8

RESULT 2968
AAZ95163
ID AAZ95163 standard; DNA; 24 BP.
XX
AC AAZ95163;
XX
DT 05-JUN-2000 (first entry)
XX
DE Forward primer #9 used to sequence UGT2B7 polymorphic fragments.
XX
KW UDP-glucuronosyltransferase 2B7; UGT2B7; polymorphism; metabolism; SNPs;
KW drug interaction; detect; human; single nucleotide polymorphism; primer;
KW ss.
XX
OS Synthetic.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US016675.
XX
PR 28-JUL-1998; 98US-0094391P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions.
XX
PS Example 2; Page 22; 72pp; English.
XX
CC This sequence represents a primer used to sequence polymorphic fragments
CC of the human UDP-glucuronosyltransferase 2B7 (UGT2B7) gene. UDP-
CC glucuronosyltransferases (UGTs) are a family of enzymes that catalyse the
CC glucuronic acid conjugation of a wide range of endogenous and exogenous
CC substrates. The UGT2B gene subfamily encode steroid metabolizing isoforms
CC in the liver. Alteration of the expression or function of UGTs may effect
CC drug metabolism. The invention relates to non-chromosomal nucleic acid
CC molecules, which comprise human UGT2B sequence polymorphisms (see
CC AAZ95051-Z95110). Probes which detect the UGT2B locus polymorphisms can
CC be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines
XX
SQ Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 24;
Best Local Similarity 94.1%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAA 2802
||||||| |||||||||
Db 1 AAAAAAAGAAAAAAAAA 17

RESULT 2969
AAD46030
ID AAD46030 standard; DNA; 24 BP.
XX
AC AAD46030;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human UGT2B7 DNA sequencing forward primer #9.
XX
KW Human; UDP-glucoronosyl transferase; UGT; UGT2B7; toxicity; cancer;
KW therapy; epirubicin; cytostatic; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200259375-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002083.
XX
PR 26-JAN-2001; 2001US-0264534P.
XX
PA (UYCH-) UNIV CHICAGO.
XX
PI Ratain MJ, Innocenti F, Das S, Iyer L, Sawyer M;
XX
DR WPI; 2002-691534/74.
XX
PT Determining the dose of a UGT2B7-glucuronidated drug for treating cancer,
PT comprises determining the level of UGT2B7 activity or expression in a
PT patient.
XX

```
PS   Disclosure; Page 53; 160pp; English.
XX
CC   The invention relates to an UDP-glucoronosyl transferase (UGT) enzyme,
CC   UGT2B7. The invention also relates to compositions and methods for
CC   optimising UGT2B7 substrate dosings and for predicting UGT2B7 substrate
CC   toxicity. The method is useful in determining the dose of a UGT2B7-
CC   glucuronidated drug that may be used in treating cancer patients. It is
CC   also useful in determining persons at risk for epirubicin toxicity, in
CC   reducing or eliminating side effects associated with epirubicin
CC   treatment, and in ways of increasing the efficacy of dosage regimens. The
CC   present sequence is a primer used for sequencing human UGT2B7 DNA
XX
SQ   Sequence 24 BP; 16 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 24;
  Best Local Similarity   94.1%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||| |||||||||
Db          1 AAAAAAAGAAAAAAAAA 17


RESULT 2970
AAC96418/c
ID   AAC96418 standard; DNA; 25 BP.
XX
AC   AAC96418;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #20.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   76.0%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAA 2800
              | |  |||  || ||||||||||||
Db         25 GGTCAAATCTAAGAAAAAAAAAAAA 1


RESULT 2971
AAC96237
ID   AAC96237 standard; DNA; 25 BP.
XX
AC   AAC96237;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #204.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 47; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 2 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   76.0%;  Pred. No. 3.7e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||||  |  | ||| |
Db          1 TTTTTTTTTTTTTGCAAGTAGAACG 25


RESULT 2972
AAC96175/c
ID   AAC96175 standard; DNA; 25 BP.
XX
AC   AAC96175;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #142.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
```

KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 46; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 25;
Best Local Similarity 94.1%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAA 2799
||| ||||||||||||
Db 17 TTGGAAAAAAAAAAAA 1

RESULT 2973
AAC96624/c
ID AAC96624 standard; DNA; 25 BP.
XX
AC AAC96624;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #1.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 54; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 25;
Best Local Similarity 94.1%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAA 2798
| ||||||||||||||
Db 17 ACTGAAAAAAAAAAAA 1

RESULT 2974
AAC95821/c
ID AAC95821 standard; DNA; 25 BP.
XX
AC AAC95821;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #1.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 40; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX

```
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              | ||||||||||||||||
Db         17 ACTGAAAAAAAAAAAAA 1


RESULT 2975
AAC95722
ID   AAC95722 standard; DNA; 25 BP.
XX
AC   AAC95722;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #19.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
              |||||||||||||| ||
Db          1 TTTTTTTTTTTTAAATT 17


RESULT 2976
AAC96424
ID   AAC96424 standard; DNA; 25 BP.
XX
AC   AAC96424;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #26.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
              |||||||||||||| ||
Db          1 TTTTTTTTTTTTAAATT 17


RESULT 2977
ABL57069
ID   ABL57069 standard; DNA; 25 BP.
XX
AC   ABL57069;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon oligonucleotide probe.
XX
KW   Molecular beacon; probe; fluorophore; nanoparticle;
KW   nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .25
FT                   /*tag=  a
FT   misc_binding    1. .21
FT                   /*tag=  e
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-21 of
FT                   sequence in ABL57071"
```

```
FT   misc_binding    1. .20
FT                   /*tag=  d
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-20 of
FT                   sequence in ABL57070"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5' disulfide group"
FT   modified_base   25
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' amino group"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 1; Page 22; 62pp; English.
XX
CC   The present sequence is an oligonucleotide probe that was used in a
CC   molecular beacon in examples from the invention. The probe has a hairpin
CC   structure in the native state. The disulfide group at the 5' end of the
CC   probe was covalently linked to the 5' phosphate via a (CH2)6 spacer, and
CC   the primary amino group at the 3' was attached to the 3' hydroxyl via a
CC   (CH2)7 spacer. An amino-reactive dye, such as fluorescein, rhodamine 6G
CC   or Texas Red, was covalently linked to the 3'-amino group. A
CC   monomaleimido-gold nanoparticle was then covalently linked to the 5'
CC   sulfhydryl group to form the molecular beacon. In the native state with
CC   hybridised termini, the proximity of the fluorophore and quencher (gold
CC   nanoparticle) in the molecular beacon is such that little or no
CC   fluorescence is detectable. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence (e.g. the
CC   sequence in ABL57070 or ABL57071), the hairpin undergoes a conformational
CC   change resulting in an increase in fluorescence, the extent of which is
CC   proportional to the amount of binding partner present. Single mismatch
CC   detection was demonstrated. The invention relates generally to the use of
CC   metal surface quenchers such as particles or films for high sensitivity
CC   applications in, for example, detection and diagnostic systems
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          6 TTTTTTTTTTTTTTCT 22


RESULT 2978
ABL57077
ID   ABL57077 standard; DNA; 25 BP.
XX
AC   ABL57077;
XX
DT   22-JUL-2002  (first entry)

XX
DE   Molecular beacon oligonucleotide probe.
XX
KW   Molecular beacon; probe; fluorophore; nanoparticle;
KW   nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .22
FT                   /*tag=  a
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "5' amine"
FT   misc_binding    6. .21
FT                   /*tag=  d
FT                   /bound_moiety= "Target oligonucleotide"
FT                   /note= "Forms double-stranded region with bases 1-16 of
FT                   sequence in ABL57075"
FT   modified_base   25
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' DABCYL"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is an oligonucleotide probe that was used in a
CC   molecular beacon in an example from the invention. A rhodamine 6G dye was
CC   attached to the primary amine at the 5' end of the oligonucleotide, which
CC   had DABCYL attached to its 3' end. A rhodamine-DNA-gold conjugate
CC   molecular beacon (see ABL57069) was also used. In the native state with
CC   hybridised termini, the proximity of the fluorophore and quencher (gold
CC   nanoparticle) in the molecular beacon is such that little or no
CC   fluorescence is detectable. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, the hairpin
CC   undergoes a conformational change resulting in an increase in
CC   fluorescence, the extent of which is proportional to the amount of
CC   binding partner present. Single mismatch detection was demonstrated. The
CC   invention relates generally to the use of metal surface quenchers such as
CC   particles or films for high sensitivity applications in, for example,
CC   detection and diagnostic systems
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          6 TTTTTTTTTTTTTTCT 22
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RESULT 2979
ADA14835
ID   ADA14835 standard; DNA; 25 BP.
XX
AC   ADA14835;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin oligonucleotide, #1, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= thiol group"
FT   misc_binding    6. .20
FT                   /*tag=  b
FT                   /bound_moiety= "Target sequence #1"
FT                   /note= "Forms a doube-stranded region with the target
FT                   sequence shown in example 2"
FT   modified_base   25
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= amino group"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 2; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
CC   complementary probe. Also claimed is a microarray comprising the hairpin
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide, #1,
CC   used in an example of the invention.
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
                ||||||||||||||| |
Db          6 TTTTTTTTTTTTTTCT 22


RESULT 2980
AAD57902
ID   AAD57902 standard; DNA; 25 BP.
XX
AC   AAD57902;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Oligonucleotide used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Linked to Au particle"
FT   modified_base   25
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Linked to Dye"
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20B; 146pp; English.
XX
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CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is an
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||| |
Db          6 TTTTTTTTTTTTTTCT 22


RESULT 2981
AAH28298/c
ID   AAH28298 standard; RNA; 29 BP.
XX
AC   AAH28298;
XX
DT   05-SEP-2001  (first entry)
XX
DE   3' untranslated region sequence from neuronal cadherin gene.
XX
KW   mRNA protein complex; tumour development; cell aging; death;
KW   ribonomic profile; RNA-binding protein; ss.
XX
OS   Unidentified.
XX
PN   WO200148480-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035583.
XX
PR   28-DEC-1999;   99US-0173338P.
XX
PA   (KEEN/) KEENE J D.
XX
PI   Keene JD,  Tenenbaum SA,  Carson C;
XX
DR   WPI; 2001-425706/45.
XX
PT   Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT   sample comprising the complex with ligand that binds to a component of
PT   the complex and separating complex by binding ligand with a binding
PT   molecule.
XX
PS   Example 6; Page 31; 49pp; English.
XX
CC   The specification describes a method for partitioning endogenous cellular
CC   mRNA-protein (mRNP) complexes. The method comprises contacting a
CC   biological sample comprising mRNP complex with ligand that specifically
CC   binds a component of mRNP complex, separating mRNP complex by binding the
CC   ligand with a molecule specific for ligand, which is attached to the
CC   solid support and then collecting the mRNP complex by removing the
CC   complex from the support. The method is useful for in vivo partitioning
CC   of cellular mRNA protein complexes in a biological sample. The method is
CC   useful for determining the ribonomic profile of a cell which has numerous
CC   uses including monitoring of tumour development, state of growth or state
CC   of development, perturbations of a biological system such as disease,
CC   drug or toxin treatment and the state of cell aging or death,
CC   distinguishing ribonomic profiles among organisms, to discriminate
CC   between transcriptional and post-transcriptional contributions to gene
CC   expression and to track the movement of RNAs through RNP complexes,
CC   including the interactions of combinations of proteins with RNAs in RNP
CC   complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC   untranslated region (UTR) of mRNA of various genes. The sequences contain
CC   target sequences for RNA-binding proteins
XX
SQ   Sequence 29 BP; 4 A; 1 C; 0 G; 0 T; 24 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 29;
  Best Local Similarity   76.0%;  Pred. No. 4.2e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              ||||   |||||||   ||||||||
Db         25 AGAAAATAAAAAAATTTAAAAAAAA 1


RESULT 2982
ADA26182/c
ID   ADA26182 standard; DNA; 29 BP.
XX
AC   ADA26182;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:27.
XX
KW   genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;
KW   characteristic; single nucleotide polymorphism; SNP; genotyping;
KW   chromosome 1; gene; ds.
XX
OS   Synthetic.
OS   Oryza sativa.
XX
PN   WO2003070934-A1.
XX
PD   28-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-JP001317.
XX
PR   25-FEB-2002; 2002JP-00048115.
XX
PA   (PLAN-) PLANT GENOME CENT CO LTD.
XX
PI   Minobe Y,  Monna L,  Kitazawa N,  Yoshino R,  Suzuki J;
XX
DR   WPI; 2003-697617/66.
XX
PT   Judging the genotype of a region around a plant sd-1 gene with
PT   polymorphism-obtained markers isolated by positional cloning, useful in
PT   genotyping for examination of semi-dwarf character of rice.
XX
PS   Disclosure; Page 15; 104pp; Japanese.
XX
CC   The present invention describes a method for judging the genotype of a
CC   region around a plant semi-dwarf (sd-1) gene in which polymorphisms are
CC   present, by detecting the polymorphisms. Also described: (1) examining
CC   semi-dwarf characteristics of a plant using the judgment method with
CC   detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA
CC   regions, which are primers for judging the genotype of a region around a
CC   plant sd-1 gene; (3) reagents for judging the genotype of a region around
CC   a plant sd-1 gene containing these oligonucleotides; and (4) reagents for
CC   examining the semi-dwarf character of a plant containing the
CC   oligonucleotides. The method is for judging the genotype of a region
CC   around a plant sd-1 gene, which is applicable in genotyping by (d)CAPS
CC   ((derived) cleaved amplified polymorphic sequence) for examination of the
CC   semi-dwarf character of rice to identify desirable strains e.g. with high
CC   crop yield, pest resistance and resistance to flooded water. The method
CC   is easy and quick, in which a seedling is required for studying single
CC   nucleotide polymorphisms (SNPs) for genotyping, without needing
CC   cultivation of seedling to fully-grown plant for judging heterozygote and
CC   distinguishing morphology. The present sequence represents a rice sd-1
CC   DNA fragment, which is given in the exemplification of the present
CC   invention. Rice sd-1 is located on chromosome 1.
XX
SQ   Sequence 29 BP; 0 A; 6 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 29;
```

```
  Best Local Similarity   76.0%;  Pred. No. 4.2e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | ||  |||| ||| |||| |||||
Db         27 AAAAAAGAAAGAAAGAAAAGAAAAA 3


RESULT 2983
AAV06769/c
ID   AAV06769 standard; DNA; 33 BP.
XX
AC   AAV06769;
XX
DT   02-JUN-1998  (first entry)
XX
DE   Oligonucleotide containing a pentanucleotide loop.
XX
KW   Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
KW   circular; bridged; hairpin; detection; pentanucleotide loop; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   repeat_region   1. .14
FT                   /*tag=  a
FT   misc_structure  15. .19
FT                   /*tag=  b
FT                   /note= "pentanucleotide loop"
XX
PN   WO9714708-A1.
XX
PD   24-APR-1997.
XX
PF   29-MAR-1996;   96WO-US004525.
XX
PR   04-OCT-1995;   95US-0004778P.
XX
PA   (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI   Kool ET;
XX
DR   WPI; 1997-245044/22.
XX
PT   New C-5 thiol-substituted nucleoside derivatives - whose presence in
PT   oligo:nucleotide(s) allows formation of covalent cross-links between non-
PT   complementary DNA domains.
XX
PS   Example 7; Page 89; 122pp; English.
XX
CC   This sequence represents an oligonucleotide containing a pentanucleotide
CC   loop. The invention relates to C-5 thiol-substituted nucleoside
CC   derivatives which can be incorporated into an RNA or DNA strand during
CC   synthesis of oligonucleotides. These compounds can be in the form of
CC   cross-linked linear, cross-linked hairpin or bridged circular oligo-
CC   nucleotides. The oligonucleotides may be used for detection and isolation
CC   of target nucleic acids, or for targeting drugs to specific cell types
CC   (e.g. for treatment of Alzheimer's disease, beta-thalassemia,
CC   osteogenesis imperfecta, arthritis, sickle cell anaemia or viral
CC   infections). The presence of the nucleoside derivatives in a linear
CC   oligonucleotide allows the formation of covalent crosslinks between non-
CC   complementary DNA domains
XX
SQ   Sequence 33 BP; 0 A; 8 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.4;  DB 1;  Length 33;
  Best Local Similarity   76.0%;  Pred. No. 4.3e+03;
  Matches   19;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | ||  ||| ||||| || ||||||
Db         29 AAAAAAGAAGAAAAAGAAGAAAAAA 5


RESULT 2984
AAF82119
ID   AAF82119 standard; DNA; 16 BP.
XX
AC   AAF82119;
XX
DT   27-JUN-2001  (first entry)
XX
DE   Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
KW   Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
KW   diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001025389-A.
XX
PD   30-JAN-2001.
XX
PF   15-JUL-1999;   99JP-00201279.
XX
PR   15-JUL-1999;   99JP-00201279.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-303742/32.
XX
PT   TSA7005 gene, encoding a polypeptide useful for the diagnosis and
PT   treatment of diseases associated with its expression.
XX
PS   Example 1; Page 24; 25pp; Japanese.
XX
CC   The present sequence represents a PCR primer which is used in an example
CC   from the present invention for the isolation of human TSA7005 gene. The
CC   human TSA7005 protein shares 32% homology with human and mouse Reg
CC   proteins, and 34% homology with the rat Reg protein. TSA7005 has
CC   pancreatic beta cell growth activity and hypoglycaemic activity. The
CC   TSA7005 protein can be used for the diagnosis and treatment of diseases
CC   associated with the gene and its expression product
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||:|
Db          1 TTTTTTTTTTTTTTHA 16


RESULT 2985
AAF82119/c
ID   AAF82119 standard; DNA; 16 BP.
XX
AC   AAF82119;
XX
DT   27-JUN-2001  (first entry)
XX
DE   Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
KW   Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
KW   diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001025389-A.
XX
PD   30-JAN-2001.
XX
PF   15-JUL-1999;   99JP-00201279.
XX
```

```
PR   15-JUL-1999;   99JP-00201279.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-303742/32.
XX
PT   TSA7005 gene, encoding a polypeptide useful for the diagnosis and
PT   treatment of diseases associated with its expression.
XX
PS   Example 1; Page 24; 25pp; Japanese.
XX
CC   The present sequence represents a PCR primer which is used in an example
CC   from the present invention for the isolation of human TSA7005 gene. The
CC   human TSA7005 protein shares 32% homology with human and mouse Reg
CC   proteins, and 34% homology with the rat Reg protein. TSA7005 has
CC   pancreatic beta cell growth activity and hypoglycaemic activity. The
CC   TSA7005 protein can be used for the diagnosis and treatment of diseases
CC   associated with the gene and its expression product
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2799
              |:|||||||||||||
Db         16 TDAAAAAAAAAAAAAA 1


RESULT 2986
AAH27758
ID   AAH27758 standard; DNA; 16 BP.
XX
AC   AAH27758;
XX
DT   15-AUG-2001  (first entry)
XX
DE   Primer used in human LUNX cDNA isolation.
XX
KW   LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001078772-A.
XX
PD   27-MAR-2001.
XX
PF   07-SEP-1999;   99JP-00253186.
XX
PR   07-SEP-1999;   99JP-00253186.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-313367/33.
XX
PT   Polynucleotide encoding LUNX gene product useful for the detection of
PT   cancer especially micrometastatic cancer.
XX
PS   Example 1; Page 27; 30pp; Japanese.
XX
CC   This invention relates to the human LUNX protein and the polynucleotide
CC   sequence encoding it. The invention includes a vector containing a LUNX
CC   polynucleotide, a host cell transformed with the vector, and an antibody
CC   that binds to LUNX. The gene can be used for cancer diagnosis and
CC   diagnosis of micrometastatic cancer and for the production of the LUNX
CC   gene product. The present sequence represents a primer used in the
CC   isolation of cDNA encoding human LUNX
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||:|
Db          1 TTTTTTTTTTTTTTVA 16


RESULT 2987
AAH27758/c
ID   AAH27758 standard; DNA; 16 BP.
XX
AC   AAH27758;
XX
DT   15-AUG-2001  (first entry)
XX
DE   Primer used in human LUNX cDNA isolation.
XX
KW   LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001078772-A.
XX
PD   27-MAR-2001.
XX
PF   07-SEP-1999;   99JP-00253186.
XX
PR   07-SEP-1999;   99JP-00253186.
XX
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-313367/33.
XX
PT   Polynucleotide encoding LUNX gene product useful for the detection of
PT   cancer especially micrometastatic cancer.
XX
PS   Example 1; Page 27; 30pp; Japanese.
XX
CC   This invention relates to the human LUNX protein and the polynucleotide
CC   sequence encoding it. The invention includes a vector containing a LUNX
CC   polynucleotide, a host cell transformed with the vector, and an antibody
CC   that binds to LUNX. The gene can be used for cancer diagnosis and
CC   diagnosis of micrometastatic cancer and for the production of the LUNX
CC   gene product. The present sequence represents a primer used in the
CC   isolation of cDNA encoding human LUNX
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2799
              |:|||||||||||||
Db         16 TBAAAAAAAAAAAAAA 1


RESULT 2988
AAD44145
ID   AAD44145 standard; DNA; 16 BP.
XX
AC   AAD44145;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #5 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
```

```
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 1.7e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTT 2179
              |:|||||||||||||
Db          1 CVTTTTTTTTTTTTT 16


RESULT 2989
AAX18388
ID   AAX18388 standard; DNA; 17 BP.
XX
AC   AAX18388;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 29.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 16


RESULT 2990
AAX18388/c
ID   AAX18388 standard; DNA; 17 BP.
XX
AC   AAX18388;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 29.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
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```
              :|||||||||||||||
Db         16 BAAAAAAAAAAAAAAA 1


RESULT 2991
AAS06666
ID   AAS06666 standard; DNA; 17 BP.
XX
AC   AAS06666;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human differential display primer generic sequence.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 17
FT                   /*tag=  a
FT                   /note= "Optionally absent"
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Claim 29; Page 55; 77pp; English.
XX
CC   The sequence represents a generic downstream PCR primer for use in DDRT-
CC   PCR experiments which demonstrate the method of the invention. The method
CC   relates to evaluating a cellular response to an environmental compound,
CC   comprising determining or comparing the expression levels of at least one
CC   endogenous gene e.g by differential display of reverse transcribed mRNAs
CC   by PCR (DDRT-PCR). The method can be adapted to identify compounds that
CC   act on the level of endogenous gene expression through activating nuclear
CC   receptors. The method is useful in toxicological analysis, diagnostics,
CC   for diagnosing cancer (e.g. testicular, breast, prostate and
CC   endometrium), asthma, hypospadia, cryptorchism and/or allergy, and for
CC   evaluating the efficiency of a treatment for hormonal deficiency or
CC   hormonal replacement therapy, in a human such as a post-menopausal
CC   female. The method is also useful for identifying environmental chemicals
CC   or pharmaceutical compositions that interact with endocrine systems, and
CC   for detecting chemicals that pose a health threat. Expression levels of
CC   endogenous genes are determined rapidly using a sensitive technique, and
CC   the expression of any gene can be monitored. The assays are far more
CC   informative than the currently used assays, and significantly reduces the
CC   number of animals required for the testing, as it is expected that
CC   essentially all the animals in a test group will respond to the compound
XX
SQ   Sequence 17 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              |||||||||||||||:
Db          1 AAGCTTTTTTTTTTTV 16


RESULT 2992
AAS14174
ID   AAS14174 standard; DNA; 17 BP.
XX
AC   AAS14174;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Modified Poly-T Primer #1 used in construction of probe sets.
XX
KW   WRAP-Probe; gene expression array; global amplification; RNA array; ss;
KW   tissue microarray; drug discovery assay; reporter binding site; forensic;
KW   diagnostic; genomic analysis; universal linker; poly-T primer.
XX
OS   Synthetic.
XX
PN   WO200166802-A1.
XX
PD   13-SEP-2001.
XX
PF   09-MAR-2001; 2001WO-US007508.
XX
PR   09-MAR-2000; 2000US-0187982P.
XX
PA   (GENE-) GENETAG TECHNOLOGY INC.
XX
PI   Shafer DA;
XX
DR   WPI; 2001-596845/67.
XX
PT   Novel probe sets with common universal linkers at one or both ends (WRAP
PT   probes) for gene expression arrays to provide global amplification of
PT   probe set and to provide common equivalent signaling regardless of
PT   length.
XX
PS   Disclosure; Page 88; 97pp; English.
XX
CC   The invention relates to a probe set for gene expression arrays to
CC   provide common equivalent signalling per probe and global amplification
CC   of the set. The probe set has a pool of modified cDNA probes, each probe
CC   having a central target specific segment copied from a portion of a
CC   single mRNA transcript and a universal linker (a WRAP-Probe) located on
CC   one or both terminal ends. The universal linker has reporter binding
CC   sites to join common reporters to the probes and primer binding sites to
CC   copy and amplify the probe. The probes and reporters are useful in
CC   diagnostic or drug discovery assays for a wide range of biomedical
CC   samples, including detection of nucleic acids and gene expression
CC   profiles in human diagnostics, forensics and genomic analysis. The
CC   methods are useful for amplifying and identifying any unknown DNA
CC   fragment and also for improving sensitivity with tissue microarrays or
CC   RNA arrays. The methods improve the quantification of gene expression and
CC   allow highly improved detection of rare transcripts or very small
CC   samples. This sequence represents a poly-T primer used in the
CC   construction of probe sets
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 16
```

```
RESULT 2993
AAS14174/c
ID   AAS14174 standard; DNA; 17 BP.
XX
AC   AAS14174;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Modified Poly-T Primer #1 used in construction of probe sets.
XX
KW   WRAP-Probe; gene expression array; global amplification; RNA array; ss;
KW   tissue microarray; drug discovery assay; reporter binding site; forensic;
KW   diagnostic; genomic analysis; universal linker; poly-T primer.
XX
OS   Synthetic.
XX
PN   WO200166802-A1.
XX
PD   13-SEP-2001.
XX
PF   09-MAR-2001; 2001WO-US007508.
XX
PR   09-MAR-2000; 2000US-0187982P.
XX
PA   (GENE-) GENETAG TECHNOLOGY INC.
XX
PI   Shafer DA;
XX
DR   WPI; 2001-596845/67.
XX
PT   Novel probe sets with common universal linkers at one or both ends (WRAP
PT   probes) for gene expression arrays to provide global amplification of
PT   probe set and to provide common equivalent signaling regardless of
PT   length.
XX
PS   Disclosure; Page 88; 97pp; English.
XX
CC   The invention relates to a probe set for gene expression arrays to
CC   provide common equivalent signalling per probe and global amplification
CC   of the set. The probe set has a pool of modified cDNA probes, each probe
CC   having a central target specific segment copied from a portion of a
CC   single mRNA transcript and a universal linker (a WRAP-Probe) located on
CC   one or both terminal ends. The universal linker has reporter binding
CC   sites to join common reporters to the probes and primer binding sites to
CC   copy and amplify the probe. The probes and reporters are useful in
CC   diagnostic or drug discovery assays for a wide range of biomedical
CC   samples, including detection of nucleic acids and gene expression
CC   profiles in human diagnostics, forensics and genomic analysis. The
CC   methods are useful for amplifying and identifying any unknown DNA
CC   fragment and also for improving sensitivity with tissue microarrays or
CC   RNA arrays. The methods improve the quantification of gene expression and
CC   allow highly improved detection of rare transcripts or very small
CC   samples. This sequence represents a poly-T primer used in the
CC   construction of probe sets
XX
SQ   Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
              :|||||||||||||||
Db         16 BAAAAAAAAAAAAAA 1


RESULT 2994
ABA05917/c
ID   ABA05917 standard; DNA; 20 BP.
XX
AC   ABA05917;
XX
DT   05-MAR-2002  (first entry)
XX
DE   Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.
XX
KW   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW   PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
PN   EP1152063-A1.
XX
PD   07-NOV-2001.
XX
PF   03-MAY-2000; 2000EP-00109436.
XX
PR   03-MAY-2000; 2000EP-00109436.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Schroeder KH,  Koike K;
XX
DR   WPI; 2002-068256/10.
XX
PT   Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT   risk for hepatocellular carcinoma, comprises identifying full length HBV
PT   transcripts and truncated HBV transcripts in a serum sample.
XX
PS   Example 1; Page 6; 25pp; English.
XX
CC   The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC   stages comprising identification of full length HBV transcripts (I) and
CC   truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC   is indicative of a particular infection stage. The method is useful for
CC   diagnosing HBV infection stages and determining the risk for developing
CC   hepatocellular carcinoma. The present sequence is that of a HBV
CC   diagnostic PCR primer, useful for the invention
XX
SQ   Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAA 2799
              ||  | ||||||||||||||
Db         20 GAGCTAAAAAAAAAAAAAAA 1


RESULT 2995
ABZ88879
ID   ABZ88879 standard; DNA; 20 BP.
XX
AC   ABZ88879;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
```

```
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4121; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              ||||   ||||||||||||
Db          1 GAAACTTAAAAAAAAAAAAA 20


RESULT 2996
AAC82913/c
ID   AAC82913 standard; DNA; 20 BP.
XX
AC   AAC82913;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #6.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              | || | ||||||||||||||
Db         20 ACAACTTAAAAAAAAAAAAA 1


RESULT 2997
AAQ95389
ID   AAQ95389 standard; DNA; 20 BP.
XX
AC   AAQ95389;
XX
DT   08-FEB-1996  (first entry)
XX
DE   Primer A (Group 2, Set B) for marker IL-9, chromosome 5.
XX
KW   primer; polymerase chain reaction; PCR; linkage study; locus;
KW   microsatellite marker sequence; automated genotyping; allele;
KW   polymorphism; detection; Homo sapiens; ss.
XX
OS   Synthetic.
XX
PN   WO9515400-A1.
XX
PD   08-JUN-1995.
XX
PF   05-DEC-1994;   94WO-US013945.
XX
PR   03-DEC-1993;   93US-00160837.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Levitt RC;
XX
DR   WPI; 1995-215278/28.
XX
PT   Kit for automated genotyping contg. pairs of PCR primers - designed to
PT   amplify polymorphic nucleotide repeat sequences, arranged in sets each
PT   with a characteristic fluorescence label, useful e.g. in detection of
PT   disease related genetic rearrangement.
XX
PS   Claim 4; Fig 7B-2; 104pp; English.
XX
CC   The method aims to provide a collection of highly reproducible
CC   microsatellite marker sequences (MMS) at approx. 10-50 cM intervals
CC   throughout the human genome which can be detectably labelled. The MSS are
CC   polymorphic, simple sequence repeats and can be used in automated
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CC   genotyping, esp. fluorescence-based. The primers correspond to the unique
CC   DNA sequence surrounding each marker, and PCR is used to detect each
CC   polymorphism. When the MSS show considerable polypmorphism (ie. a
CC   difference in the number of repeats) between individuals, the markers can
CC   be particularly informative. The MSS can be ideal for linkage studies.
CC   Kits comprise at least 4 groups, of at least 3 sets, each comprising
CC   labelled primers for PCR amplification of the DNA. Group 2 primer pairs
CC   are shown in AAQ95369-416. The published size range of the IL-9 allele is
CC   271-283 bp, and the degree of heterozygosity in the population is about
CC   63%
XX
SQ   Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1860 CCACACACTTAGCCATTGAA 1879
              || ||| |||||||||||  |
Db          1 CCCCACTCTTAGCCATTGTA 20


RESULT 2998
AAT10129/c
ID   AAT10129 standard; DNA; 20 BP.
XX
AC   AAT10129;
XX
DT   21-AUG-1996  (first entry)
XX
DE   Sequence #1 used in the method of the invention.
XX
KW   Vascular endothelial growth factor; VEGF; antisense oligonucleotide;
KW   therapy; abnormal angiogenesis; cancer; rheumatoid arthritis; diabetes;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9600286-A1.
XX
PD   04-JAN-1996.
XX
PF   07-JUN-1995;   95WO-JP001121.
XX
PR   27-JUN-1994;   94JP-00145146.
PR   21-NOV-1994;   94JP-00311130.
XX
PA   (TOAG ) TOA GOSEI KK.
XX
PI   Uchida K,  Uchida T,  Tanaka Y,  Matsuda Y,  Kondo S;
XX
DR   WPI; 1996-068870/07.
XX
PT   Anti-sense polynucleotide complementary to VEGF sequence - inhibit growth
PT   factor expression and are used for diagnosis and treatment of cancer and
PT   other diseases.
XX
PS   Example 1; Page 45; 66pp; Japanese.
XX
CC   AAT10129 and AAT10130 represent oligonucleotides used within the
CC   invention. These sequences were used to determine the antisense
CC   oligonucleotides of the invention (see AAT10121-T10128). These sequences
CC   are antisense oligonucleotides complementary to at least 8 consecutive
CC   nucleotides of the vascular endothelial growth factor (VEGF) gene (see
CC   AAT10120). These antisense sequences inhibit the expression of VEGF to
CC   below 30% of normal expression. The antisense oligonucleotides may be
CC   used in diagnosis and treatment of diseases involving VEGF expression and
CC   associated abnormal angiogenesis, such as cancer, rheumatoid arthritis
CC   and diabetes
XX
SQ   Sequence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||| || ||||| |||||||
Db         20 TTTGTTGTTTTTGTTTTTT 1


RESULT 2999
AAT50899/c
ID   AAT50899 standard; DNA; 20 BP.
XX
AC   AAT50899;
XX
DT   26-AUG-1997  (first entry)
XX
DE   Probe #13 for interleukin-6 receptor.
XX
KW   Probe; interleukin-6 receptor; IL-6R; cytokine; cellular proliferation;
KW   transmembrane glycoprotein receptor; signal transducer; gp130; inhibitor;
KW   IL-6; cancer; renal cell carcinoma; autoimmune disease; viral infection;
KW   therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .20
FT                   /*tag=  a
FT                   /note= "optionally phosphorothioated"
XX
PN   EP747386-A2.
XX
PD   11-DEC-1996.
XX
PF   07-JUN-1996;   96EP-00304315.
XX
PR   07-JUN-1995;   95US-00484666.
PR   07-JUN-1995;   95US-00486408.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Brown SJ,  Dattagupta N,  Naidu YM;
XX
DR   WPI; 1997-023093/03.
XX
PT   Oligo:nucleotide(s) complementary to interleukin-6 receptor mRNA - for
PT   treating proliferative diseases, e.g. cancer, auto-immune diseases or
PT   viral infections.
XX
PS   Claim 1; Page 16; 18pp; English.
XX
CC   AAT50887-T50904 represent oligonucleotides of the invention. These
CC   sequences are all probes for interleukin-6 receptor (IL-6R) mRNA. IL-6 is
CC   one of the most well characterised of the cytokines. It functions through
CC   interacting with at least two transmembrane glycoprotein receptor
CC   molecules on the surface of target cells. The receptors are the IL-6R,
CC   and the signal transducer gp130. Signal transduction by IL-6 involves the
CC   concerted action of both IL-6R and gp130. IL-6 overproduction is
CC   implicated in many different disease states, particularly in cellular
CC   proliferation associated with these diseases. These sequences bind to the
CC   IL-6R coding sequence, thereby inhibiting IL-6R production. The sequences
CC   therefore inhibit the functioning of IL-6. These sequences can be used
CC   for inhibiting disease-associated cellular proliferation. The
CC   oligonucleotides are especially useful for treating cancer (e.g. renal
CC   cell carcinoma), autoimmune diseases or viral infections. They can also
CC   be used as probes for detecting IL-6 receptor mRNA, especially for
CC   evaluating the effectiveness of drugs in reducing IL-6 receptor mRNA
CC   levels
XX
SQ   Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
```

```
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAGCAGG 470
              | |||| |||| ||||||||
Db         20 CTCAGGAAGCCGGCAGCAGG 1


RESULT 3000
AAT91100
ID   AAT91100 standard; DNA; 20 BP.
XX
AC   AAT91100;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Bovine lysosomal alpha-mannosidase (LAMAN) gene PCR primer mp5UT1F.
XX
KW   LAMAN; lysosomal alpha-mannosidase; alpha-mannosidosis; cattle;
KW   diagnosis; screening; genetic test; PCR; primer; RFLP;
KW   restriction fragment length polymorphism; ss.
XX
OS   Synthetic.
OS   Bos taurus.
XX
PN   WO9726369-A1.
XX
PD   24-JUL-1997.
XX
PF   15-JAN-1997;   97WO-GB000109.
XX
PR   15-JAN-1996;   96NO-00000163.
XX
PA   (HEAL/) HEALY P.
PA   (DZIE/) DZIEGLEWSKA H.
XX
PI   Berg T,  Tollersrud OK,  Nilssen O;
XX
DR   WPI; 1997-385352/35.
XX
PT   Diagnosis and screening for bovine alpha-mannosidosis - by detecting
PT   mutation(s) in alpha-mannosidase gene, also nucleic acid encoding the
PT   enzyme and derived oligo:nucleotide primers.
XX
PS   Example 2; Page 22; 85pp; English.
XX
CC   Forward primer mp5UT1F is based on a 1500 bp amplicon produced from
CC   bovine fibroblast genomic DNA using primers (see AAT91098-99) based on
CC   the bovine alpha-mannosidase (LAMAN) gene (see AAT91086). It was used
CC   with reverse primer mp262 (see AAT91101) to obtain an 800 bp RT-PCR
CC   product that constituted a 5' part of LAMAN cDNA. This was combined with
CC   a previously obtained PCR cDNA fragment (see AAT91096-97) to produce a
CC   full-length clone (see AAT91086) for LAMAN (see AAW26682). Mutations in
CC   the LAMAN gene cause bovine alpha-mannosidosis, and can be detected using
CC   claimed PCR primers (see AAT91088-93)
XX
SQ   Sequence 20 BP; 2 A; 5 C; 11 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGA 70
              | ||||| |||||| ||||| |
Db          1 GTGGCGGCGGCGGCTGCAGA 20


RESULT 3001
AAV47995/c
ID   AAV47995 standard; DNA; 20 BP.
XX
AC   AAV47995;
XX
DT   19-OCT-1998  (first entry)
XX
DE   Human B7-1 targetted oligonucleotide 13810.
XX
KW   ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
KW   cell proliferation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages"
XX
PN   WO9829124-A1.
XX
PD   09-JUL-1998.
XX
PF   16-DEC-1997;   97WO-US023270.
XX
PR   31-DEC-1996;   96US-00777266.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Vickers TA;
XX
DR   WPI; 1998-387783/33.
XX
PT   New oligo:nucleotide(s) that modulate expression of B7 proteins - used
PT   for, e.g. controlling activation and proliferation of T cells,
PT   particularly for treatment, diagnosis and prevention of inflammation.
XX
PS   Example 1; Page 33; 120pp; English.
XX
CC   The oligonucleotides which specifically hybridise to B7 modulate its
CC   expression (and thus T cell activation and proliferation). This is
CC   particularly useful for treatment and prevention of inflammation and
CC   autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
CC   Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
CC   (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
CC   rhinitis, allergy, cancer and metastases. The oligonucleotides may also
CC   be used to manipulate T cell activation ex vivo; to determine or detect
CC   B7 protein expression; for diagnosis; as assay and purification reagents,
CC   and to study physiological roles of B7 proteins
XX
SQ   Sequence 20 BP; 6 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGG 560
              ||| |||||||||| || |||
Db         20 GCCTCACCTCTCCTGGTTGG 1


RESULT 3002
AAZ37559
ID   AAZ37559 standard; DNA; 20 BP.
XX
AC   AAZ37559;
XX
DT   07-JAN-2000  (first entry)
XX
DE   Human mdm2 phosphorothioate oligodeoxynucleotide #89.
XX
KW   Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW   antisense; modulation; oligonucleotide; expression; inhibition;
KW   hyperproliferation; blood cancer; brain cancer; breast cancer;
KW   lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KW   restenosis; ss.
XX
OS   Synthetic.
```

OS Homo sapiens.
XX
PN WO9949065-A1.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999; 99WO-US006702.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX
DR WPI; 1999-610754/52.
XX
PT New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Example 9; Page 49; 157pp; English.
XX
CC AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention describes
CC novel nucleotide antisense compounds, targetted to the 5' untranslated,
CC translation termination codon, or 3' untranslated region of a nucleic
CC acid encoding human mdm2, that modulates expression of human mdm2. The
CC oligonucleotides mediate their effect by antisense inhibition of
CC hyperproliferative gene expression. The antisense compound is used to
CC treat an animal having a disease or condition associated with mdm2,
CC particularly a hyperproliferative condition, more particularly cancer,
CC especially of the blood, brain, breast, lung or soft tissue, or
CC psoriasis, fibrosis, atherosclerosis or restenosis
XX
SQ Sequence 20 BP; 4 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2313 CAATTTGTTGCTGCTTGTCA 2332
              |||| ||||| ||||| |||
Db          1 CAATATGTTGTTGCTTCTCA 20
```

RESULT 3003
AAX36657
ID AAX36657 standard; DNA; 20 BP.
XX
AC AAX36657;
XX
DT 13-JUL-1999 (first entry)
XX
DE PCR primer for marker D2S113.
XX
KW PCR primer; detection; glaucoma allele; haplotype analysis; human; GLC1B;
KW chromosome 2; chromosome 6; GLC6p25; haplotype profile;
KW presymptomatic glaucoma; symptomatic glaucoma; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916899-A2.
XX
PD 08-APR-1999.
XX
PF 29-SEP-1998; 98WO-CA000924.
XX
PR 30-SEP-1997; 97CA-02217097.
XX
PA (UYLA-) UNIV LAVAL.
XX
PI Raymond V, Morissette J, Falardeau P, Cote G, Anctil J;
XX
DR WPI; 1999-263704/22.
XX
PT Haplotype analyses for indirect detection of glaucoma.
XX
PS Claim 7; Page 27; 41pp; English.
XX
CC This sequence represents a PCR primer used in the method of the
CC invention. The method is for detecting the presence of alleles for
CC glaucoma comprising haplotype analysis of human chromosome 2 and 6
CC respectively, where the haplotypes are associated with loci GLC1B and
CC GLC6p25 respectively. The primers are used to amplify gene sequences to
CC generate information necessary to compile haplotype profiles. The
CC haplotype profiles can be used to detect presymptomatic and symptomatic
CC glaucoma. They can also be used to localise, isolate and identify the
CC GLC1B and GLC6p25 loci so that detection of individuals with glaucoma is
CC enhanced. The haplotype analyses also provide means for identification
CC and following of mutant alleles in pedigrees or populations.
CC Identification of presymptomatic individuals using the methods allows
CC intervention in the disease process and obviates the impact of inheriting
CC a mutant allele causing disease, by medically disrupting the initiation
CC or progression of the disease
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1332 GCTTGTCTCATTTCAGCCTG 1351
              |||||| |||| ||| ||||
Db          1 GCTTGTTTCATCTCACCCTG 20
```

RESULT 3004
AAZ06095
ID AAZ06095 standard; DNA; 20 BP.
XX
AC AAZ06095;
XX
DT 07-OCT-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB001939.
XX
PR 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis.
XX
PS Disclosure; Page 1824; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs

```
CC   encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC   against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC   be used to control growth of the microorganism. Chlamydia trachomatis is
CC   responsible for a large number of diseases, e.g. eye diseases such as
CC   conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC   conjunctivitis; genital diseases such as nongonococcal uretritis,
CC   epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC   pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC   The polypeptides of the invention may be of use in treating these
CC   diseases
XX
SQ   Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1697 CTAGCGCTGAGCTATCTCCT 1716
              || ||| ||| |||||||||
Db          1 CTCGCGATGACCTATCTCCT 20


RESULT 3005
AAZ04917
ID   AAZ04917 standard; DNA; 20 BP.
XX
AC   AAZ04917;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB001939.
XX
PR   28-NOV-1997;   97FR-00015041.
PR   17-DEC-1997;   97FR-00016034.
PR   04-NOV-1998;   98US-0107077P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-371125/31.
XX
PT   Genome sequence of Chlamydia trachomatis.
XX
PS   Disclosure; Page 1728; 1755pp; English.
XX
CC   PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC   (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC   encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC   against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC   be used to control growth of the microorganism. Chlamydia trachomatis is
CC   responsible for a large number of diseases, e.g. eye diseases such as
CC   conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC   conjunctivitis; genital diseases such as nongonococcal uretritis,
CC   epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC   pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC   The polypeptides of the invention may be of use in treating these
CC   diseases
XX
SQ   Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1082 GTAGAAGGTGAAGCTGTTCA 1101
              | ||||||||||| | ||||
Db          1 GCAGAAGGTGAAGTTCTTCA 20


RESULT 3006
AAX96826/c
ID   AAX96826 standard; DNA; 20 BP.
XX
AC   AAX96826;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1856; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1525 GAACGAAGAAAGGTTAGGAG 1544
              || ||||||||| || ||||
Db         20 GACCGAAGAAAGATTGGGAG 1


RESULT 3007
AAF32837/c
ID   AAF32837 standard; DNA; 20 BP.
```

XX
AC AAF32837;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human B7-1 mRNA antisense oligonucleotide SEQ ID NO: 34.
XX
KW Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;
KW autoimmune disorder; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
XX
PN WO200074687-A1.
XX
PD 14-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US014471.
XX
PR 04-JUN-1999; 99US-00326186.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX
DR WPI; 2001-049991/06.
XX
PT Novel compound for diagnosing, preventing and treating immune disorders,
PT comprising an oligonucleotide that specifically hybridizes with a nucleic
PT acid sequence encoding B7 protein.
XX
PS Example 1; Page 45; 162pp; English.
XX
CC The present invention provides sequences of antisense oligonucleotides
CC targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences.
CC The antisense sequences have phosphorothioate backbones and some
CC nucleotides are 2'-methoxyethoxy residues. The sequences can be used in
CC the treatment of inflammatory and autoimmune disorders, including asthma,
CC juvenile diabetes mellitus, myasthenia gravis, Graves' disease,
CC rheumatoid arthritis, allograft rejection, inflammatory bowel disease,
CC multiple sclerosis, psoriasis, systemic lupus erythematosus, contact
CC dermatitis, rhinitis, allergies and cancer
XX
SQ Sequence 20 BP; 6 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 541 GCCCCACCTCTCCGGGCTGG 560
||| ||||||||| || |||
Db 20 GCCTCACCTCTCCTGGTTGG 1

RESULT 3008
AAF32944/c
ID AAF32944 standard; DNA; 20 BP.
XX
AC AAF32944;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human B7-1 antisense oligonucleotide SEQ ID NO: 141.
XX
KW Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;
KW autoimmune disorder; phosphorothioate backbone; ss.
XX
OS Homo sapiens.
XX
PN WO200074687-A1.
XX
PD 14-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US014471.
XX
PR 04-JUN-1999; 99US-00326186.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX
DR WPI; 2001-049991/06.
XX
PT Novel compound for diagnosing, preventing and treating immune disorders,
PT comprising an oligonucleotide that specifically hybridizes with a nucleic
PT acid sequence encoding B7 protein.
XX
PS Example 12; Page 75; 162pp; English.
XX
CC The present invention provides sequences of antisense oligonucleotides
CC targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences.
CC The antisense sequences have phosphorothioate backbones and some
CC nucleotides are 2'-methoxyethoxy residues. The sequences can be used in
CC the treatment of inflammatory and autoimmune disorders, including asthma,
CC juvenile diabetes mellitus, myasthenia gravis, Graves' disease,
CC rheumatoid arthritis, allograft rejection, inflammatory bowel disease,
CC multiple sclerosis, psoriasis, systemic lupus erythematosus, contact
CC dermatitis, rhinitis, allergies and cancer
XX
SQ Sequence 20 BP; 6 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 541 GCCCCACCTCTCCGGGCTGG 560
||| ||||||||| || |||
Db 20 GCCTCACCTCTCCTGGTTGG 1

RESULT 3009
AAF80713
ID AAF80713 standard; DNA; 20 BP.
XX
AC AAF80713;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #87.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN US6184212-B1.
XX
PD 06-FEB-2001.
XX
PF 26-MAR-1999; 99US-00280805.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
XX
DR WPI; 2001-190948/19.
XX
PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
PT acid molecule encoding human mdm-2 useful for modulating the expression
PT of human mdm-2 and reducing hyperproliferation of human cells.
XX
PS Example 9; Col 27; 77pp; English.
XX
CC The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the

```
CC   3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC   The invention is useful for reducing hyperproliferation of human cells,
CC   modulating the expression of mdm2 in human cells or tissues or in vitro.
CC   The hyperproliferative disorder includes cancer or psoriasis
XX
SQ   Sequence 20 BP; 4 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2313 CAATTTGTTGCTGCTTGTCA 2332
              |||| ||||| ||||| |||
Db          1 CAATATGTTGTTGCTTCTCA 20


RESULT 3010
AAC84794/c
ID   AAC84794 standard; DNA; 20 BP.
XX
AC   AAC84794;
XX
DT   20-APR-2001  (first entry)
XX
DE   Human TLR4 gene exon 4 amplifying forward primer.
XX
KW   TLR4; toll receptor 4; innate immunity; gram-negative bacteria; sepsis;
KW   respiratory distress syndrome; LPS; lipopolysaccharide; asthma; ARDS;
KW   chronic airway disease; arthritis; inflammatory disease; SIRS; human;
KW   systematic inflammatory response syndrome; pyelonephritis; bronchitis;
KW   acute respiratory distress syndrome; gall bladder disease; pneumonia;
KW   cystic fibrosis; antibacterial; antiinflammatory; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200077204-A1.
XX
PD   21-DEC-2000.
XX
PF   08-JUN-2000; 2000WO-US015723.
XX
PR   10-JUN-1999;   99US-00329515.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (LORE/) LORENZ E.
XX
PI   Lorenz E,  Schwartz DA,  Schutte BC;
XX
DR   WPI; 2001-061872/07.
XX
PT   Identifying humans at risk of, or having indication associated with
PT   altered innate immunity involves detecting or determining whether DNA
PT   amplified from a biological sample encodes a portion of variant toll
PT   receptor 4.
XX
PS   Example 1; Page 31; 97pp; English.
XX
CC   The invention relates to human toll receptor 4 (TLR4) nucleic acid and
CC   methods to identify polymorphisms at the human TLR4 locus and to identify
CC   individuals at risk of, or having, an indication associated with altered
CC   innate immunity. A variant TLR4 nucleic acid is useful as a diagnostic
CC   reagent for detecting a polymorphism in human TLR4 gene. Since the
CC   presence of TLR4 mutation is associated with gram-negative sepsis,
CC   severity of sepsis, pre-term delivery and respiratory distress syndrome
CC   in pre-term infants, agents which alter TLR4 activity are useful for
CC   preventing or ameliorating infection by gram-negative bacteria, sepsis
CC   induced by gram-negative bacteria, LPS (lipopolysaccharide) induced
CC   chronic airway disease, asthma, arthritis, local and systemic
CC   inflammatory disease conditions such as systematic inflammatory response
CC   syndrome (SIRS) or acute respiratory distress syndrome (ARDS),
CC   pyelonephritis, gall bladder disease, pneumonia, bronchitis, chronic
CC   obstructive pulmonary disease, local gram-negative bacterial infection
CC   and cystic fibrosis. Sequences AAC84776-823 represent PCR primers for
CC   amplifying the exons of human TLR4 gene
XX
SQ   Sequence 20 BP; 6 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1166 TTAACCAGACCTCATCTTGG 1185
              ||| |||| ||||||| |||
Db         20 TTACCCAGTCCTCATCCTGG 1


RESULT 3011
AAC82910/c
ID   AAC82910 standard; DNA; 20 BP.
XX
AC   AAC82910;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #3.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 3 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1971 TTACCTTGAAAAAAAGAAAA 1990
              | ||||| ||||||| ||||
Db         20 TCACCTTAAAAAAAAAAAAA 1


RESULT 3012
AAC82909
```

ID AAC82909 standard; DNA; 20 BP.
XX
AC AAC82909;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human beta-actin derived oligonucleotide #2.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
PS Example; Fig 1; 8pp; German.
XX
CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
SQ Sequence 20 BP; 2 A; 0 C; 4 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||  | |
Db          1 TTTTTTTTTTTTTAAGGTGG 20
```

RESULT 3013
AAC82914
ID AAC82914 standard; DNA; 20 BP.
XX
AC AAC82914;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human beta-actin derived oligonucleotide #7.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
PS Example; Fig 1; 8pp; German.
XX
CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||| | || |
Db          1 TTTTTTTTTTTTTAAGCTGT 20
```

RESULT 3014
AAF99949
ID AAF99949 standard; DNA; 20 BP.
XX
AC AAF99949;
XX
DT 12-JUL-2001 (first entry)
XX
DE Synthetic oligonucleotide #15.
XX
KW Oligonucleotide purification; liquid chromatography;
KW hydrophobic protective group; deprotection; ds.
XX
OS Synthetic.
XX
PN JP2000342265-A.
XX
PD 12-DEC-2000.
XX
PF 02-JUN-1999; 99JP-00154974.
XX
PR 02-JUN-1999; 99JP-00154974.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 2001-268251/28.
XX
PT A process for purification of oligonucleotides using liquid
PT chromatography.
XX
PS Example 1; Page 4; 13pp; Japanese.
XX

```
CC   The present sequence is an oligonucleotide provided in a specification
CC   relating to the simplified purification of oligonucleotides by liquid
CC   chromatography. The process comprises: (a) pouring oligonucleotides
CC   protected with a hydrophobic group and oligonucleotide with no protective
CC   group into a liquid chromatography column packed with an acid and alkali
CC   resistant packing agent, such as polystyrene resin; (b) pouring a mixed
CC   developing solvent composed of a buffer made from a volatile salt and a
CC   water soluble organic solvent at a suitable concentration gradient into
CC   the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into
CC   the column to deprotect the oligonucleotides protected with the
CC   hydrophobic group; (d) pouring a mixed developing solvent composed of a
CC   buffer made from a volatile salt, particularly 0.05-0.5 N aqueous
CC   ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water
CC   soluble organic solvent at a suitable concentration gradient to elute the
CC   deprotected oligonucleotides; and (e) removal of the solvent and the salt
CC   from the eluted oligonucleotides
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||| |||| |||| ||||
Db          1 TTTTTCTTTTGTTTTATTTT 20


RESULT 3015
AAS29328
ID   AAS29328 standard; DNA; 20 BP.
XX
AC   AAS29328;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human mdm2 antisense oligonucleotide 31728.
XX
KW   Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW   atherosclerosis; tumour; cytostatic; anti psoriatic;
KW   anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= All phosphorothioate linkages,
FT                    additionally bases 1-6 and bases 15-20 are 2'-O-
FT                    methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
PN   US2001016575-A1.
XX
PD   23-AUG-2001.
XX
PF   02-JAN-2001; 2001US-00752983.
XX
PR   26-MAR-1998;   98US-00048810.
PR   26-MAR-1999;   99US-00280805.
XX
PA   (MIRA/) MIRAGLIA L J.
PA   (NERO/) NERO P.
PA   (GRAH/) GRAHAM M J.
PA   (MONI/) MONIA B P.
PA   (COWS/) COWSERT L M.
XX
PI   Miraglia LJ,  Nero P,  Graham MJ,  Monia BP,  Cowsert LM;
XX
DR   WPI; 2001-535565/59.
XX
PT   An antisense compound, useful for treating e.g. cancer, comprises
PT   nucleobases targeted a region (e.g. translation termination codon region)
PT   of a nucleic acid encoding human mdm2.
XX
PS   Example 9; Page 15; 81pp; English.
XX
CC   The present invention relates to antisense compounds, 8-30 nucleobases in
CC   length targeted to the 5' untranslated region, translation termination
CC   codon region, 3' untranslated region, coding region or translation start
CC   site of a nucleic acid encoding human mdm2, where the antisense compound
CC   modulates the expression of human mdm2. The antisense oligonucleotides of
CC   the invention are useful for encoding human mdm2 and for inhibiting the
CC   expression of human mdm2. They may be used for treating an animal having
CC   a disease or condition associated with amplification of mdm2 gene or
CC   overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC   (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC   fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC   and chronic myelogenous leukemia. The antisense compound may be
CC   administered with a chemotherapeutic agent to overcome drug resistance.
CC   The antisense compound reduces hyperproliferation of human cells. The
CC   method, which involves the use of the antisense compound, is also useful
CC   for detecting the role of mdm2 expression in various cell functions and
CC   physiological processes and useful in both clinical research and
CC   diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC   oligonucleotides of the present invention
XX
SQ   Sequence 20 BP; 4 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2313 CAATTTGTTGCTGCTTGTCA 2332
              |||| ||||| ||||| |||
Db          1 CAATATGTTGTTGCTTCTCA 20


RESULT 3016
AAH80594
ID   AAH80594 standard; cDNA; 20 BP.
XX
AC   AAH80594;
XX
DT   11-SEP-2003  (revised)
DT   19-SEP-2001  (first entry)
XX
DE   Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 558.
XX
KW   Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW   disease diagnosis; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6251588-B1.
XX
PD   26-JUN-2001.
XX
PF   10-FEB-1998;   98US-00021701.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2001-424456/45.
XX
PT   Predicting the potential of an oligonucleotide to hybridize to a target
PT   nucleotide sequence, useful for evaluating oligonucleotide probe
PT   sequences, by identifying a oligonucleotides based on the evaluation of
PT   parameters.
XX
PS   Example 2; Col 65; 342pp; English.
XX
CC   The present invention describes a method for predicting the potential of
```

```
CC   an oligonucleotide to hybridise to a (complementary) target nucleotide
CC   sequence, involving identifying a subset of oligonucleotides within the
CC   predetermined number of unique oligonucleotides based on the evaluation
CC   of the parameter. Oligonucleotides in the subset are identified that are
CC   clustered along a region of the nucleotide sequence that is hybridisable
CC   to the target nucleotide sequence. This is useful for evaluating
CC   oligonucleotide probe sequences. The present sequence is an
CC   oligonucleotide described in the exemplification of the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 20 BP; 2 A; 4 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              |||||| |||||||||  ||
Db          1 TTTTTTCTTTTTTAACCCTG 20


RESULT 3017
ABA91532/c
ID   ABA91532 standard; DNA; 20 BP.
XX
AC   ABA91532;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA oligonucleotide AGT02020 used to test RNase H cleavage.
XX
KW   Nucleic acid detection; probe; mismatch; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    13
FT                   /*tag=  a
FT                   /note= "mismatch to target DNA"
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 5; Page 49; 72pp; English.
XX
CC   The present sequence is that of oligonucleotide AGT02020, which contains
CC   a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
CC   one of a set of oligonucleotides (see ABA91532-37) containing
CC   mismatch(es) to the target DNA that were tested in a hybridisation/RNase
CC   H cleavage assay. The results showed that 2 mismatches between the target
CC   and the probe ablated RNase H cleavage. The effect of one mismatch site
CC   was less than that of two mismatch sites, and showed a polarity effect,
CC   with stronger inhibition shown in assays with AGT02020 than in assays
CC   using an oligonucleotide in which the mismatch was at an adjacent
CC   position. The invention provides probes for nucleic acid hybridisation.
CC   The probes form a hairpin structure comprising a double-stranded stem and
CC   a single-stranded loop, and are capable of both intramolecular and
CC   intermolecular hybridisation. The double-stranded stem may comprise a
CC   methylphosphonate DNA:RNA hybrid that is resistant to RNase H cleavage.
CC   When the probe hybridises with a target DNA, the RNA strand in the
CC   DNA:RNA duplex becomes sensitive to RNase H treatment and can be removed.
CC   Arrays and methods for nucleic acid hybridisation using the probes are
CC   provided
XX
SQ   Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||   |||||||||
Db         20 TTTTTTTCAAATTTTTTTTT 1


RESULT 3018
ABA91537/c
ID   ABA91537 standard; DNA; 20 BP.
XX
AC   ABA91537;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA oligonucleotide AGT02025 used to test RNase H cleavage.
XX
KW   Nucleic acid detection; probe; mismatch; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    12
FT                   /*tag=  a
FT                   /note= "mismatch to target DNA"
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 5; Page 50; 72pp; English.
XX
CC   The present sequence is that of oligonucleotide AGT02025, which contains
CC   a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
CC   one of a set of oligonucleotides (see ABA91532-37) containing
CC   mismatch(es) to the target DNA that were tested in a hybridisation/RNase
CC   H cleavage assay. The results showed that 2 mismatches between the target
CC   and the probe ablated RNase H cleavage. The effect of one mismatch site
CC   was less than that of two mismatch sites, and showed a polarity effect,
CC   with weaker inhibition shown in assays with AGT02021 than in assays using
CC   an oligonucleotide in which the mismatch was at an adjacent position.
CC   Oligonucleotides in which the mismatch was G or C rather than A showed
CC   similar inhibition of RNase H cleavage. The invention provides probes for
CC   nucleic acid hybridisation. The probes form a hairpin structure
CC   comprising a double-stranded stem and a single-stranded loop, and are
```

```
CC   capable of both intramolecular and intermolecular hybridisation. The
CC   double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
CC   is resistant to RNase H cleavage. When the probe hybridises with a target
CC   DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
CC   treatment and can be removed. Arrays and methods for nucleic acid
CC   hybridisation using the probes are provided
XX
SQ   Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |  |||||||||
Db         20 TTTTTTTATAATTTTTTTTT 1


RESULT 3019
ABA91534/c
ID   ABA91534 standard; DNA; 20 BP.
XX
AC   ABA91534;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA oligonucleotide AGT02022 used to test RNase H cleavage.
XX
KW   Nucleic acid detection; probe; mismatch; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    12
FT                   /*tag=  a
FT                   /note= "mismatch to target DNA"
FT   misc_feature    13
FT                   /*tag=  b
FT                   /note= "mismatch to target DNA"
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 5; Page 50; 72pp; English.
XX
CC   The present sequence is that of oligonucleotide AGT02022, which contains
CC   a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
CC   one of a set of oligonucleotides (see ABA91532-37) containing
CC   mismatch(es) to the target DNA that were tested in a hybridisation/RNase
CC   H cleavage assay. The results showed that 2 mismatches between the target
CC   and the probe ablated RNase H cleavage. The invention provides probes for
CC   nucleic acid hybridisation. The probes form a hairpin structure
CC   comprising a double-stranded stem and a single-stranded loop, and are
CC   capable of both intramolecular and intermolecular hybridisation. The
CC   double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
CC   is resistant to RNase H cleavage. When the probe hybridises with a target
CC   DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
CC   treatment and can be removed. Arrays and methods for nucleic acid
CC   hybridisation using the probes are provided
XX
SQ   Sequence 20 BP; 16 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              ||||||| |  |||||||||
Db         20 TTTTTTTCCAATTTTTTTTT 1


RESULT 3020
ABA02210/c
ID   ABA02210 standard; DNA; 20 BP.
XX
AC   ABA02210;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Human/mouse C/EBP phosphorothioate antisense oligonucleotide, SEQ ID:22.
XX
KW   Human; C/EBP alpha; CCAAT/enhancer-binding protein alpha; CEBPA;
KW   transcription factor; tissue development; cellular function;
KW   proliferation; differentiation; adipocyte; energy metabolism;
KW   chondrogenic; ovulation; follicular development;
KW   hepatic steroid-induced cell cycle arrest; GLUT2 promoter regulation;
KW   hormonal metabolic regulation; granulocyte development; cancer;
KW   tumour formation; infection; inflammation; expression inhibition;
KW   antisense therapy; quantitative real-time PCR primer; ss.
XX
OS   Homo sapiens.
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
XX
PN   US6306655-B1.
XX
PD   23-OCT-2001.
XX
PF   13-JUN-2000; 2000US-00593589.
XX
PR   13-JUN-2000; 2000US-00593589.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Butler MM,  Wyatt J;
XX
DR   WPI; 2002-040202/05.
XX
PT   New antisense oligonucleotides for modulating the expression of
PT   CCAAT/Enhancer-binding proteins alpha, particularly useful for
PT   preventing, delaying or treating infection, inflammation or tumor
PT   formation.
XX
PS   Example 15; Col 42; 44pp; English.
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```
XX
CC   Sequences ABA02205-ABA02282 represent antisense oligonucleotides targeted
CC   to the human CCAAT/enhancer-binding protein alpha (C/EBP alpha) gene,
CC   which inhibit its expression. The antisense oligonucleotides were
CC   designed to target different regions of the human C/EBP alpha RNA, and
CC   were analysed for their effect on C/EBP alpha mRNA levels by quantitative
CC   real-time PCR. A similar investigation on mouse C/EBP alpha expression
CC   was performed using a subset of the antisense oligonucleotides that were
CC   capable of hybridising to mouse C/EBP alpha mRNA. The C/EBP family of
CC   proteins are a family of transcription factors which regulate the
CC   expression of wide range of genes that control normal tissue development,
CC   cellular function, cellular proliferation and functional differentiation.
CC   C/EBP alpha (also known as CEBPA) is primarily found in tissues involved
CC   in energy metabolism which have a capacity to metabolise lipids,
CC   cholesterol and other sterols. It is thought to be involved in the
CC   regulation of adipocyte and chondrogenic differentation, and is also
CC   involved in follicular development and ovulation, steroid-induced cell
CC   cycle arrest in the liver, in controlling glucose transporter GLUT2
CC   promoter activity, in the hormonal regulation of metabolism, and in
CC   granulocyte development. The oligonucleotides of the invention are useful
CC   for diagnosis, prevention and treatment of conditions associated with
CC   C/EBP expression, such as cancer, tumour formation, infection, or
CC   inflammation
XX
SQ   Sequence 20 BP; 2 A; 9 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        212 GAGGATCGCCACGACGGGAG 231
              |||| |||||| | ||||||
Db         20 GAGGCTCGCCATGCCGGGAG 1


RESULT 3021
ABL45622/c
ID   ABL45622 standard; DNA; 20 BP.
XX
AC   ABL45622;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 21q22.1 PCR primer SEQ ID NO:2666.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones.
XX
PS   Claim 6; Page 57; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention
XX
SQ   Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1178 CATCTTGGAGGACGAAATGA 1197
              | || ||||||| |||||||
Db         20 CCTCATGGAGGAAGAAATGA 1


RESULT 3022
ABL94262/c
ID   ABL94262 standard; DNA; 20 BP.
XX
AC   ABL94262;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Human C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:28.
XX
KW   Human; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EPB2; LAP;
KW   TCF5; CRP2; NFIL6; IL6DBP; NF-M; AGP/EBP; Apc/EBP; transcription factor;
KW   tissue development; cellular function; proliferation; differentiation;
KW   hormone responsiveness; oxidative stress response;
KW   IL-6 signalling mediator; interleukin-6; carbohydrate metabolism;
KW   immunity; Th1 response; female fertility; gluconeogenesis; ovarian;
KW   cancer; tumour formation; type II; diabetes; infection; inflammation;
KW   expression inhibition; phosphorothioate; antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
XX
PN   US6271030-B1.
XX
PD   07-AUG-2001.
XX
PF   14-JUN-2000; 2000US-00593711.
XX
PR   14-JUN-2000; 2000US-00593711.
XX
PA   (ISIS-) ISIS PHARM INC.
```

```
XX
PI   Monia BP,  Butler MM,  Wyatt J;
XX
DR   WPI; 2002-214451/27.
XX
PT   Novel antisense compound targeted to nucleic acids encoding human or
PT   mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for
PT   inhibiting expression of human or mouse C/EBP beta in cells/tissues.
XX
PS   Claim 1; Col 42; 69pp; English.
XX
CC   Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted
CC   to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)
CC   gene, which inhibit its expression. The antisense oligonucleotides were
CC   designed to target different regions of the human and/or mouse C/EBP
CC   alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels
CC   by quantitative real-time PCR. The C/EBP family of proteins are a family
CC   of transcription factors which regulate the expression of a wide range of
CC   genes that control normal tissue development, cellular function, cellular
CC   proliferation and functional differentiation. C/EBP beta (also known as
CC   C/EPB2, LAP, TCF5, CRP2, NFIL6, IL6DBP, NF-M, AGP/EBP and Apc/EBP)
CC   primarily regulates hormone responsiveness and oxidative stress responses
CC   and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is
CC   thought to be involved in carbohydrate metabolism, immunity, the Th1
CC   response, female fertility and gluconeogenic pathways. C/EBP beta is
CC   expressed in the liver, lung, spleen, kidney, brain, and testis, with the
CC   highest expression found in the lung. It is also expressed at a higher
CC   level in malignant ovarian tissue compared with normal ovarian tissue,
CC   and its expression in pancreas is upregulated in response to chronically
CC   elevated levels of glucose, indicating that it is involved in the
CC   impairment of insulin secretion in type II diabetes. The oligonucleotides
CC   of the invention are useful for diagnosis, prevention and treatment of
CC   conditions associated with C/EBP beta expression, such as cancer
CC   (particularly ovarian cancer), tumour formation, diabetes (particularly
CC   type II diabetes), infection, or inflammation
XX
SQ   Sequence 20 BP; 2 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        266 TCCGCCGGGCAGCACCTCTA 285
              ||| |||||||||||||  | |
Db         20 TCCTCCGGGCAGCACCACGA 1


RESULT 3023
ABX04655
ID   ABX04655 standard; DNA; 20 BP.
XX
AC   ABX04655;
XX
DT   14-JAN-2003  (first entry)
XX
DE   Human endogenous retrovirus k (herv-k) associated probe #27.
XX
KW   Human; endogenous retrovirus; herv; prostate cancer; testicular cancer;
KW   multiple sclerosis; insulin-dependent diabetes mellitus; HML-2 protease;
KW   cancer; transgenic animal; probe; ss.
XX
OS   Human endogenous retrovirus.
XX
PN   WO200246477-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US047824.
XX
PR   07-DEC-2000; 2000US-0251830P.
PR   07-DEC-2001; 2001US-00016604.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Garcia P,  Hardy SF,  Williams LT,  Escobedo J;
XX
DR   WPI; 2002-691475/74.
XX
PT   Novel isolated polypeptides useful for diagnosis of prostate cancer.
XX
PS   Claim 18; Page 146; 152pp; English.
XX
CC   The invention describes novel isolated polypeptides (I, Ib) useful for
CC   diagnosing prostate cancer comprising obtaining a patient sample
CC   containing prostate cells and detecting the presence or absence of an
CC   expression product of a HML-2 endogenous retrovirus in a patient sample.
CC   Polynucleotides associated with (I) are useful for diagnosis or treatment
CC   of testicular cancer, multiple sclerosis or insulin-dependent diabetes
CC   mellitus. An inhibitor of a HML-2 protease and a transdominant negative
CC   mutant of HML-2 cORF are also useful in the manufacture of a medicament
CC   for treating prostate cancer. (I) and (Ib) are useful for generating
CC   antibodies specific to the polypeptides associated with cancer, as
CC   targets for therapeutic intervention, and in immunising a transgenic
CC   animal. This sequence represents a probe used for detecting the presence
CC   of human endogenous retrovirus (herv) of the HML-2 sub-group in prostate
CC   tissue
XX
SQ   Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||  |||||||  ||
Db          1 GAAAAAAATCAAAAAAAGAA 20


RESULT 3024
ABZ85316/c
ID   ABZ85316 standard; DNA; 20 BP.
XX
AC   ABZ85316;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
```

XX
PS Claim 15; SEQ ID NO 558; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 11 A; 1 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1760 ATTCATTAAGCTTTTTTTTT 1779
              ||||| ||| |||||||| |
Db         20 ATTCAATAAACTTTTTTTGT 1
```

RESULT 3025
ABZ90374/c
ID ABZ90374 standard; DNA; 20 BP.
XX
AC ABZ90374;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Disclosure; SEQ ID NO 5616; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||| |||||| |||| ||||
Db         20 TTTGTTTTTTGTTTTGTTTT 1
```

RESULT 3026
ABZ85667
ID ABZ85667 standard; DNA; 20 BP.
XX
AC ABZ85667;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Claim 15; SEQ ID NO 909; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 5 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTT 2183
||| ||| ||| ||||||||
Db 1 CCTCTTTCTTTCTTTTTTTT 20

RESULT 3027
ABZ85670
ID ABZ85670 standard; DNA; 20 BP.
XX
AC ABZ85670;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Claim 15; SEQ ID NO 912; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2185
|||| ||||||| | |||||
Db 1 TTTTCTTTTTTTCTATTTTT 20

RESULT 3028
ABZ88438
ID ABZ88438 standard; DNA; 20 BP.
XX
AC ABZ88438;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Disclosure; SEQ ID NO 3680; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2778 TAGAATTGAAAAAAAAAAAA 2797
| || || ||||||||||||
Db 1 TTGACTTCAAAAAAAAAAAA 20

RESULT 3029
ABZ90373/c
ID ABZ90373 standard; DNA; 20 BP.
XX
AC ABZ90373;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX
PS Disclosure; SEQ ID NO 5615; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2170 TTTTTTTTTTTTTTTTTAAC 2189
|||| |||| ||||| ||||
Db 20 TTTTGTTTTGTTTTTCTAAC 1

RESULT 3030
ABZ91225
ID ABZ91225 standard; DNA; 20 BP.
XX
AC ABZ91225;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

```
XX
PS   Disclosure; SEQ ID NO 6467; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||| |||||| |||||| ||
Db          1 GAAGAAAAAACAAAAAACAA 20


RESULT 3031
ABX12581
ID   ABX12581 standard; DNA; 20 BP.
XX
AC   ABX12581;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human cytochrome P450, CYP3AX, PCR primer #7.
XX
KW   Human; cytochrome P450; CYP3AX; cancer; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002160479-A1.
XX
PD   31-OCT-2002.
XX
PF   09-NOV-2001; 2001US-00007814.
XX
PR   30-MAY-2000; 2000US-00583447.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Wojnowski L,  Gellner K,  Eiselt R;
XX
DR   WPI; 2003-288110/28.
XX
PT   New polynucleotide encoding a cytochrome P450 (CYP) 3AX polypeptide,
PT   useful for diagnosing or treating disorders related to the expression of
PT   a molecular variant CYP3AX gene, e.g. cancer.
XX
PS   Example 3; Page 18; 52pp; English.
XX
CC   The invention relates to a polynucleotide which encodes a cytochrome P450
CC   (CYP) 3AX polypeptide. The polynucleotide is useful in diagnosing or
CC   treating a disorder related to the expression of a molecular variant
CC   CYP3AX gene in a subject, such as cancer. It may also be used for
CC   identifying and obtaining drug candidates and inhibitors for therapy of
CC   disorders related to the malfunction of CYP3AX encoding genes. The
CC   present sequence represents a CYP3AX PCR primer of the invention
XX
SQ   Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1863 CACACTTAGCCATTGAAATG 1882
              || |||| ||||| ||||||
Db          1 CAAACTTTGCCATGGAAATG 20


RESULT 3032
ACC49194
ID   ACC49194 standard; DNA; 20 BP.
XX
AC   ACC49194;
XX
DT   20-JUN-2003  (first entry)
XX
DE   Human ribonuclease L antisense oligonucleotide SEQ ID NO:11.
XX
KW   Human; ribonuclease L; antisense modulation; cytostatic; antimicrobial;
KW   antiinflammatory; antitumour; ribonuclease L expression inhibitor;
KW   antisense gene therapy; infection; aberrant apoptosis; cancer; tumour;
KW   inflammation; phosphorothioate; 2'-O-methoxyethyl; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls (2'-MOEs)"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls (2'-MOEs)"
XX
PN   WO2003023011-A2.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028729.
XX
PR   12-SEP-2001; 2001US-00954679.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ward DT,  Watt AT;
XX
DR   WPI; 2003-313248/30.
XX
PT   Novel antisense compound which is targeted to nucleic acid encoding
PT   ribonuclease L, and inhibits expression of ribonuclease L protein, useful
PT   for treating diseases or conditions resulting from infections and
PT   aberrant apoptosis.
XX
PS   Claim 3; Page 77; 106pp; English.
XX
CC   The present invention describes a compound (I) of 8-50 nucleobases in
CC   length targeted to a nucleic acid molecule (II) encoding ribonuclease L
CC   (III), and which specifically hybridises with (II) and inhibits
CC   expression of (III), where (I) specifically hybridises with at least an 8
CC   -nucleobase portion of an active site on (II). (I) has cytostatic,
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CC   antimicrobial, antiinflammatory and antitumour activities, and can be
CC   used as a ribonuclease L expression inhibitor and in antisense gene
CC   therapy. (I) is useful for inhibiting the expression of ribonuclease L in
CC   cells or tissues, and for treating an animal having a disease condition
CC   associated with ribonuclease L, e.g. infection, aberrant apoptosis or
CC   cancer. (I) is also useful for modulating the process of RNA-mediated
CC   interference (RNAi) in a cell or animal. (I) is also useful
CC   prophylactically, e.g. to prevent or delay infection, inflammation or
CC   tumour formation. (I) is useful as a tool in differential and/or
CC   combinatorial analyses to elucidate expression patterns of a portion or
CC   the entire complement of genes expressed within cells and tissues. (I) is
CC   also useful for research, therapeutics and diagnostics. (I) is also
CC   useful for distinguishing functions of various members of a biological
CC   pathway, and in antisense gene therapy. The present sequence represents a
CC   human ribonuclease L chimeric phosphorothioate antisense oligonucleotide,
CC   which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 7 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1412 ATCAAAGAAGCCCTGATTGT 1431
              ||||||||||| ||| |||
Db          1 ATCAAAGAAGCTTTGAGTGT 20


RESULT 3033
AAL53968/c
ID   AAL53968 standard; DNA; 20 BP.
XX
AC   AAL53968;
XX
DT   18-FEB-2003  (first entry)
XX
DE   DNA mutation detection related ribonucleotide, SEQ ID No 18.
XX
KW   Detecting; point mutation; hybridising; target DNA; duplex; RNase H;
KW   single nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   US2002142308-A1.
XX
PD   03-OCT-2002.
XX
PF   30-MAR-2001; 2001US-00823634.
XX
PR   30-MAR-2001; 2001US-00823634.
XX
PA   (DATT/) DATTAGUPTA N.
PA   (TSEN/) TSENG T.
XX
PI   Dattagupta N,  Tseng T;
XX
DR   WPI; 2003-102506/09.
XX
PT   Detecting point mutation in DNA strand, by hybridizing target DNA strand
PT   having mutation with test DNA strand to form duplex, contacting the
PT   duplex with RNase H and determining the cleavage of test strand by RNase
PT   H.
XX
PS   Example 5; Fig 4; 26pp; English.
XX
CC   The invention relates to a novel method for detecting a point mutation in
CC   a DNA strand. The novel method comprises hybridising a target DNA strand
CC   containing or suspected of containing a point mutation with a test
CC   nucleic acid strand complementary to the DNA strand to form a target DNA
CC   strand/test nucleic acid strand duplex, contacting the duplex with an
CC   RNase H, and determining whether the ribonucleotide residues within the
CC   nucleotide sequence are cleaved by RNase H. The method is useful for
CC   detecting a point mutation in a DNA strand, where the point mutation to
CC   be detected is a single nucleotide polymorphism, preferably a
CC   polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian
CC   or human genome. The method is useful to detect any nucleic acids from
CC   any species of organisms such as Acintobacter, Bacillus, Candida,
CC   Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
CC   This polynucleotide sequence represents a ribonucleotide relating to the
CC   mutation detecting method of the invention
XX
SQ   Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              |||||||||  | |||||||
Db         20 TTTTTTTTTAATATTTTTTT 1


RESULT 3034
AAL61401
ID   AAL61401 standard; DNA; 20 BP.
XX
AC   AAL61401;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Human FXR antisense oligonucleotide, ISIS 145348.
XX
KW   Human; farnesoid X receptor; FXR; cardiovascular disease; gene therapy;
KW   atherosclerosis; hypercholesterolaemia; NR1H4; bile acid receptor; BAR;
KW   retinoid X receptor-interacting protein 14; phosphorothioate backbone;
KW   RIP14; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT   .               methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003044167-A2.
XX
PD   30-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036691.
XX
PR   15-NOV-2001; 2001US-00002491.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Watt AT;
XX
DR   WPI; 2003-468767/44.
XX
PT   New antisense oligonucleotides for modulating human farnesoid X receptor
PT   (FXR) expression, useful for treating conditions associated with FXR in
PT   humans, e.g. cardiovascular disease, atherosclerosis or
PT   hypercholesterolemia.
XX
PS   Claim 3; Page 75; 127pp; English.
XX
```

```
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of human farnesoid X receptor (FXR). FXR is
CC   also known as NR1H4, retinoid X receptor-interacting protein 14 (RIP14)
CC   and bile acid receptor (BAR). The antisense oligonucleotide is useful for
CC   inhibiting the expression of human FXR in cells or tissues. It is
CC   particularly useful for treating or preventing a disease or condition
CC   associated with FXR in a human, e.g. cardiovascular disease,
CC   atherosclerosis or hypercholesterolaemia. The antisense compound is
CC   useful for diagnostics, therapeutics, prophylaxis, or as research
CC   reagents or kits. It is also used in gene therapy. The present sequence
CC   is an antisense oligonucleotide targetted to human FXR DNA. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1892 TGTGCCCTAGATCAACAGAT 1911
              | | |||||| |||||||||
Db          1 TTTTCCCTAGTTCAACAGAT 20


RESULT 3035
ADC98404
ID   ADC98404 standard; DNA; 20 BP.
XX
AC   ADC98404;
XX
DT   01-JAN-2004  (first entry)
XX
DE   ITGA12 polymorphism marker PCR primer S primer seq.
XX
KW   low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;
KW   single nucleotide polymorphism; SNP; PCR primer; ss; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003054218-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US040948.
XX
PR   20-DEC-2001; 2001US-0342711P.
PR   04-NOV-2002; 2002US-0423559P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA,  Valdes A,  Townley DJ,  Mangion J,  Galwey N,  Bennett S;
PI   Mckay I,  Schafer A;
XX
DR   WPI; 2003-559156/52.
XX
PT   Determining whether an individual is predisposed to susceptibility to low
PT   bone mineral density (BMD) and/or bone damage, involves identifying
PT   polymorphisms in associated genes.
XX
PS   Example 8; Page 237; 246pp; English.
XX
CC   The present invention describes a method of determining whether an
CC   individual is predisposed to susceptibility to low bone mineral density
CC   (BMD) and/or bone damage comprising identifying whether the individual
CC   has at least one polymorphism in a polynucleotide encoding a protein,
CC   where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,
CC   see ADC98235 to ADC98315). An agent identified in an method from the
CC   present invention which can be used for the prevention or treatment of a
CC   disease resulting in susceptibility to low BMD and/or bone damage is
CC   useful in the manufacture of a medicament for use in modulating the
CC   susceptibility to low BMD and/or bone damage. The disease associated with
CC   low BMD and/or bone damage is osteoporosis. The present PCR primer
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              | ||||| |||| |||||||
Db          1 TGTTTTTATTTTGTTTTTTA 20


RESULT 3036
ADD21524
ID   ADD21524 standard; DNA; 20 BP.
XX
AC   ADD21524;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human mdm2 antisense oligonucleotide #87.
XX
KW   antisense oligonucleotide; human; mdm2; hyperproliferation;
KW   hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW   atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KW   2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2003048315-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038281.
XX
PR   04-DEC-2001; 2001US-00005344.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Miraglia LJ,  Nero PS,  Graham MJ,  Monia BP,  Koller E,  Chiang MY;
PI   Manoharan M;
XX
DR   WPI; 2003-577263/54.
XX
PT   Novel antisense compound targeted to 5' untranslated region, coding
PT   region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT   useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT   mdm2 expression.
XX
PS   Example 9; SEQ ID NO 89; 289pp; English.
XX
CC   The invention comprises antisense oligonucleotides which are targeted to
CC   the human mdm2 gene. The antisense oligonucleotides of the invention are
CC   useful for reducing hyperproliferation of human cells. The antisense
CC   oligonucleotides are also useful for treating: hyperproliferative
CC   disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC   restenosis. The antisense oligonucleotides are also useful for modulating
CC   apoptosis, and for increasing expression of p21. The present DNA sequence
CC   represents a human mdm2 gene antisense oligonucleotide of the invention.
CC   The present sequence contains 2'-methoxyethoxy-residues and has a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 4 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2313 CAATTTGTTGCTGCTTGTCA 2332
              |||| ||||| ||||| |||
Db          1 CAATATGTTGTTGCTTCTCA 20
```

```
RESULT 3037
ADD81485
ID   ADD81485 standard; DNA; 20 BP.
XX
AC   ADD81485;
XX
DT   29-JAN-2004  (first entry)
XX
DE   HIV PRT antisense derived probe #414.
XX
KW   ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW   large array; minimum oligonucleotide synthesis; probe.
XX
OS   Human immunodeficiency virus.
XX
PN   US2003054346-A1.
XX
PD   20-MAR-2003.
XX
PF   15-FEB-2001; 2001US-00784674.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (SHAN/) SHANNON K W.
PA   (WOLB/) WOLBER P K.
PA   (DELE/) DELENSTARR G C.
PA   (WEBB/) WEBB P G.
PA   (KINC/) KINCAID R H.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2003-743746/70.
XX
PT   Predicting potential of oligonucleotides to hybridize to target
PT   nucleotide sequence comprises determining and evaluating for each
PT   oligonucleotide a parameter predictive of the oligonucleotides ability to
PT   hybridize with target.
XX
PS   Example 2; SEQ ID NO 558; 423pp; English.
XX
CC   The invention relates to a method of predicting the potential of
CC   oligonucleotides to hybridise to target nucleotide sequences. The method
CC   is useful for predicting the potential of an oligonucleotide to hybridise
CC   to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC   contains chemically modified nucleotides. The method is also useful for
CC   predicting the potential of the oligonucleotides to hybridise to a
CC   complementary target nucleotide sequence. The method is useful to predict
CC   efficient hybridisation oligonucleotides for each of multiple target
CC   sequences therefore very large arrays may be constructed and tested with
CC   minimum synthesis of oligonucleotides. The present sequence represents a
CC   HIV PRT antisense derived probe.
XX
SQ   Sequence 20 BP; 2 A; 4 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              |||||| |||||||||  ||
Db          1 TTTTTTCTTTTTTAACCCTG 20


RESULT 3038
ADE27772/c
ID   ADE27772 standard; DNA; 20 BP.
XX
AC   ADE27772;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human B7-1 mRNA targeted oligonucleotide SEQ ID 34.
XX
KW   ss; human; B7-1; inflammatory skin disorder; antisense; psoriasis;
KW   contact dermatitis; atopic dermatitis; seborrheic dermatitis;
KW   nummular dermatitis; generalised exfoliative dermatitis; eczema;
KW   critical costimulatory molecule.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003176374-A1.
XX
PD   18-SEP-2003.
XX
PF   09-MAY-2001; 2001US-00851871.
XX
PR   31-DEC-1996;   96US-00777266.
PR   04-JUN-1999;   99US-00326186.
PR   25-MAY-2000; 2000WO-US014471.
XX
PA   (BENN/) BENNETT C F.
PA   (VICK/) VICKERS T A.
PA   (KARR/) KARRAS J G.
XX
PI   Bennett CF,  Vickers TA,  Karras JG;
XX
DR   WPI; 2003-863863/80.
XX
PT   Treating an inflammatory skin disorder such as psoriasis comprises
PT   topically applying an antisense compound targeted to the nucleic acid
PT   encoding human B7 protein.
XX
PS   Example 1; SEQ ID NO 34; 88pp; English.
XX
CC   The invention relates to a method of treating an inflammatory skin
CC   disorder in an individual by topically applying an antisense compound
CC   targeted to a nucleic acid molecule encoding a human B7 protein. The
CC   invention is for treating an inflammatory skin disorder in individual.
CC   The skin disorder is psoriasis, contact dermatitis, atopic dermatitis,
CC   seborrheic dermatitis, nummular dermatitis, generalised exfoliative
CC   dermatitis or eczema. The invention effectively modulates critical
CC   costimulatory molecules such as the B7 protein. The present sequence
CC   represents a human B7-1 targeted oligonucleotide.
XX
SQ   Sequence 20 BP; 6 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGG 560
              ||| |||||||||  || |||
Db         20 GCCTCACCTCTCCTGGTTGG 1


RESULT 3039
ADE27879/c
ID   ADE27879 standard; DNA; 20 BP.
XX
AC   ADE27879;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human B7-1 targeted oligonucleotide SEQ ID 141.
XX
KW   ss; human; B7-1; inflammatory skin disorder; antisense; psoriasis;
KW   contact dermatitis; atopic dermatitis; seborrheic dermatitis;
KW   nummular dermatitis; generalised exfoliative dermatitis; eczema;
KW   critical costimulatory molecule.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003176374-A1.
```

```
XX
PD   18-SEP-2003.
XX
PF   09-MAY-2001; 2001US-00851871.
XX
PR   31-DEC-1996;   96US-00777266.
PR   04-JUN-1999;   99US-00326186.
PR   25-MAY-2000; 2000WO-US014471.
XX
PA   (BENN/) BENNETT C F.
PA   (VICK/) VICKERS T A.
PA   (KARR/) KARRAS J G.
XX
PI   Bennett CF,  Vickers TA,  Karras JG;
XX
DR   WPI; 2003-863863/80.
XX
PT   Treating an inflammatory skin disorder such as psoriasis comprises
PT   topically applying an antisense compound targeted to the nucleic acid
PT   encoding human B7 protein.
XX
PS   Example 12; SEQ ID NO 141; 88pp; English.
XX
CC   The invention relates to a method of treating an inflammatory skin
CC   disorder in an individual by topically applying an antisense compound
CC   targeted to a nucleic acid molecule encoding a human B7 protein. The
CC   invention is for treating an inflammatory skin disorder in individual.
CC   The skin disorder is psoriasis, contact dermatitis, atopic dermatitis,
CC   seborrheic dermatitis, nummular dermatitis, generalised exfoliative
CC   dermatitis or eczema. The invention effectively modulates critical
CC   costimulatory molecules such as the B7 protein. The present sequence
CC   represents a human B7-1 targeted oligonucleotide.
XX
SQ   Sequence 20 BP; 6 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        541 GCCCCACCTCTCCGGGCTGG 560
              ||| ||||||||| || |||
Db         20 GCCTCACCTCTCCTGGTTGG 1


RESULT 3040
AAZ26235/c
ID   AAZ26235 standard; DNA; 21 BP.
XX
AC   AAZ26235;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 424.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 17 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||| | || |
Db         21 TTTTTTTTTTTTTCATCTCT 2


RESULT 3041
ABK15655/c
ID   ABK15655 standard; DNA; 21 BP.
XX
AC   ABK15655;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Anchored oligo-dt reverse primer.
XX
KW   ss; lipoxygenase; RCI-1; transgenic; plant; plant antifungal;
KW   rice chemically induced cDNA; promoter; transit peptide; plastid;
KW   fungal mycotoxin inhibitor; plant breeding; PCR; primer.
XX
OS   Synthetic.
XX
PN   WO200206490-A1.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-EP008085.
XX
PR   13-JUL-2000; 2000GB-00017275.
PR   15-SEP-2000; 2000GB-00022739.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Dudler R,  Schaffrath U,  Lawton KA;
XX
DR   WPI; 2002-188550/24.
XX
PT   Novel isolated nucleic acid encoding a promoter which is capable of
```

PT driving chemically inducible but not wound- or pathogen-inducible
PT expression of an associated nucleotide sequence.
XX
PS Example 3; Page 30; 88pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (a promoter of
CC rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase)
CC capable of driving chemically-inducible but not wound- or pathogen-
CC inducible expression of an associated nucleotide sequence. Also included
CC are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the
CC lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide
CC which directs expressed proteins to the plastid, a vector comprising the
CC promoter or fragments and a transgenic plant comprising the vector. The
CC promoter or fragments are useful for expressing a nucleotide sequence of
CC interest. The transit peptide is useful for targeting an associated
CC protein of interest to plastids. A nucleic acid which expresses
CC polypeptide having lipoxygenase activity is useful for inhibiting fungal
CC mycotoxins when transformed into a plant. The lipoxygenase is useful for
CC inhibiting fungal mycotoxins. The promoter is useful for regulating
CC transcription of a chemically inducible but not wound or pathogen
CC inducible gene, which involves applying a chemical regulator to a plant
CC or seed containing a chemically regulatable nucleotide sequence.
CC Transgenic plants as described above are useful for breeding improved
CC plant lines that for example increase the effectiveness of conventional
CC methods such as herbicide or pesticide treatment or allow to dispense
CC with the methods due to their modified genetic properties. New crops with
CC improved stress tolerance can be obtained that, due to their optimised
CC genetic equipment yield harvested product of better quality than products
CC that were not able to tolerate comparable adverse developmental
CC conditions. The present sequence is an anchored oligo-dt reverse RT-PCR
CC primer (reverse transcriptase PCR) used to isolate the cDNA encoding rice
CC lipoxygenase
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 1 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3e+03;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2785 GAAAAAAAAAAAAAAA 2800
              :|||||||||||||||
Db         21 BAAAAAAAAAAAAAAA 6
```

RESULT 3042
AAZ25989/c
ID AAZ25989 standard; DNA; 21 BP.
XX
AC AAZ25989;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 178.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 3 A; 8 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1374 AGGCCATCTGTGCCGCGGTG 1393
              |||||||||  ||||||| |
Db         21 AGGCCATCTTCGCCGCGGCG 2
```

RESULT 3043
AAX25672/c
ID AAX25672 standard; DNA; 21 BP.
XX
AC AAX25672;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human endogenous retrovirus W primer GAG4782.
XX
KW Clone; human endogenous retrovirus; genome; autoimmune disease; primer;
KW multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes;
KW disseminated lupus erythematosus; pregnancy; chromosomal marker; PCR;
KW amplification; ss.
XX
OS Synthetic.
OS Human endogenous retrovirus.
XX
PN WO9902696-A1.
XX
PD 21-JAN-1999.
XX
PF 06-JUL-1998; 98WO-FR001442.
XX
PR 07-JUL-1997; 97FR-00008815.
XX
PA (INMR) BIO MERIEUX.
XX
PI Beseme F, Blond J, Bouton O, Mandrand B, Mallet F;
XX
DR WPI; 1999-120897/10.
XX
PT New nucleic acid sequences from human endogenous retrovirus-W - expressed

PT exclusively in placenta and useful in diagnosis and therapy of autoimmune
PT disease, and abnormal or failed pregnancy.
XX
PS Example 5; Page 85; 106pp; French.
XX
CC This sequence represents a primer used to analyse the human endogenous
CC retrovirus (HERV) W genome (AAX25665). Nucleic acids, their fragments or
CC peptides encoded by them derived from the HERV-W genome are markers of
CC autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis,
CC disseminated lupus erythematosus, insulin-dependent diabetes and related
CC pathologies) and of abnormal or unsuccessful pregnancy and can be used as
CC chromosomal markers for susceptibility to these conditions, or proximity
CC markers of genes associated with this susceptibility
XX
SQ Sequence 21 BP; 6 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2673 AGTGTGTGTGGGTGAAATGG 2692
||||| || |||| ||||||
Db 21 AGTGTCTGAGGGTCAAATGG 2

RESULT 3044
AAX14731
ID AAX14731 standard; DNA; 21 BP.
XX
AC AAX14731;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix third strand of Beta-globin gene nucleotides 917-937.
XX
KW Triplex formation; DNA detection; triple helix; identification; bacteria;
KW oncogene; virus; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 17-18; 168pp; English.
XX
CC The present sequence represents a polynucleotide that is able to form a
CC triple helix with a double stranded sequence. Cytosine bases in the
CC present can be replaced with 5-methylcytosine for increased triplex
CC stability. The present sequence is used in the assay of the invention,
CC where it can be part of the anchor DNA or reporter DNA sequence. The
CC assay comprises adding a sample containing double-stranded DNA test
CC sequences to an aqueous medium containing at least one complex of anchor
CC DNA, attached to a solid support, and reporter DNA, where either a part
CC of the anchor DNA or reporter DNA is designed to form a triple-strand
CC structure with part of the test sequence. Triplex formation results in
CC displacement of the reporter DNA which is detected as an indication of
CC the presence of the DNA test sequence. The method is used to detect DNA
CC sequences, particularly for identification of bacteria (by detecting
CC genes for ribosomal RNA) in clinical samples, but also detection of
CC oncogenes and Hepatitis B virus
XX
SQ Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTT 2183
||| || |||||||||| |||
Db 1 CCTCTTCTTTTTTTTCTTT 20

RESULT 3045
AAA11484/c
ID AAA11484 standard; DNA; 21 BP.
XX
AC AAA11484;
XX
DT 30-JUN-2000 (first entry)
XX
DE Human dysferlin PCR primer #129.
XX
KW Dysferlin; anti-dystrophic; gene therapy; muscular dystrophy; human;
KW skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis;
KW limb girdle muscular dystrophy-2B; brain-specific; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200011157-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019395.
XX
PR 25-AUG-1998; 98US-0097927P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;
XX
DR WPI; 2000-237646/20.
XX
PT Novel dysferlin genes and related proteins useful for diagnosis, risk
PT identification and treatment of hereditary muscular dystrophies and other
PT dysferlin related disorders.
XX
PS Claim 8; Page 134; 146pp; English.
XX
CC This invention describes a novel human dysferlin nucleic acid (I) and its
CC encoding protein (II), which has anti-dystrophic activity and can be used
CC for gene therapy. Introduction of (I), a vector comprising (I) or
CC dysferlin into a cell of a mammal can be used to decrease the symptoms of
CC muscular dystrophy. The dysferlin gene is normally expressed in skeletal
CC muscle cells and is selectively mutated in several families with the
CC hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle
CC muscular dystrophy-2B. The primers and oligonucleotides derived from (I)
CC can be used in diagnosis of or risk identification for dysferlin-related
CC disorders in patients, fetus, or pre-embryos. Expression of brain-
CC specific dysferlin may be important as a marker for normal neural
CC development. Dysferlin DNA or subgenomic coding sequences can be used for
CC therapy of the hereditary muscular dystrophies. AAX82919-X82945 represent
CC PCR primers used in the method of the invention
XX
SQ Sequence 21 BP; 6 A; 1 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        335 CCACCCTACTTTCCCCCTCC 354
              || ||||||| ||||| |||
Db         21 CCTCCCTACTGTCCCCTTCC 2
```

RESULT 3046
AAA11497/c
ID AAA11497 standard; DNA; 21 BP.
XX
AC AAA11497;
XX
DT 30-JUN-2000 (first entry)
XX
DE Human dysferlin PCR primer #142.
XX
KW Dysferlin; anti-dystrophic; gene therapy; muscular dystrophy; human;
KW skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis;
KW limb girdle muscular dystrophy-2B; brain-specific; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200011157-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019395.
XX
PR 25-AUG-1998; 98US-0097927P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;
XX
DR WPI; 2000-237646/20.
XX
PT Novel dysferlin genes and related proteins useful for diagnosis, risk
PT identification and treatment of hereditary muscular dystrophies and other
PT dysferlin related disorders.
XX
PS Claim 8; Page 135; 146pp; English.
XX
CC This invention describes a novel human dysferlin nucleic acid (I) and its
CC encoding protein (II), which has anti-dystrophic activity and can be used
CC for gene therapy. Introduction of (I), a vector comprising (I) or
CC dysferlin into a cell of a mammal can be used to decrease the symptoms of
CC muscular dystrophy. The dysferlin gene is normally expressed in skeletal
CC muscle cells and is selectively mutated in several families with the
CC hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle
CC muscular dystrophy-2B. The primers and oligonucleotides derived from (I)
CC can be used in diagnosis of or risk identification for dysferlin-related
CC disorders in patients, fetus, or pre-embryos. Expression of brain-
CC specific dysferlin may be important as a marker for normal neural
CC development. Dysferlin DNA or subgenomic coding sequences can be used for
CC therapy of the hereditary muscular dystrophies. AAX82919-X82945 represent
CC PCR primers used in the method of the invention
XX
SQ Sequence 21 BP; 1 A; 5 C; 9 G; 6 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1263 TCAGCCAAGACCGGACACCC 1282
              |||||||| || || |||||
Db         20 TCAGCCAACACAGGGCACCC 1
```

RESULT 3047
AAA36939/c
ID AAA36939 standard; DNA; 21 BP.
XX
AC AAA36939;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human dysferlin exon amplification primer SEQ ID NO:201.
XX
KW Human; dysferlin; mutant; identification; chromosome 2p12-14; detection;
KW muscular dystrophy; diagnosis; hereditary muscular dystrophy;
KW miyoshi myopathy; limb girdle muscular dystrophy; primer; amplification;
KW screening; ss.
XX
OS Homo sapiens.
XX
PN WO200011016-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019394.
XX
PR 25-AUG-1998; 98US-0097930P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Brown RH, Liu J, Hoffman E, Chou F;
XX
DR WPI; 2000-246531/21.
XX
PT Dysferlin polynucleotide, its mutant form useful for diagnosis and
PT treatment of hereditary muscular dystrophies e.g. miyoshi myopathy and
PT limb girdle muscular dystrophy.
XX
PS Disclosure; Page 32; 136pp; English.
XX
CC The present invention describes an isolated dysferlin DNA of 20-25
CC nucleotides in length, comprising a nucleotide sequence specifically
CC selected from nucleotides 911-913, 929-948, 1019-1038, 1392-1411, 1424-
CC 1443, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 2241-2260,
CC 2864-2883, 2978-2997, 3057-3076, 3198-3217, 3252-3271, 4356-4375, 4665-
CC 4684, 5015-5034, 5610-5629, 5726-5735, 6035-6054, 6179-6198, 6243-6263
CC and 6529-6548 of the human dysferlin nucleotide sequence given in
CC AAA36744. Dysferlin nucleotide sequences containing specific mutations
CC can be used for diagnosing a patient, a foetus or a pre-embryo at risk of
CC developing a dysferlin associated disorder by detecting mutations in the
CC dysferlin gene in biological samples from patients. Alternatively, the
CC biological sample containing genomic DNA can be incubated with a
CC restriction enzyme, preferably BanII, Bsp1286I, RsaI, HhaI, HaeIII,
CC Bsp1286, NlaIV, NlaIII, BcgI, AvaII, BstEII, PleI, HaeI, AluI, ApoI,
CC Tsp509I, SalI, HincII, TaqI, HinfI, TfiI, SfaNI or FokI and the presence
CC or absence of a restriction enzyme site in the sample is detected as an
CC indication of the presence or absence of a particular mutation in the
CC sample. Dysferlin polynucleotides are useful for treating hereditary
CC muscular dystrophies such as miyoshi myopathy (MM) and limb girdle
CC muscular dystrophy-2B (LGMB-2B). MM and LGMB-2B map to the human
CC chromosome 2p12-14 region between the genetic markers D2S292 and D2S286.
CC The present sequence represents a primer for human dysferlin
XX
SQ Sequence 21 BP; 6 A; 1 C; 12 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        335 CCACCCTACTTTCCCCCTCC 354
              || ||||||| ||||| |||
Db         21 CCTCCCTACTGTCCCCTTCC 2
```

RESULT 3048
AAA36952/c
ID AAA36952 standard; DNA; 21 BP.
XX
AC AAA36952;
XX
DT 03-AUG-2000 (first entry)

```
XX
DE   Human dysferlin exon amplification primer SEQ ID NO:214.
XX
KW   Human; dysferlin; mutant; identification; chromosome 2p12-14; detection;
KW   muscular dystrophy; diagnosis; hereditary muscular dystrophy;
KW   miyoshi myopathy; limb girdle muscular dystrophy; primer; amplification;
KW   screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200011016-A1.
XX
PD   02-MAR-2000.
XX
PF   25-AUG-1999;   99WO-US019394.
XX
PR   25-AUG-1998;   98US-0097930P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Brown RH,  Liu J,  Hoffman E,  Chou F;
XX
DR   WPI; 2000-246531/21.
XX
PT   Dysferlin polynucleotide, its mutant form useful for diagnosis and
PT   treatment of hereditary muscular dystrophies e.g. miyoshi myopathy and
PT   limb girdle muscular dystrophy.
XX
PS   Disclosure; Page 32; 136pp; English.
XX
CC   The present invention describes an isolated dysferlin DNA of 20-25
CC   nucleotides in length, comprising a nucleotide sequence specifically
CC   selected from nucleotides 911-913, 929-948, 1019-1038, 1392-1411, 1424-
CC   1443, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 2241-2260,
CC   2864-2883, 2978-2997, 3057-3076, 3198-3217, 3252-3271, 4356-4375, 4665-
CC   4684, 5015-5034, 5610-5629, 5726-5735, 6035-6054, 6179-6198, 6243-6263
CC   and 6529-6548 of the human dysferlin nucleotide sequence given in
CC   AAA36744. Dysferlin nucleotide sequences containing specific mutations
CC   can be used for diagnosing a patient, a foetus or a pre-embryo at risk of
CC   developing a dysferlin associated disorder by detecting mutations in the
CC   dysferlin gene in biological samples from patients. Alternatively, the
CC   biological sample containing genomic DNA can be incubated with a
CC   restriction enzyme, preferably BanII, Bsp1286I, RsaI, HhaI, HaeIII,
CC   Bsp1286, NlaIV, NlaIII, BcgI, AvaII, BstEII, PleI, HaeI, AluI, ApoI,
CC   Tsp509I, SalI, HincII, TaqI, HinfI, TfiI, SfaNI or FokI and the presence
CC   or absence of a restriction enzyme site in the sample is detected as an
CC   indication of the presence or absence of a particular mutation in the
CC   sample. Dysferlin polynucleotides are useful for treating hereditary
CC   muscular dystrophies such as miyoshi myopathy (MM) and limb girdle
CC   muscular dystrophy-2B (LGMB-2B). MM and LGMB-2B map to the human
CC   chromosome 2p12-14 region between the genetic markers D2S292 and D2S286.
CC   The present sequence represents a primer for human dysferlin
XX
SQ   Sequence 21 BP; 1 A; 5 C; 9 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1263 TCAGCCAAGACCGGACACCC 1282
              ||||||| || || |||||
Db         20 TCAGCCAACACAGGGCACCC 1


RESULT 3049
AAZ52058
ID   AAZ52058 standard; DNA; 21 BP.
XX
AC   AAZ52058;
XX
DT   18-JUL-2000  (first entry)
XX
DE   5'PCR primer L1-5 for preparation of DNA construct for scFv expression.
XX
KW   PCR primer; humanised antibody-901; Hu-901; monoclonal antibody;
KW   gene therapy; recombinant adenovirus vector; anti-IgE antibody;
KW   anti-immunoglobulin E; scFv; single chain variable fragment; allergy;
KW   antiallergic; ss.
XX
OS   Homo sapiens.
OS   Mus sp.
XX
PN   WO200015260-A1.
XX
PD   23-MAR-2000.
XX
PF   16-SEP-1999;   99WO-US021646.
XX
PR   16-SEP-1998;   98US-0100639P.
XX
PA   (TANO-) TANOX INC.
XX
PI   Liou RS,  Thomas D;
XX
DR   WPI; 2000-271264/23.
XX
PT   New nucleic acids encoding anti-IgE antibodies such as Hu-901 or their
PT   fragments, useful in the gene therapy of allergic diseases.
XX
PS   Example 1; Page 10; 52pp; English.
XX
CC   The present sequence is the 5'PCR primer L1-5 used for the preparation of
CC   DNA construct for scFv (single chain variable fragment) expression of
CC   anti-IgE without signal peptide. This primer was used to obtain a 330-bp
CC   DNA fragment of the Hu-901 light chain variable region cells by using the
CC   pHCMV-VL1-huCkappa plasmid DNA as the template. Humanised anti-IgE genes
CC   are incorporated in the genome of a recombinant adenovirus vector as an
CC   independent transcriptional unit, and packaged into infectious virus
CC   particles. Upon infection of host, the recombinant adenovirus vector will
CC   direct the production of either intact anti-IgE antibody or an scFv
CC   fragment in the serum, which will bind free circulating IgE, resulting in
CC   the reduction of free serum IgE. The binding of the antibody or fragment
CC   to IgE-bearing B cells may lower IgE levels by down-regulating IgE
CC   production by these B cells. These methods are useful in the gene therapy
CC   of allergic diseases
XX
SQ   Sequence 21 BP; 4 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        602 TCCGACCTGCTGCTGCCCCA 621
              |||||| | |||||| ||||
Db          1 TCCGACATCCTGCTGACCCA 20


RESULT 3050
AAZ75737/c
ID   AAZ75737 standard; DNA; 21 BP.
XX
AC   AAZ75737;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:10093.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
```

```
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 2382; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 21 BP; 10 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1112 GACTTTGCCTATGTCTGTGA 1131
              || |||| |||| |||||||
Db         21 GATTTTGACTATTTCTGTGA 2


RESULT 3051
AAZ75372
ID   AAZ75372 standard; DNA; 21 BP.
XX
AC   AAZ75372;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:9728.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 2304; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2180
              || |||||||||||||  ||
Db          1 TCCCCTTTTTTTTTTCCTT 20


RESULT 3052
AAC72800
ID   AAC72800 standard; DNA; 21 BP.
XX
AC   AAC72800;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #1753.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
```

```
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 21 BP; 6 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        924 CACCTGAATGCTTAAATGCC 943
              ||||| ||||||  ||||||
Db          1 CACCTTAATGCTCTAATGCC 20


RESULT 3053
AAC72803
ID   AAC72803 standard; DNA; 21 BP.
XX
AC   AAC72803;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #1755.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 21 BP; 6 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        924 CACCTGAATGCTTAAATGCC 943
              ||||| ||||||  ||||||
Db          1 CACCTTAATGCTCTAATGCC 20


RESULT 3054
AAA80353/c
ID   AAA80353 standard; DNA; 21 BP.
XX
AC   AAA80353;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human ASTH1I 5' region polymorphic site, SEQ ID NO:100 (a).
XX
KW   ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KW   bronchial hyperreactivity; ets family; transcription factor;
KW   splice variant; genetic predisposition; polymorphism; antibody;
KW   drug screening; prophylaxis; therapy; diagnosis;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(10. .12,TA)
FT                   /*tag=  a
XX
PN   US6087485-A.
XX
PD   11-JUL-2000.
XX
PF   21-JAN-1998;   98US-00009913.
XX
PR   21-JAN-1997;   97US-0035663P.
PR   01-JUL-1997;   97US-0051432P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  North M,  Cardon L,  Buckler A;
PI   Brooks-Wilson AR,  Carey AH;
XX
DR   WPI; 2000-505109/45.
XX
PT   New nucleic acids other than naturally occurring chromosomes encoding
PT   ASTH1 protein, for e.g. screening compositions that modulate expression
PT   or function of ASTH1 proteins or as diagnostics for genetic
PT   predisposition to asthma.
XX
PS   Example; Col 41-42; 131pp; English.
XX
CC   The invention relates to the ASTH1 locus on the short arm of human
CC   chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
CC   are associated with a genetic predisposition to asthma and bronchial
CC   hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
CC   directions with the ASTH1 locus, and have similar patterns of expression
CC   and common sequence motifs. They are both expressed in trachea, lung and
CC   several other tissues. ASTH1I and ASTH1J are novel members of the ets
CC   family of transcription factors, which have been implicated in the
CC   activation of a variety of genes including the TCRa gene and cytokine
CC   genes known to be important in the aetiology of asthma. Both ASTH1I and
CC   ASTH1J mRNAs are alternatively spliced. Alternative splicing of
CC   transcripts has no effect on the open reading frame of ASTH1J, as the
CC   exons involved are all 5' to the start codon in exon b. In contrast,
CC   alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
CC   isoforms. The invention also encompasses mouse asth1j protein. The ASTH1
```

CC nucleic acids are useful as diagnostics to identify a hereditary
CC predisposition to asthma, as probes for identifying ASTH1 related genes,
CC for identifying expression of the gene in a biological specimen, and for
CC generating genetically modified non-human animals or site specific gene
CC modifications in cell lines. The encoded ASTH1 proteins are useful as
CC immunogens to raise specific antibodies; in drug screening for
CC compositions that mimic or modulate activity or expression of ASTH1I
CC and/or ASTH1J (including altered forms of these proteins); and as a
CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
CC antibodies are useful in the identification of individuals predisposed to
CC development of asthma, and for modulation of gene activity in vivo for
CC prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
CC proteins or active fragments thereof may be used to modulate or reduce
CC bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC represent polymorphic sites within the ASTH1J or ASTH1I genes
XX
SQ Sequence 21 BP; 8 A; 0 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1968 TATTTACCTTGAAAAAAAGA 1987
              ||||| |||| ||||||| |
Db         21 TATTTTCCTTAAAAAAAAAA 2
```

RESULT 3055
AAF29175
ID AAF29175 standard; DNA; 21 BP.
XX
AC AAF29175;
XX
DT 06-APR-2001 (first entry)
XX
DE DNA encoding an E-coil peptide used as a tag.
XX
KW Virus like particle; VPL; tumour; autoimmune disease; infectious disease;
KW molecule interaction identification; ds.
XX
OS Synthetic.
XX
PN WO200102551-A2.
XX
PD 11-JAN-2001.
XX
PF 26-JUN-2000; 2000WO-EP006144.
XX
PR 30-JUN-1999; 99EP-00112451.
PR 30-JUN-1999; 99US-0141268P.
PR 21-MAR-2000; 2000EP-00106109.
PR 15-MAY-2000; 2000EP-00110363.
XX
PA (EVOT-) EVOTEC BIOSYSTEMS AG.
XX
PI Hunt N;
XX
DR WPI; 2001-103004/11.
XX
PT Selectively incorporating or encapsulating proteinaceous target molecules
PT into virus like particles, useful for preparation of a medicament for
PT treating/preventing disease, comprises co-expressing target and signal
PT molecules in cells.
XX
PS Disclosure; Page 73; 125pp; English.
XX
CC This invention relates to selectively incorporating or encapsulating
CC proteinaceous target molecules into virus like particles (VLPs)
CC comprising co-expressing target and signal molecules in a cell. The
CC method of encapsulating target molecules can be used in the production of
CC virus like particles which can be used for preparing a medicament for
CC treating or preventing a genetic disease, tumours, autoimmune or
CC infectious diseases. The VLPs can also be used for identifying and
CC characterising the interactions between target molecules, also for
CC identifying potential pharmaceutically active substances and for the
CC identification of analytes in diagnostic applications. The present
CC sequence represents DNA encoding an E-coil used in the production of
CC coiled coil tagged target and signal molecules for use in the
CC construction of the virus like particles of the invention
XX
SQ Sequence 21 BP; 4 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1388 GCGGTGTCTGCCCTGCAGAA 1407
              | |||||| |||||| ||||
Db          1 GAGGTGTCCGCCCTGGAGAA 20
```

RESULT 3056
AAH88904
ID AAH88904 standard; DNA; 21 BP.
XX
AC AAH88904;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human polymorphic oligonucleotide M33494 fragment #19.
XX
KW Human; single nucleotide polymorphic; SNP; forensic science;
KW paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW plant breeding; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,a)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200134840-A2.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-US030766.
XX
PR 10-NOV-1999; 99US-0164596P.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Au K, Chen J, Patil N, Thomas D;
XX
DR WPI; 2001-335945/35.
XX
PT New polymorphic sites derived from the human genome are useful to
PT determine sites correlating with phenotypic traits, particularly disease,
PT and also in forensics and paternity testing.
XX
PS Claim 37; Page 9; 43pp; English.
XX
CC The present invention relates to human oligonucleotides comprising a
CC single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC sequence is one such oligonucleotide. The oligonucleotides can be used in
CC forensics, paternity testing, correlation of polymorphisms with
CC phenotypic traits, genetic mapping of phenotypic traits and marker
CC assisted breeding of animals and crop plants
XX
SQ Sequence 21 BP; 2 A; 7 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        550 CTCCGGGCTGGAGGCGGGCG 569
              | || ||||| |||||||||
Db          2 CACCTGGCTGCAGGCGGGCG 21
```

RESULT 3057
AAF81140/c
ID AAF81140 standard; DNA; 21 BP.
XX
AC AAF81140;
XX
DT 02-MAY-2001 (first entry)
XX
DE Primer used for sequencing PTGS2 exon 1 SEQ ID 246.
XX
KW Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
KW inflammation; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200107662-A1.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020114.
XX
PR 22-JUL-1999; 99US-0145170P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
XX
DR WPI; 2001-182805/18.
XX
PT New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
PT for gene therapy of inflammation and for establishing a genotype or
PT haplotype.
XX
PS Example 1b; Page 40; 118pp; English.
XX
CC This invention relates to a polynucleotide sequence that is a polymorphic
CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
CC protein is represented by AAB72199. The invention includes PCR and
CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
CC are used to isolated and characterise the PTGS2 gene sequence, and to
CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
CC especially for determining association between a particular trait, e.g. a
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
CC effects of therapeutic agents
XX
SQ Sequence 21 BP; 7 A; 9 C; 3 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1610 TGGGGGAAGAGTTTGTTACC 1629
```

```
                ||||||  ||  ||||  |||||
Db         20 TGGGGGCAGGGTTTTTTACC 1
```

RESULT 3058
ABK37488
ID ABK37488 standard; DNA; 21 BP.
XX
AC ABK37488;
XX
DT 08-MAY-2002 (first entry)
XX
DE Packaged vector plus sense RT-PCR primer.
XX
KW Viral vector; retinoic acid receptor beta-2; RARbeta2; gag-pol; env;
KW non-primate lentivirus; equine infectious anaemia virus; EIAV; cancer;
KW vesicular stomatitis virus G protein; VSV-G; neurite development;
KW neurological disorder; inflammatory disorder; dermatological disorder;
KW autoimmune disorder; cardiovascular disorder; nerve growth factor; NGF;
KW neurite outgrowth; gene therapy; RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200175135-A1.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-GB001478.
XX
PR 30-MAR-2000; 2000WO-GB001211.
PR 04-OCT-2000; 2000GB-00024300.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman AJ, Maden M, Corcoran JPT;
XX
DR WPI; 2002-010796/01.
XX
PT Novel viral vector useful in preparation of medicament to cause neurite
PT development or for treatment of neurological disorder, comprises a
PT sequence encoding a receptor, preferably retinoic acid receptor beta-2.
XX
PS Example 7; Page 114; 241pp; English.
XX
CC The present invention relates to viral vectors comprising a nucleic acid
CC sequence encoding retinoic acid receptor beta-2 (RARbeta2). The vector is
CC preferably based on or derived from a lentivirus, more preferably non-
CC primate such as equine infectious anaemia virus (EIAV), and comprises
CC deleted regions of the gag-pol genes. The vector may be engineered to
CC replace all or part of the env gene with env sequences from other RNA
CC viruses (e.g. gene encoding vesicular stomatitis virus G, VSV-G protein),
CC by a method of pseudotyping, to broaden the infectious spectrum of the
CC viral vector. The viral vectors of the invention are useful in the
CC preparation of a medicament, or in gene therapy to stimulate neurite
CC development, or for the treatment of a neurological disorder (e.g.
CC Parkinson's disease and spinal cord injuries). The vectors are also
CC useful for treating cancers, inflammatory disorders, dermatological
CC disorders, autoimmune disorders, cardiovascular disorders, ulcers,
CC haemophilia, liver cirrhosis, bone marrow transplantation or other
CC transplantation complications. The vectors eliminate the need for
CC administration of nerve growth factor (NGF) to a subject, enable neurite
CC outgrowth to be promoted in adult neural tissue, and enable RARbeta2 to
CC be introduced into non-dividing mammalian cells such as neuronal cells.
CC The present sequence represents a primer used in the methods of the
CC present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2209 AATGGGAGACTCTTTGAAAT 2228
```

```
                  | |||||||| |||||| ||
Db          1 ATTGGGAGACCCTTTGACAT 20
```

RESULT 3059
ABK37472
ID ABK37472 standard; DNA; 21 BP.
XX
AC ABK37472;
XX
DT 08-MAY-2002 (first entry)
XX
DE Packaging signal assay plus sense RT-PCR primer.
XX
KW Viral vector; retinoic acid receptor beta-2; RARbeta2; gag-pol; env;
KW non-primate lentivirus; equine infectious anaemia virus; EIAV; cancer;
KW vesicular stomatitis virus G protein; VSV-G; neurite development;
KW neurological disorder; inflammatory disorder; dermatological disorder;
KW autoimmune disorder; cardiovascular disorder; nerve growth factor; NGF;
KW neurite outgrowth; gene therapy; RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200175135-A1.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-GB001478.
XX
PR 30-MAR-2000; 2000WO-GB001211.
PR 04-OCT-2000; 2000GB-00024300.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman AJ, Maden M, Corcoran JPT;
XX
DR WPI; 2002-010796/01.
XX
PT Novel viral vector useful in preparation of medicament to cause neurite
PT development or for treatment of neurological disorder, comprises a
PT sequence encoding a receptor, preferably retinoic acid receptor beta-2.
XX
PS Example 5; Page 106; 241pp; English.
XX
CC The present invention relates to viral vectors comprising a nucleic acid
CC sequence encoding retinoic acid receptor beta-2 (RARbeta2). The vector is
CC preferably based on or derived from a lentivirus, more preferably non-
CC primate such as equine infectious anaemia virus (EIAV), and comprises
CC deleted regions of the gag-pol genes. The vector may be engineered to
CC replace all or part of the env gene with env sequences from other RNA
CC viruses (e.g. gene encoding vesicular stomatitis virus G, VSV-G protein),
CC by a method of pseudotyping, to broaden the infectious spectrum of the
CC viral vector. The viral vectors of the invention are useful in the
CC preparation of a medicament, or in gene therapy to stimulate neurite
CC development, or for the treatment of a neurological disorder (e.g.
CC Parkinson's disease and spinal cord injuries). The vectors are also
CC useful for treating cancers, inflammatory disorders, dermatological
CC disorders, autoimmune disorders, cardiovascular disorders, ulcers,
CC haemophilia, liver cirrhosis, bone marrow transplantation or other
CC transplantation complications. The vectors eliminate the need for
CC administration of nerve growth factor (NGF) to a subject, enable neurite
CC outgrowth to be promoted in adult neural tissue, and enable RARbeta2 to
CC be introduced into non-dividing mammalian cells such as neuronal cells.
CC The present sequence represents a primer used in the methods of the
CC present invention
XX
SQ Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2209 AATGGGAGACTCTTTGAAAT 2228
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```
                  | |||||||| |||||| ||
Db          1 ATTGGGAGACCCTTTGACAT 20
```

RESULT 3060
ABL44934
ID ABL44934 standard; DNA; 21 BP.
XX
AC ABL44934;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1978.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 43; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 21 BP; 3 A; 0 C; 10 G; 8 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1939 GGTAATGGTTGGTTTTTGTG 1958
                | ||||||| | |||| |||||
Db          2 GGTAATGATGGGTTGTTGTG 21
```

RESULT 3061
ABS97218
ID ABS97218 standard; DNA; 21 BP.
XX

```
AC   ABS97218;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human CYP4502E1 promoter polymorphism #4.
XX
KW   Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 3; Page 103; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   polymorphic DNA sequence of the invention
XX
SQ   Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1072 GACATCCTTAGTAGAAGGTG 1091
                ||| |||| ||||||||||
Db          1 GACTACCTTCGTAGAAGGTG 20


RESULT 3062
ABK89936
ID   ABK89936 standard; DNA; 21 BP.
XX
AC   ABK89936;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Virus like particle associated E-coil DNA sequence.
XX
KW   Protein incorporation; protein encapsulation; virus like particle;
KW   proteinaceous target molecule complex; signal molecule;
KW   substance enrichment; recombinant molecule; pharmaceutical screening;
KW   functional genomics analysis; viral maturation;
KW   cell surface protein-mediated activity; receptor-mediated activity;
KW   ion channel-mediated activity; coiled-coil structure; ds.
XX
OS   Synthetic.
XX
PN   EP1219705-A1.
XX
PD   03-JUL-2002.
XX
PF   29-DEC-2000; 2000EP-00128686.
XX
PR   29-DEC-2000; 2000EP-00128686.
XX
PA   (EVOT-) EVOTEC OAI AG.
XX
PI   Hunt N;
XX
DR   WPI; 2002-521946/56.
XX
PT   Selectively incorporating a proteinaceous target molecule complex into a
PT   virus like particle for screening or purifying recombinant molecules
PT   comprises co-expressing target molecules in recombinant cells with signal
PT   molecules.
XX
PS   Disclosure; Page 31; 68pp; English.
XX
CC   The present invention relates to a method for selectively incorporating
CC   or encapsulating a proteinaceous target molecule complex into a virus
CC   like particle, or physically associating a two component proteinaceous
CC   target molecule complex with a virus like particle comprising co-
CC   expressing target molecules in recombinant cells together with signal
CC   molecules. The method is useful for achieving enrichment of substances
CC   (e.g. proteins, polynucleotides, oligonucleotides, organic molecules of
CC   lower molecular weight or ion) in a medium in which cells are arranged
CC   when the virus-like particles are released in the medium, where the virus
CC   -like particles incorporate, encapsulate or are associated with the
```

```
CC   substances. The virus-like particles are useful for concentrating,
CC   isolating or purifying recombinant molecules. They are particularly
CC   useful in pharmaceutical screening and functional genomics, e.g. for
CC   detecting compounds influencing viral maturation, identifying modulators
CC   of cell surface protein-mediated activity or identifying modulators of
CC   receptor- or ion channel-mediated activity. The present sequence
CC   represents a coil DNA sequence used in the methods of the present
CC   invention
XX
SQ   Sequence 21 BP; 4 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1388 GCGGTGTCTGCCCTGCAGAA 1407
              | |||||| |||||| ||||
Db          1 GAGGTGTCCGCCCTGGAGAA 20


RESULT 3063
ABZ69339
ID   ABZ69339 standard; DNA; 21 BP.
XX
AC   ABZ69339;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human SLC11A3 coding sequence PCR primer #17.
XX
KW   Human; hereditary haemochromatosis; HH; ferroportin 1 gene; SLC11A3;
KW   mutation; iron transport; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003002589-A1.
XX
PD   09-JAN-2003.
XX
PF   01-JUL-2002; 2002WO-US020771.
XX
PR   29-JUN-2001; 2001US-0301429P.
PR   10-OCT-2001; 2001US-00973180.
XX
PA   (UYRO-) UNIV ROTTERDAM ERASMUS.
PA   (DEAN/) DEAN D D.
XX
PI   Dean DD,  Van Duijn CM,  Heutink P,  Oostra BA;
XX
DR   WPI; 2003-201489/19.
XX
PT   New isolated DNA sequence and polypeptide, useful for diagnosing a
PT   patient as having an increased risk of developing hereditary
PT   hemochromatosis disease or anemia, or screening potential therapeutic
PT   agents for treating the disease.
XX
PS   Disclosure; Page 28; 66pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   ferroportin 1 (SLC11A3) gene, and describes the A734C base change present
CC   in the gene which causes hereditary haemochromatosis (HH). This affects
CC   SLC11A3 mediated iron transport. The sequences can be used in the
CC   diagnosis and treatment of hereditary haemochromatosis and anaemia. The
CC   present sequence is a PCR primer used to isolate the sequences in the
CC   exemplification of the invention
XX
SQ   Sequence 21 BP; 7 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   85.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2703 TTGAACTCTCTGCCTGTAAA 2722
              ||||| | | ||||||||||
Db          1 TTGAAATGTATGCCTGTAAA 20


RESULT 3064
ADC16521
ID   ADC16521 standard; RNA; 21 BP.
XX
AC   ADC16521;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Short interfering double-stranded RNA oligonucleotide SEQ ID NO:246.
XX
KW   expression interference; expression inhibition; target gene;
KW   short interfering double stranded RNA; cytostatic; gene therapy;
KW   proliferative disease; cancer; ds.
XX
OS   Synthetic.
XX
PN   WO2003012052-A2.
XX
PD   13-FEB-2003.
XX
PF   30-JUL-2002; 2002WO-US024226.
XX
PR   30-JUL-2001; 2001US-0308640P.
PR   08-APR-2002; 2002US-0370970P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (CARN-) CARNEGIE INST WASHINGTON.
PA   (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI   Caplen NJ,  Morgan RA,  Fire A,  Parrish S,  Mousses S;
PI   Kallioniemi O,  Cornelison JR,  Alton EW,  Griesenbach U;
XX
DR   WPI; 2003-248169/24.
XX
PT   New RNA comprising double stranded RNA and a 3' or 5' overhang having a
PT   length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse
PT   genetic and/or therapeutic tools for interfering or inhibiting expression
PT   of a target gene.
XX
PS   Claim 71; SEQ ID NO 246; 176pp; English.
XX
CC   The present invention describes an RNA (I) used for the interference or
CC   inhibition of expression of a target gene, where (I) comprises double
CC   stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang
CC   having a length of 0-nucleotide to 5-nucleotides on each strand, where
CC   the sequence of the double stranded RNA is substantially identical to a
CC   portion of a mRNA or transcript of the target gene. Also described: (1)
CC   interfering with or inhibiting the expression of a target gene in a cell
CC   by exposing the cell to an amount of (I); (2) a gene silencing array
CC   comprising a substantially flat substrate, and addressably arrayed
CC   different double-stranded RNAs; (3) an array-based method of assessing a
CC   phenotypic effect of a double-stranded RNA on a target gene; (4)
CC   validating a gene as a potential drug target for a disease or condition;
CC   (5) selecting an optimised sequence of a double-stranded RNA for
CC   interference with or inhibition of expression of a target gene in a cell;
CC   and (6) a short double-stranded RNA effective for interfering with or
CC   inhibiting expression of a target gene comprising any of 311 20-78
CC   nucleotide sequences (see ADC16276 to ADC16586). (I) has cytostatic
CC   activity, and can be used in gene therapy. The RNAs are useful as reverse
CC   genetic and/or therapeutic tools for interfering or inhibiting expression
CC   of a target gene. They are useful for treating proliferative diseases,
CC   e.g. cancer.
XX
SQ   Sequence 21 BP; 6 A; 7 C; 4 G; 0 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 21;
  Best Local Similarity   65.0%;  Pred. No. 3e+03;
  Matches   13;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       1176 CTCATCTTGGAGGACGAAAT 1195
              |:||:| : ||||||| |:
Db          1 CUCAUCAUCGAGGACGACAU 20
```

RESULT 3065
AAT78995
ID AAT78995 standard; DNA; 22 BP.
XX
AC AAT78995;
XX
DT 13-JAN-1998 (first entry)
XX
DE Mouse Huntington's disease gene intron 1 3' acceptor site.
XX
KW Huntington's disease; animal model; transgenic animal; mouse; therapy;
KW drug screening; Hdh gene; ss.
XX
OS Mus musculus.
XX
PN CA2178022-A.
XX
PD 02-DEC-1996.
XX
PF 03-JUN-1996; 96CA-02178022.
XX
PR 01-JUN-1995; 95US-00457273.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Hayden M, Lin B, Nasir J;
XX
DR WPI; 1997-298677/28.
XX
PT Mouse Huntington's Disease gene - useful for generating transgenic mice
PT as a model of Huntington's Disease.
XX
PS Disclosure; Page 60; 69pp; English.
XX
CC This oligonucleotide comprises the 5' acceptor site of intron 1 of the
CC mouse Huntington's disease (HD) gene (see also AAT78974). The splice site
CC sequences for the first 5 exons of the mouse and human HD genes were
CC compared (see AAT78985-T79002). Targeted disruption of the murine HD
CC gene, e.g. at exon 5, can be used to examine the function of the HD gene
CC and its role in development. Transgenic mice can be used as models of HD
XX
SQ Sequence 22 BP; 1 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2157 TTTTTCTCCTTTTTTTTTT 2176
              |||| ||||| ||||||| |
Db          1 TTTTCCTCCTGTTTTTTGT 20
```

RESULT 3066
AAV81783/c
ID AAV81783 standard; DNA; 22 BP.
XX
AC AAV81783;
XX
DT 10-MAR-1999 (first entry)
XX
DE Rat ALK-7 PCR primer 4077.
XX
KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; PCR primer; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN WO9849317-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US008439.
XX
PR 28-APR-1997; 97US-0044428P.
PR 20-MAY-1997; 97US-0047222P.
PR 11-JUN-1997; 97US-0049477P.
PR 11-JUN-1997; 97US-0049756P.
PR 18-JUN-1997; 97US-0049914P.
PR 23-OCT-1997; 97US-0063595P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
PI Courtneidge SA, App H, Hui TH;
XX
DR WPI; 1999-009434/01.
XX
PT New nucleic acid encoding specific protein tyrosine phosphatases - useful
PT for identifying specific modulators for treatment and prevention of
PT cancer and neurodegenerative disease.
XX
PS Example 23; Page 132; 193pp; English.
XX
CC The present invention describes isolated, enriched or purified nucleic
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC above proteins, other than ALK-7, are protein tyrosine phosphatases
CC (PTPs) and are used to identify substances that modulate their activity
CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These
CC substances are used to treat or prevent diseases associated with abnormal
CC signal transduction pathways that involve the proteins, particularly
CC cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is
CC a type I receptor serine/threonine kinase) are used to promote neuronal
CC survival, particularly for treating Alzheimer's, Parkinson's or
CC Huntington's diseases. Nucleic acid fragments of the polynucleotides
CC encoding the proteins can be used as probes to identify and clone related
CC sequences; to detect protein-encoded RNA; to generate transgenic animals
CC and in gene therapy (optionally after mutation). Ab are used to determine
CC the proteins. The present sequence represents a PCR primer for rat ALK-7
XX
SQ Sequence 22 BP; 4 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        885 ACAAAGTGACAGTGGCTGAA 904
              ||| |||||| ||||||| |
Db         21 ACATAGTGACCGTGGCTGGA 2
```

RESULT 3067
AAC61618
ID AAC61618 standard; DNA; 22 BP.
XX
AC AAC61618;
XX
DT 19-FEB-2001 (first entry)
XX
DE Probe specific for mannose binding protein (MBP) gene allele C.
XX
KW Human; mannose binding protein; MBP; immune system;
KW bioelectronic microchip; single nucleotide polymorphism; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200058522-A1.
XX
PD 05-OCT-2000.

XX
PF 28-MAR-2000; 2000WO-US008617.
XX
PR 30-MAR-1999; 99US-0126865P.
XX
PA (NANO-) NANOGEN INC.
XX
PI Giles PN, Dillon PJ, Wu DJ, Foster CB, Chanock SJ;
XX
DR WPI; 2000-638354/61.
XX
PT Detecting single nucleotide polymorphism by utilizing a bioelectronic
PT microchip having several test sites.
XX
PS Example 1; Page 11; 46pp; English.
XX
CC Reporter probes AAC61609-20 were used to discriminate against different
CC alleles of the human mannose binding protein (MBP) gene. MBP is a
CC component of the innate immune system and is capable of opsonizing
CC pathogenic microorganisms. Inheritance of variant forms of MBP gives rise
CC to a subtle immunologic defect that can be enhanced during a period of
CC immunosuppression. Four distinct alleles of the MBP gene have been
CC identified. The method of the invention is used for detecting single
CC nucleotide polymorphisms (SNPs) in MBP. The method utilises electronic
CC circuitry on silicon microchips. The method provides accurate
CC discrimination of amplified DNA samples following electronic transport,
CC concentration, and attachment of DNA to selected electrodes (test sites).
CC The test sites make up organised arrays of samples that are distinguished
CC by using internal controls of dual labelled reporters comprising wild
CC type and mismatched sequences to validate the SNP genotype. Multiples of
CC SNPs in target nucleic acids from a patient sample source or a SNP in
CC target nucleic acids of multiple patient sample sources can also be
CC detected using the electronically addressable microchip
XX
SQ Sequence 22 BP; 10 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1198 GATGGCAGCTAGGAAGAACA 1217
|||||| | |||||||| |
Db 2 GATGGCACCAAGGAAGAAAA 21

RESULT 3068
AAD14545/c
ID AAD14545 standard; DNA; 22 BP.
XX
AC AAD14545;
XX
DT 01-NOV-2001 (first entry)
XX
DE Arabidopsis thaliana ABF4 amplifying 5' PCR primer.
XX
KW Abscisic acid responsive element; ABRE; ABRE-binding factor; ABF;
KW stress treatment; transgenic plant; environmental stress; PCR primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN US6232461-B1.
XX
PD 15-MAY-2001.
XX
PF 19-SEP-2000; 2000US-00665309.
XX
PR 12-OCT-1999; 99US-00416050.
XX
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI Kim SY;
XX
DR WPI; 2001-366358/38.
XX
PT New nucleic acid encoding abscisic acid responsive element binding factor
PT 4, useful for generating transgenic plants, which are tolerant to
PT multiple environmental stresses.
XX
PS Disclosure; Col 5; 42pp; English.
XX
CC The invention relates to nucleic acid encoding the Abscisic acid
CC responsive element (ABRE)-binding factor 4 (ABF4). ABF4 belongs to the
CC ABF family of factors which bind abscisic acid responsive elements in
CC plants. Expression of ABFs is inducible by abscisic acid and various
CC stress treatments. ABFs have the potential to activate a large number of
CC abscisic acid/stress responsive genes and thus a nucleic acid molecule
CC encoding ABF4 is useful for generating transgenic plants that are
CC tolerant to multiple environmental stresses. The present sequence is a 5'
CC PCR primer which is used to isolate full length Arabidopsis thaliana ABF4
CC from clone 19
XX
SQ Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2084 CTCTAAACCCCGTGTTCAAA 2103
| ||||| ||| ||||||||
Db 21 CCCTAAAACCCTTGTTCAAA 2

RESULT 3069
AAS03330/c
ID AAS03330 standard; cDNA; 22 BP.
XX
AC AAS03330;
XX
DT 29-AUG-2001 (first entry)
XX
DE ABRE binding factor 4, 5' PCR primer.
XX
KW Abscisic acid response element; ABRE; ABRE binding factor; ABF4;
KW basic leucine zipper; bZIP; transgenic plant; stress responsive gene;
KW environmental stress response; ss; PCR primer.
XX
OS Arabidopsis thaliana.
XX
PN US6218527-B1.
XX
PD 17-APR-2001.
XX
PF 19-SEP-2000; 2000US-00664800.
XX
PR 12-OCT-1999; 99US-00416050.
XX
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI Kim SY;
XX
DR WPI; 2001-281059/29.
XX
PT Isolated nucleic acid molecule for generating environmental-stress
PT tolerant transgenic plants, encodes abscisic acid responsive element-
PT binding factor 3.
XX
PS Disclosure; Col 5; 43pp; English.
XX
CC The sequence represents a 5' PCR primer used to isolate a cDNA encoding
CC abscisic acid response element (ABRE) binding factor 4, ABF4, a novel
CC bZIP (basic leucine zipper) class transcription factor. The nucleic acid
CC encoding an ABF can be used to generate transgenic plants that are
CC tolerant to multiple environmental stresses e.g. drought, high salt, and
CC cold/freezing. Expression of the binding factor is inducible by abscisic
CC acid and various stress treatments, and can transactivate an abscisic
CC acid responsive element (ABRE)-containing a reporter gene in yeast. The

```
CC   binding factor can activate a number of abscisic acid/stress responsive
CC   genes
XX
SQ   Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
              | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 3070
AAS01584
ID   AAS01584 standard; DNA; 22 BP.
XX
AC   AAS01584;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human fibrillin-1 (FBN1) CpG island 5'-bisulfite PCR primer.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 15q21; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 21; Page 34; 125pp; English.
XX
CC   The present sequence for 5'-bisulfite PCR primer is used to study the
CC   methylation state of human fibrillin-1 (FBN1) which maps to chromosome
CC   15q21.1. The methylation state of specific regions within CpG islands
CC   associated with a novel T-type calcium channel CACNA1G gene correlate
CC   with several cancerous phenotypes involving various tissue and cell
CC   types. Since aberrant methylation of normally unmethylated CpG islands is
CC   often observed in immortalised and transformed cells, CACNA1G is
CC   implicated in cellular proliferative disorders e.g. leukaemia,
CC   colorectal, lung, breast and other cancers. The nucleic acid coding for
CC   CACNA1G is useful as a marker for screening cancer and age related
CC   diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC   amplification of a CpG-containing nucleic acid, where the primer
CC   hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC   be used for detecting aberrant methylation. The CpG island sequences
CC   (AAS01677-AAS01692) are selected from genes encoding CACNA1G,
CC   apolipoprotein B (APOB), caudal type homeobox transcription factor 2
CC   (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G
CC   protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
CC   HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
CC   activated receptor 2 (PAR2), paired-like homeodomain transcription factor
CC   2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
CC   SDC4) or a MINT31 sequence
XX
SQ   Sequence 22 BP; 3 A; 0 C; 3 G; 15 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   77.3%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
              ||||||| || : |||| ||||
Db          1 TTTTTTTATTGYGTTAATTTTG 22


RESULT 3071
AAS01637/c
ID   AAS01637 standard; DNA; 22 BP.
XX
AC   AAS01637;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human fibrillin-1 (FBN1) 5'-target sequence for bisulfite PCR.
XX
KW   Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW   cellular proliferative disorder; colorectal cancer; age related disease;
KW   apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW   CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW   G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW   HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW   PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW   patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW   chromosome 15q21; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119845-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025479.
XX
PR   15-SEP-1999;   99US-00398522.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J;
XX
DR   WPI; 2001-244777/25.
XX
PT   New nucleic acid molecule for use as a marker for screening cancer,
PT   comprises the coding region for a T-type calcium channel and regulatory
PT   sequences associated with the channel.
XX
PS   Claim 20; Page 37; 125pp; English.
XX
CC   The present sequence for human fibrillin-1 (FBN1) 5'-target sequence
CC   (complementary to the 5'-bisulfite PCR primer) is used to study the
CC   methylation state of FBN1 which maps to chromosome 15q21.1. The
CC   methylation state of specific regions within CpG islands associated with
CC   a novel T-type calcium channel CACNA1G gene correlate with several
CC   cancerous phenotypes involving various tissue and cell types. Since
CC   aberrant methylation of normally unmethylated CpG islands is often
CC   observed in immortalised and transformed cells, CACNA1G is implicated in
CC   cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast
CC   and other cancers. The nucleic acid coding for CACNA1G is useful as a
CC   marker for screening cancer and age related diseases. A diagnostic kit
CC   containing primers (AAS01574-AAS01623) for amplification of a CpG-
CC   containing nucleic acid, where the primer hybridises with a target
CC   polynucleotide sequence (AAS01627-AAS01676), can be used for detecting
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```
CC   aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are
CC   selected from genes encoding CACNA1G, apolipoprotein B (APOB), caudal
CC   type homeobox transcription factor 2 (CDX2), epidermal growth factor
CC   receptor (EGFR), FBN1, G protein-coupled receptor 37 (GPR37), heat shock
CC   70kD protein 6 (HSP70B'; HSPA6), RasGAP-related protein (IQGAP2), klotho
CC   (KL), proteinase-activated receptor 2 (PAR2), paired-like homeodomain
CC   transcription factor 2 (PITX2), patched A and B (PTCHA; PTCHB) and
CC   syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence
XX
SQ   Sequence 22 BP; 15 A; 3 C; 0 G; 3 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   77.3%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
             ||||||| || : |||| ||||
Db         22 TTTTTTTATTGYGTTAATTTTG 1


RESULT 3072
AAS07849/c
ID   AAS07849 standard; DNA; 22 BP.
XX
AC   AAS07849;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Abscisic acid responsive element binding factor 4 (ABF4) PCR primer #1.
XX
KW   Abscisic acid responsive element binding factor; ABF; bZIP; ss; G/ABRE;
KW   G-box-like ABRE; coupling element-like ABRE; C/ABRE; transgenic plant;
KW   stress responsive gene; environmental stress; cress; PCR primer.
XX
OS   Arabidopsis sp.
XX
PN   EP1097999-A2.
XX
PD   09-MAY-2001.
XX
PF   29-JUN-2000; 2000EP-00305459.
XX
PR   04-NOV-1999;   99KR-00048477.
XX
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-337113/36.
XX
PT   Nucleic acid encoding novel transcription factors that bind to various
PT   abscisic acid responsive elements, for generating stress tolerant
PT   transgenic plants.
XX
PS   Disclosure; Page 5; 37pp; English.
XX
CC   The sequence represents a PCR primer used to isolate DNA encoding an
CC   abscisic acid responsive element binding factor (ABF) protein. ABFs are
CC   bZIP class transcription factors that can bind to two classes of abscisic
CC   acid responsive elements (ABRE), namely G-box-like ABREs (G/ABRE) and
CC   coupling element-like ABREs (C/ABRE). Expression of ABF is inducible by
CC   abscisic acid and various stress treatments and they can transactivate an
CC   ABRE-containing reporter gene in yeast. Therefore, the ABFs are useful
CC   for activating a large number of abscisic acid or stress responsive genes
CC   and for generating transgenic plants that are tolerant to multiple
CC   environmental stresses
XX
SQ   Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
             | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 3073
AAD08919/c
ID   AAD08919 standard; DNA; 22 BP.
XX
AC   AAD08919;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Arabidopsis thaliana ABF4 amplifying 5' PCR primer.
XX
KW   Abscisic acid responsive element binding factor; ABF; ABRE;
KW   bZIP class transcription factor; transgenic plant; PCR primer; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6245905-B1.
XX
PD   12-JUN-2001.
XX
PF   14-SEP-2000; 2000US-00661569.
XX
PR   12-OCT-1999;   99US-00416050.
XX
PA   (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI   Kim SY;
XX
DR   WPI; 2001-380516/40.
XX
PT   New abscisic acid responsive element binding factor 2 useful for
PT   activating abscisic acid/stress responsive genes, and generating
PT   transgenic plants that are tolerant to multiple environmental stresses.
XX
PS   Disclosure; Col 5; 42pp; English.
XX
CC   The patent discloses novel abscisic acid (ABA) responsive element (ABRE)
CC   binding factors (ABFs). ABFs are basic leucine zipper (bZIP) class
CC   transcription factors that bind to both G-box-like ABREs (G/ABREs) and
CC   coupling element like ABREs (C/ABREs). ABFs have the potential to
CC   activate a large number of abscisic acid/stress responsive genes, and are
CC   therefore used to generate transgenic plants that are tolerant to
CC   multiple environmental stresses. The present sequence is a 5' PCR primer
CC   which is used to isolate full length Arabidopsis thaliana ABF4 from clone
CC   19
XX
SQ   Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2084 CTCTAAACCCCGTGTTCAAA 2103
             | ||||| ||| ||||||||
Db         21 CCCTAAAACCCTTGTTCAAA 2


RESULT 3074
AAS00383/c
ID   AAS00383 standard; cDNA; 22 BP.
XX
AC   AAS00383;
XX
DT   25-MAY-2001  (first entry)
XX
DE   5' PCR primer #2 used to isolate full length ABF3 and ABF4.
XX
KW   Abscisic acid responsive element binding factor 1; ABF1; plant hormone;
KW   drought; ABA-responsive element; ABRE; ABRE-binding factor; ABF;
```

KW basic leucine zipper; bZIP; G/ABRE; C/ABRE; transgenic plant;
KW environmental stress; ss; PCR primer.
XX
OS Arabidopsis thaliana.
XX
PN US6194559-B1.
XX
PD 27-FEB-2001.
XX
PF 12-OCT-1999; 99US-00416050.
XX
PR 12-OCT-1999; 99US-00416050.
XX
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI Kim SY;
XX
DR WPI; 2001-217937/22.
XX
PT New nucleic acid molecule encoding Abscisic acid responsive element
PT binding factor 1 (ABF1) which can be used to generate transgenic plants
PT that are tolerant to multiple environmental stresses.
XX
PS Disclosure; Col 6; 42pp; English.
XX
CC The sequence represents 5' PCR primer #2 used to isolate full length
CC abscisic acid responsive element binding factors, ABF3 and ABF4, from an
CC Arabidopsis cDNA library. Abscisic acid (ABA) is a major plant hormone
CC involved in response to adverse environmental conditions such as drought,
CC high salt and cold/freezing. This response involves induced expression of
CC various genes. ABA-responsive elements (ABREs) are cis-regulatory
CC elements that mediate the ABA-modulated gene and interact with a novel
CC class of ABRE-binding factors (ABFs). ABFs are basic leucine zipper
CC (bZIP) class transcription factors that bind to both G/ABREs and C/ABREs.
CC ABFs have the potential to activate a large number of ABA/stress
CC responsive genes and can be used to generate transgenic plants that are
CC tolerant to multiple environmental stresses
XX
SQ Sequence 22 BP; 6 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2084 CTCTAAACCCCGTGTTCAAA 2103
|| ||||| ||| ||||||||
Db 21 CCCTAAAACCCTTGTTCAAA 2

RESULT 3075
ABL44301
ID ABL44301 standard; DNA; 22 BP.
XX
AC ABL44301;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1345.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 4; Page 31; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 22 BP; 7 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2119 TTTAGGAAACTTGTAGAAAC 2138
|| ||||||||| ||| |||
Db 1 TTGAGGAAACTTCTAGGAAC 20

RESULT 3076
ABX97353
ID ABX97353 standard; DNA; 22 BP.
XX
AC ABX97353;
XX
DT 20-MAY-2003 (first entry)
XX
DE Human NOV-associated reverse primer from primer-probe set Ag791.
XX
KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200272757-A2.
XX
PD 19-SEP-2002.
XX
PF 08-MAR-2002; 2002WO-US006908.
XX
PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.

PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
PI Lepley DM, Rieger DK;
XX
DR WPI; 2002-723332/78.
XX
PT NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
PS Example C; Page 723; 1103pp; English.
XX
CC This invention describes novel human NOVX polypeptides which have
CC cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX13460-ABX13462 and ABX97186-ABX97593 represent PCR primers
CC and probes used in the amplification and isolation of the NOVX
CC polynucleotides represented in ABX97008-ABX97185 which encode the
CC polypeptides represented in ABU65041-ABU65218
XX
SQ Sequence 22 BP; 6 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1413 TCAAAGAAGCCCTGATTGTC 1432
||||||| |||| |||||
Db 3 TCAAAGAAACCCTTGTTGTC 22

RESULT 3077
ACF42669/c
ID ACF42669 standard; DNA; 22 BP.
XX
AC ACF42669;
XX
DT 29-SEP-2003 (first entry)
XX
DE Human ALMS1 PCR primer Ex7mR.
XX
KW Human; ALMS1; chromosome 2; 2p13; Alstrom disease; retinal dystrophy;
KW cardiomyopathy; endocrinopathy; diabetes; Alstrom syndrome; cardiant;
KW ophthalmological; antidiabetic; hepatotropic; nephrotropic; gene therapy;
KW PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003034072-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-GB004658.
XX
PR 15-OCT-2001; 2001GB-00024621.
PR 22-OCT-2001; 2001GB-00025318.
PR 07-JAN-2002; 2002GB-00000248.
PR 08-FEB-2002; 2002GB-00003039.
PR 08-FEB-2002; 2002GB-00003040.
XX
PA (UYSO-) UNIV SOUTHAMPTON.
XX
PI Wilson DI, Hearn T, Walker M;
XX
DR WPI; 2003-393556/37.
XX
PT Diagnosing the presence of, or susceptibility to, retinal dystrophy,
PT cardiomyopathy, endocrinopathy, diabetes, or Alstrom syndrome in an
PT individual, comprises detection or modulation of the ALMS1 protein or
PT gene region.
XX
PS Disclosure; Page 39; 121pp; English.
XX
CC The present invention describes a method of diagnosing the presence of,
CC or susceptibility to, retinal dystrophy, cardiomyopathy, endocrinopathy,
CC diabetes, or Alstrom syndrome in an individual. The method comprises
CC typing in a sample from the individual the ALMS1 protein or ALMS1 gene
CC region of the individual, or detecting aberrant ALMS1 activity. Human
CC ALMS1 is located to chromosome 2, more specifically to 2p13. ALMS1 has
CC ophthalmological, cardiant, antidiabetic, hepatotropic and nephrotropic
CC activities, and can be used in gene therapy. The method is useful for

```
CC   diagnosing the presence of, or susceptibility to, retinal dystrophy,
CC   cardiomyopathy, endocrinopathy (e.g. liver disease or renal impairment),
CC   diabetes, or Alstrom syndrome in an individual. ALMS1 sequences can be
CC   used in an agent that prevents or treats retinal dystrophy,
CC   cardiomyopathy, endocrinopathy or diabetes is useful in manufacturing a
CC   medicament for treating a patient who has been diagnosed as having or
CC   being susceptible to retinal dystrophy, cardiomyopathy, endocrinopathy or
CC   diabetes. ACF42632 to ACF42747 and ABR82113 to ABR82118 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 22 BP; 2 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        734 CAGACAGTCATTCGCAAAGG 753
              ||||||| ||||| || |||
Db         21 CAGACAGCCATTCACAGAGG 2


RESULT 3078
ABZ58799/c
ID   ABZ58799 standard; DNA; 22 BP.
XX
AC   ABZ58799;
XX
DT   14-APR-2003  (first entry)
XX
DE   Cinnamycin cinA gene fragment amplifying primer FTP28.
XX
KW   Cinnamycin; bacterium; cinA; cinM; cinX; cinT; cinH; cinY; antibiotic;
KW   food additive; antibacterial; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200288367-A1.
XX
PD   07-NOV-2002.
XX
PF   29-APR-2002; 2002WO-GB001983.
XX
PR   27-APR-2001; 2001GB-00010432.
XX
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PA   (WIDD/) WIDDICK D A.
XX
PI   Bibb MJ;
XX
DR   WPI; 2003-111893/10.
XX
PT   New expression cassettes or genes isolated from Streptomyces cinnamoneus,
PT   useful for producing a library of lantibiotic-producing host cells or
PT   lantibiotics, which are useful as food additives and antibacterial
PT   agents.
XX
PS   Example 3; Page 60; 111pp; English.
XX
CC   The invention relates to expression cassettes or sets of nucleic acids
CC   comprising various open reading frames selected from (a) a cinA open
CC   reading frame (orf), a cinM orf, and optionally a cinX orf; or (b) a cinA
CC   orf, a cinM orf, a cinT orf, a cinH orf, a cinY orf, and optionally a
CC   cinX orf. The expression cassettes, set of nucleic acids, (set of)
CC   vectors, or methods are useful for producing a library of lantibiotic-
CC   producing host cells or a library of lantibiotics. These are particularly
CC   useful for producing lantibiotic cinnamycin or its modified versions. The
CC   lantibiotics are useful as antibiotics having efficacy and utility as
CC   food additives and antibacterial agents against Propionibacterium acnes
CC   and problematic pathogens, e.g. methicillin-resistant Staphylococcus
CC   aureus (which has or is developing resistance to many commonly used
CC   antibiotics), or Streptococcus pneumoniae. Sequences ABZ58796-799
CC   represent PCR primers used in the construction of a cinA deletion
XX
SQ   Sequence 22 BP; 5 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 22;
  Best Local Similarity   85.0%;  Pred. No. 3.3e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        591 CCTACCGCCGCTCCGACCTG 610
              |||||| ||||| | |||||
Db         22 CCTACCACCGCTTCTACCTG 3


RESULT 3079
ABT33591
ID   ABT33591 standard; DNA; 22 BP.
XX
AC   ABT33591;
XX
DT   22-MAY-2003  (first entry)
XX
DE   NOV reverse PCR primer SEQ ID No 507.
XX
KW   Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
KW   vulnerary; virucide; antibacterial; protozoacide; fungicide; nootropic;
KW   antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
KW   anticonvulsant; antiaddictive; analgesic; dermatological; keratolytic;
KW   antiseborrheic; antirheumatic; antiarthritic; antiinflammatory; anti-HIV;
KW   cytostatic; antiasthmatic; antipsoriatic; hypotensive; osteopathic;
KW   antiulcer; anorectic; antidiabetic; antiallergic; haemostatic;
KW   neuroleptic; antidepressant; antiinfertility; NOVX; human disease;
KW   NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
KW   parasitic infection; Alzheimer's disease; stroke; forensic biology;
KW   immunogen; non-human transgenic animal; gene therapy; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200281517-A2.
XX
PD   17-OCT-2002.
XX
PF   22-JAN-2002; 2002WO-US002064.
XX
PR   19-JAN-2001; 2001US-0262892P.
PR   23-JAN-2001; 2001US-0263598P.
PR   24-JAN-2001; 2001US-0263799P.
PR   25-JAN-2001; 2001US-0264117P.
PR   25-JAN-2001; 2001US-0264139P.
PR   26-JAN-2001; 2001US-0264478P.
PR   30-JAN-2001; 2001US-0263351P.
PR   02-MAR-2001; 2001US-0272870P.
PR   14-MAR-2001; 2001US-0275927P.
PR   14-MAR-2001; 2001US-0275990P.
PR   15-MAR-2001; 2001US-0276449P.
PR   20-MAR-2001; 2001US-0277358P.
PR   23-MAR-2001; 2001US-0278151P.
PR   29-MAR-2001; 2001US-0279857P.
PR   20-APR-2001; 2001US-0285140P.
PR   20-APR-2001; 2001US-0285141P.
PR   30-APR-2001; 2001US-0287484P.
PR   17-MAY-2001; 2001US-0291701P.
PR   08-JUN-2001; 2001US-0296960P.
PR   10-JUL-2001; 2001US-0304353P.
PR   10-JUL-2001; 2001US-0304355P.
PR   12-JUL-2001; 2001US-0304886P.
PR   09-AUG-2001; 2001US-0311289P.
PR   13-AUG-2001; 2001US-0311975P.
PR   16-AUG-2001; 2001US-0312937P.
PR   18-OCT-2001; 2001US-0330227P.
PR   29-NOV-2001; 2001US-0334198P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Decristofaro MF,  Padigaru M,  Miller C,  Tchernev V,  Zhong H;
PI   Zhong M,  Anderson D,  Ballinger R,  Gerlach V,  Spytek KA,  Rastelli L;
```

PI Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M;
PI Burgess CE, Eisen A, Wolenc A, Baumgartner J, Shimkets RA, Gusev V;
PI Vernet CAM, Taupier RJ, Pena C, Shenoy S, Li L, Casman S, Boldog F;
PI Fernandes E, Smithson G, Malyankar U, Taillon B, Liu X;
XX
DR WPI; 2003-058504/05.
XX
PT New polypeptides, designated as NOVX, useful for diagnosing and treating
PT infections, neurological diseases, cancer, allergy, and bone,
PT immunological, skin, renal, brain, muscle and autoimmune disorders.
XX
PS Example 3; Page 659; 672pp; English.
XX
CC The invention relates to a novel isolated polypeptide, designated NOVX
CC (NOV1 - 33), consisting of a mature form of one of 61 sequences, given in
CC the specification, or its variant, where amino acid residue(s) in the
CC variant differ from the mature form, provided that the variant differs in
CC not more than 15 % of the amino acids from the sequence of the mature
CC form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and
CC an antibody to the polypeptides, are useful for treating or preventing a
CC NOVX-associated disorder in humans and for treating a syndrome associated
CC with a human disease (NOVX-associated disorder). NOVX polypeptides and
CC the encoding nucleic acids, are useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX
CC polypeptide and polynucleotide, by measuring the level of polypeptide
CC expression or the amount of nucleic acid from a mammal and comparing it
CC with another mammal not having or not predisposed to the disease. NOVX
CC polypeptide is also useful for identifying an agent that binds to NOVX
CC and a cell expressing NOVX is useful for identifying an agent that
CC modulates the expression or activity of NOVX. The antibodies and a
CC polypeptide having 95 % sequence identity to NOVX polypeptide are useful
CC for treating a pathological state in a mammal. The antibodies are also
CC useful for determining the presence or amount of NOVX in a sample. NOVX
CC polypeptides, polynucleotides and antibodies specific for the
CC polypeptides are useful for treating or preventing disorders or syndromes
CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
CC infections. They can also treat disorders such as e.g., Alzheimer's
CC disease or a stroke. The NOVX encoding nucleic acids are useful for
CC expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in
CC a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful
CC for identifying a cell or tissue type in a biological sample, to amplify
CC DNA sequences from very small biological samples such as tissues e.g.
CC hair or skin or body fluids in forensic biology and as primers and probes
CC for use in identifying and/or cloning NOVX homologues in other cell
CC types. The NOVX proteins are useful as an immunogen to generate
CC antibodies which are useful for diagnostically monitoring protein levels
CC and modulating NOVX activity. Cells comprising NOVX nucleic acids are
CC useful for producing non-human transgenic animals which are useful for
CC studying the function and/or activity of NOVX protein and for identifying
CC and/or evaluating modulators of NOVX protein activity. The NOVX nucleic
CC acids can be used in gene therapy. This polynucleotide sequence
CC represents a NOVX PCR primer of the invention
XX
SQ Sequence 22 BP; 3 A; 2 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1606 GGCCTGGGGGAAGAGTTTGT 1625
              |||||| ||| ||||||||
Db          2 GGCCTGATGGAGGAGTTTGT 21
```

RESULT 3080
AAQ10627
ID AAQ10627 standard; DNA; 23 BP.
XX
AC AAQ10627;
XX
DT 25-MAR-2003 (revised)
DT 29-APR-1991 (first entry)
XX
DE HLA Class I locus-specific primer SGD010.BIVS3.R2NP.
XX
KW Human leukocyte antigen; major histocompatibility complex; MHC;
KW restriction fragment length polymorphic analysis; RFLP; tissue typing;
KW allele; PCR; ss.
XX
OS Synthetic.
XX
PN EP414469-A.
XX
PD 27-FEB-1991.
XX
PF 20-AUG-1990; 90EP-00309107.
XX
PR 25-AUG-1989; 89US-00398217.
PR 11-SEP-1989; 89US-00405499.
PR 16-JAN-1990; 90US-00465863.
PR 11-JUL-1990; 90US-00551239.
XX
PA (GENE-) GENETYPE AG.
PA (JEAN-) GENETYPE AG.
PA (SIMO/) SIMONS M J.
XX
PI Simons MJ;
XX
DR WPI; 1991-059664/09.
XX
PT Detection of adjacent and non:adjacent locus, e.g. HLA alleles - by
PT amplifying genomic DNA, for direct determination of haplotype.
XX
PS Claim 29; Page 49; 53pp; English.
XX
CC The primer is specific for nt 1582-1604 of HLA Class I B17 locus. It is
CC used in a method for the prodn. of RFLP fragments for an HLA locus,
CC together with a second primer making up a locus-specific primer (LSP)
CC pair. It is pref. used with a Class I-specific primer which hybridises
CC with at least two different Class I loci, pref. at least one of each of
CC A, B, and C, and most pref. all of these. The Class I primer esp.
CC hybridises with intervening sequence (IVS) III or IVS I sequences. Direct
CC determination of the haplotye is possible, providing useful information
CC for identity of individuals for e.g. paternity case and forensic
CC investigations. See also AAQ10621-Q10669. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 23 BP; 6 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1275 GGACACCCCATGGGACCAGC 1294
              |||| |||||| |||||||
Db          4 GGACCACCCATGTGACCAGC 23
```

RESULT 3081
AAV27967/c
ID AAV27967 standard; DNA; 23 BP.
XX
AC AAV27967;
XX
DT 25-SEP-1998 (first entry)
XX
DE Ataxia telangiectasia exon 5 primer 2.
XX
KW ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
KW radiation; breast cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9822621-A1.
XX

```
PD   28-MAY-1998.
XX
PF   17-NOV-1997;   97WO-US020953.
XX
PR   20-NOV-1996;   96US-00753147.
XX
PA   (VIRG-) VIRGINIA MASON RES CENT.
XX
PI   Concannon P;
XX
DR   WPI; 1998-312503/27.
XX
PT   Method of detecting ataxia telangiectasia - comprises use of primers
PT   based on intron-exon boundaries, useful for diagnosing disease in
PT   heterozygotes.
XX
PS   Claim 6; Page 5; 47pp; English.
XX
CC   The primers AAV27964-V28086 are used to amplify ataxia telangiectasia
CC   (ATM) exons and their adjacent splice junction sites. These can be used
CC   as a method of detecting a mutation in the ATM gene by comparing the PCR
CC   products of amplification from a sample from a patient suspected of
CC   having an ATM mutation with a sample from a non-mutated ATM patient This
CC   method is especially useful for diagnosing ataxia telangiectasia in
CC   heterozygotes and can be used to locate the positions of the mutation.
CC   The diagnosis of ataxia telangiectasia in patients needing therapeutic
CC   radiation will prevent fatal radiation burns and the development of
CC   breast cancer which can occur
XX
SQ   Sequence 23 BP; 14 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2260 TTGCATATTTATTTCAGATG 2279
              || |||||||||||| | ||
Db         20 TTTCATATTTATTTCTGTTG 1


RESULT 3082
AAA39504/c
ID   AAA39504 standard; DNA; 23 BP.
XX
AC   AAA39504;
XX
DT   24-AUG-2000  (first entry)
XX
DE   Human Factor V starter oligonucleotide primer #3.
XX
KW   Factor V; primer; detection; APC; activated protein C; thrombosis; ss.
XX
OS   Homo sapiens.
XX
PN   DE19848665-A1.
XX
PD   27-APR-2000.
XX
PF   22-OCT-1998;   98DE-01048665.
XX
PR   22-OCT-1998;   98DE-01048665.
XX
PA   (FARB ) BAYER AG.
XX
PI   Springer W;
XX
DR   WPI; 2000-304738/27.
XX
PT   New primers and probes from the factor V gene, useful for detecting the
PT   mutation that causes activated protein C resistance.
XX
PS   Claim 3; Page 11; 14pp; German.
XX
CC   This invention describes novel primers (I) derived from the factor V
CC   gene. (I) are used for detecting APC (activated protein C) resistance,
CC   i.e. a condition, associated with increased incidence of venous (and
CC   possibly arterial) thrombosis, and caused by a mutation in the factor V
CC   gene (G to A change at position 1691, resulting in replacement of Gln by
CC   Arg). The new method does not require restriction enzyme digestion of the
CC   amplicons nor electrophoretic separation (rather the results are read out
CC   automatically by direct measurements of the amounts of amplicons in
CC   chemiluminescent or colorimetric tests). The sensitivity of the assay is
CC   increased 10-100 times by using RNA detection probe and nucleic acid
CC   antibody, so that only small amounts of test material are required and
CC   more than 100 samples may be processed in 20 min. The primers contain 2-
CC   5, preferably 2, additional mismatches at the 3'-end to improve
CC   differentiation between wild-type and mutant sequences. AAA39502-A39508
CC   represent primers used in the method of the invention
XX
SQ   Sequence 23 BP; 10 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2256 TTATTTGCATATTTATTTCA 2275
              | ||||||| | ||||||||
Db         23 TCATTTGCAAAGTTATTTCA 4


RESULT 3083
AAA28111
ID   AAA28111 standard; DNA; 23 BP.
XX
AC   AAA28111;
XX
DT   01-DEC-2000  (first entry)
XX
DE   Human androgen shutoff gene intron/exon 30 boundary sequence.
XX
KW   Androgen-induced tumour suppressor; androgen shutoff gene 3; AS3;
KW   chromosome 13q12-13q; cell proliferation inhibitor; prostate cancer;
KW   diagnosis; treatment; cytostatic; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    15. .16
FT                   /*tag=  a
FT                   /note= "Intron/exon 30 boundary"
XX
PN   WO200050454-A1.
XX
PD   31-AUG-2000.
XX
PF   24-FEB-2000; 2000WO-US004732.
XX
PR   24-FEB-1999;   99US-0121461P.
XX
PA   (TUFT ) TUFTS COLLEGE.
XX
PI   Soto AM,  Sonnenschein C,  Geck P,  Szelei J;
XX
DR   WPI; 2000-565451/52.
XX
PT   New human androgen-induced tumor suppressor cDNA sequence termed
PT   'Androgen Shutoff Gene 3' (AS3), useful as a marker for the efficient
PT   diagnosis and treatment of prostate cancer.
XX
PS   Disclosure; Fig 5; 152pp; English.
XX
CC   This invention relates to a human androgen-induced tumour suppressor cDNA
CC   sequence termed "Androgen Shutoff Gene 3" (AS3). The AS3 gene is located
CC   on chromosome 13 at position 13q12-13q. AS3 has a role in inhibiting cell
CC   proliferation and use as a marker for the efficient diagnosis and
CC   treatment of prostate cancer. The invention includes AS3 cDNA and protein
```

CC sequences, a vector comprising the cDNA sequence, a host cell transfected
CC with the expression vector, and a method for producing an AS3 polypeptide
CC comprising culturing the transfected cells. AS3 has cytostatic activity,
CC and acts to suppress cell proliferation. The AS3 gene is useful as a
CC marker for the efficient diagnosis and treatment of prostate cancer. The
CC AS3 nucleic acid molecule can be used as a source of antisense agents for
CC sequence specific modulation of gene expression. The AS3 protein may be
CC used in the treatment of disorders caused by aberrant modification or
CC mutation of a gene encoding an AS3 protein, misregulation of the AS3 gene
CC or aberrant post-translational modification of the AS3 protein. This
CC sequence represents the boundary between a human AS3 intron and exon
XX
SQ Sequence 23 BP; 7 A; 7 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1333 CTTGTCTCATTTCAGCCTGA 1352
| | ||||||||||||||| |
Db 1 CATTTCTCATTTCAGCCTAA 20

RESULT 3084
AAH56004
ID AAH56004 standard; DNA; 23 BP.
XX
AC AAH56004;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human SCN2A PCR-SSCP PCR primer SEQ ID NO:248.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA001404.
XX
PR 26-NOV-1999; 99US-0167623P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
PS Example 4; Fig 4; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 23 BP; 2 A; 4 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1111 GGACTTTGCCTATGTCTGTG 1130
|| |||||||||| ||| ||
Db 1 GGTCTTTGCCTATTTCTATG 20

RESULT 3085
AAF70491
ID AAF70491 standard; DNA; 23 BP.
XX
AC AAF70491;
XX
DT 20-APR-2001 (first entry)
XX
DE Human DRD2 fragment 5 PCR primer SEQ ID NO:234.
XX
KW Human; dopamine receptor D2; DRD2; polymorphism; allele specific;
KW drug target isogene; detection; single nucleotide polymorphism; SNP;
KW genotype; schizophrenia; Parkinson's disease; myoclonus dystonia; MD;
KW probe; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200105832-A1.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-US019644.
XX
PR 19-JUL-1999; 99US-0144493P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
XX
DR WPI; 2001-091967/10.
XX
PT Polynucleotides comprising single nucleotide polymorphisms in the human
PT dopamine receptor D2, useful for detecting mutations associated with,
PT e.g. schizophrenia, Parkinson's and myoclonus dystonia.
XX
PS Example 1B; Page 39; 135pp; English.
XX
CC The present invention describes polynucleotides comprising single
CC nucleotide polymorphisms (SNPs) in the human dopamine receptor D2 (DRD2).
CC The polynucleotides may be used in assays to detect and characterise
CC polymorphisms in DRD2 that affect its expression and activity and are
CC involved in disorders such as schizophrenia, Parkinson's and myoclonus
CC dystonia (MD). This information would be useful for studying the
CC biological function of DRD2 as well as in identifying drugs targeting
CC this protein for the treatment of disorders related to its abnormal
CC expression or function. Polymorphisms in the DRD2 gene affect the
CC expression of active and functional polypeptides. Therefore it is
CC advantageous to detect polymorphisms in the DRD2 gene and how those
CC polymorphisms are combined in different copies of the gene. AAF70261 to
CC AAF70308 represent human DRD2 allele specific oligonucleotide probes, and
CC AAF70309 to AAF70404 represent human DRD2 allele specific oligonucleotide
CC primers which are used in the detection of DRD2 polymorphisms. AAF70405
CC to AAF70452 represent oligonucleotide primers for the detection of human
CC DRD2 polymorphisms which are given in the exemplification of the present
CC invention. AAF70453 to AAF70538 represent PCR primers for the human DRD2
CC gene which are used in examples from the present invention
XX
SQ Sequence 23 BP; 9 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

```
  Query Match           0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1143 CTAGTAAACCAGTGGCAGAA 1162
              |||| |||  ||||||||||
Db          2 CTAGCAAAAGAGTGGCAGAA 21
```

RESULT 3086
ABK90968/c
ID ABK90968 standard; DNA; 23 BP.
XX
AC ABK90968;
XX
DT 05-NOV-2002 (first entry)
XX
DE PCR primer, 22164, used to amplify human VH3 gene.
XX
KW Human; PCR; primer; ss; antiHIV; chimeric protein; HIV-1;
KW human immunodeficiency virus-1; envelope glycoprotein; env; gp120; CD4;
KW cellular receptor; immunoglobulin; Ig; V1; V2; variable region;
KW variable region-like membrane distal domain; antibody; heavy chain; VH;
KW VH3; gene therapy; HIV infection; virus replication.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259258-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-IL000060.
XX
PR 22-JAN-2001; 2001IL-00141023.
XX
PA (GAVI-) GAVISH-GALILEE BIO APPL LTD.
XX
PI Gross G, Meyuhas R;
XX
DR WPI; 2002-608450/65.
XX
PT New nucleic acid molecule encoding chimeric proteins with binding
PT specificity for a site on HIV envelope glycoprotein gp120 and a site on
PT gp120 protein or on the extracellular portion of human CD4, for
PT preventing or treating HIV infection.
XX
PS Example 4; Page 29; 48pp; English.
XX
CC The invention discloses a nucleic acid molecule encoding a functional
CC chimeric protein with binding specificity for at least two different
CC sites. At least one site is on the human immunodeficiency virus-1 (HIV-1)
CC envelope glycoprotein (env), gp120, and the other site is either on the
CC gp120 protein or on the extracellular portion of human CD4, the major
CC cellular receptor for HIV. The chimeric protein essentially comprises a
CC first binding region of a soluble extracellular portion of human CD4,
CC consisting of the immunoglobulin (Ig) variable region-like membrane
CC distal domains (V1 and V2) and a second binding region of a variable
CC region of an antibody heavy chain (VH), encoded by the VH3 gene, which is
CC capable of being attached to an adjacent and non-overlapping site on the
CC gp120 protein, or to a site on the extracellular portion of human CD4,
CC and is capable of increasing the capacity of the extracellular portion of
CC human CD4 to interact with gp120 and to block the interaction of HIV with
CC membranal CD4. These two binding regions are physically connected by a
CC linker region. The chimeric protein of the invention is useful for gene
CC therapy and for preventing and treating an HIV infection and for
CC neutralising and inhibiting virus replication and infectivity in a
CC subject, preferably a mammal. The sequence presented is the PCR primer,
CC 22164, which was used to amplify the human VH3 gene, used in the
CC construction of the VH3-CD4 (V1 and V2) chimeric protein
XX
SQ Sequence 23 BP; 3 A; 3 C; 11 G; 6 T; 0 U; 0 Other;

```
  Query Match           0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1566 CAAAAATCCTTCTCCACCGC 1585
              ||||| ||| |||||| |||
Db         20 CAAAACTCCATCTCCAGCGC 1
```

RESULT 3087
ACC47485
ID ACC47485 standard; DNA; 23 BP.
XX
AC ACC47485;
XX
DT 27-JUN-2003 (first entry)
XX
DE PCR primer for detection of the C77G mutation in the CD45 gene #1.
XX
KW CD45; viral infection; immunodeficiency disease; IDD; C77G mutant;
KW human immunodeficiency virus; HIV; HIV-1; Epstein-Barr virus; EBV;
KW poliovirus; haemophagocytic lymphohistiocytosis;
KW peripheral blood mononuclear cells; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2002103049-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-GB002785.
XX
PR 14-JUN-2001; 2001GB-00014512.
PR 30-OCT-2001; 2001US-00020758.
XX
PA (JENN-) JENNER INST VACCINE RES EDWARD.
XX
PI Tchilian E, Beverley P;
XX
DR WPI; 2003-175244/17.
XX
PT Screening human subject for susceptibility or predisposition to viral
PT infection or developing immunodeficiency disease, by detecting
PT polymorphic variants or mutations in gene encoding CD45.
XX
PS Example 1; Page 18; 39pp; English.
XX
CC The invention relates to a method for screening a human subject for
CC susceptibility to viral infection, developing immunodeficiency disease
CC (IDD) and/or a predisposition to developing severe disease following
CC viral infection, or more severe forms of IDD. The method comprises
CC detecting polymorphic variants or mutations in the gene encoding CD45, or
CC evaluating an abnormal pattern of CD45 mRNA/protein expression associated
CC with the presence of the C77G mutant allele of the CD45 gene.
CC Specifically, the viral infection referred to is human immunodeficiency
CC virus (HIV), especially HIV-1, Epstein-Barr virus (EBV) or poliovirus.
CC The method of the invention is useful for screening a subject for
CC susceptibility to haemophagocytic lymphohistiocytosis. The method is also
CC useful for identifying human subjects exhibiting functional abnormalities
CC in peripheral blood mononuclear cells. Subjects having at least one
CC mutant allele are scored as having a higher frequency of peripheral blood
CC mononuclear cells able to produce interferon gamma (IFN-gamma). The
CC method of the invention is simple, non-invasive, reliable, reproducible
CC and amenable to automation. The current sequence represents aPCR primer
CC utilised in an example from the invention for the detection of the C77G
CC mutation in the CD45 gene
XX
SQ Sequence 23 BP; 8 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

```
  Query Match           0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       1407 ACTACATCAAAGAAGCCCTG 1426
              |||||| |||||| |||| |
Db          2 ACTACAGCAAAGATGCCCAG 21


RESULT 3088
ADC42610/c
ID   ADC42610 standard; DNA; 23 BP.
XX
AC   ADC42610;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human FANCD2 PCR primer hFANCD2_exon15b_R.
XX
KW   cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;
KW   chemosensitising; ss; PCR; primer.
XX
OS   Synthetic.
XX
PN   WO2003039327-A2.
XX
PD   15-MAY-2003.
XX
PF   06-JUN-2002; 2002WO-US018153.
XX
PR   02-NOV-2001; 2001US-00998027.
PR   02-NOV-2001; 2001WO-US045561.
XX
PA   (DAND ) DANA FARBER CANCER INST.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI   D'andrea AD,  Taniguchi T,  Timmers C,  Grompe M,  Fox EA;
XX
DR   WPI; 2003-441436/41.
XX
PT   Diagnosing or determining cancer or increased risk of cancer in a
PT   patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a
PT   cancer-associated defect, that indicates cancer or increased risk of
PT   cancer.
XX
PS   Example 14; Page 101; 160pp; English.
XX
CC   The invention relates to a novel method of diagnosing or determining if a
CC   patient has cancer or is at increased risk of cancer, involving testing a
CC   Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a
CC   cancer-associated defect, where the presence of one or more cancer-
CC   associated defects is indicative of cancer or an increased risk of cancer
CC   in the patient. The method of the invention has cytostatic activity. The
CC   method is useful for determining if a patient has cancer, or is at
CC   increased risk of developing cancer, e.g. breast, ovarian or prostate
CC   cancer. A microarray of the invention is useful for determining if a
CC   patient has cancer, or is at increased risk of developing cancer, by
CC   hybridising a nucleic acid sample to the nucleic acid sequences from the
CC   array, and detecting the presence of mutations in FA/BRCA pathway genes
CC   in the nucleic acid sample from the patient, where detecting the presence
CC   of mutations is indicative of a patient who has cancer, or is at
CC   increased risk of developing cancer. A method of the invention is useful
CC   for screening a chemosensitising agent, and the agent obtained is useful
CC   for treating a patient having a cancer. The present sequence is used in
CC   the exemplification of the invention.
XX
SQ   Sequence 23 BP; 5 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2535 ACAGGGTATTAAGAATTAAG 2554
              |||||||  |||||| ||||
Db         20 ACAGGGTGCTAAGAAATAAG 1


RESULT 3089
ADD28129
ID   ADD28129 standard; DNA; 23 BP.
XX
AC   ADD28129;
XX
DT   15-JAN-2004  (first entry)
XX
DE   HIV-1 LTR region DNA fragment PNAI.
XX
KW   conjugate; peptide nucleic acid; PNA; transport mediator;
KW   addressing protein; nuclear importation; penetratin family; tat gene;
KW   rev gene; anti-HIV; primer; ss.
XX
OS   Human immunodeficiency virus 1.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    16. .17
FT                   /*tag=  a
FT                   /note= "continous DNA sequence interrupted by an
FT                   undisclosed peptide linker"
FT   modified_base   21
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally pseudo-isocytosine or cytosine"
XX
PN   WO2003006065-A2.
XX
PD   23-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-DE002564.
XX
PR   12-JUL-2001; 2001DE-01033307.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
XX
PI   Braun K,  Waldeck W,  Pipkorn R,  Braun I,  Debus J;
XX
DR   WPI; 2003-256334/25.
XX
PT   New conjugate for delivery to the cell nucleus, useful for treating
PT   infection by human immune deficiency virus, comprises targeting peptides
PT   and peptide nucleic acid.
XX
PS   Disclosure; Page 8; 30pp; German.
XX
CC   This invention describes a novel conjugate for mediating specific
CC   transport to the cell nucleus of a peptide nucleic acid (PNA) that
CC   hybridizes to an HIV (human immune deficiency virus) gene, or part of it.
CC   The conjugate comprises a transport mediator for the cell membrane, an
CC   addressing protein or peptide for nuclear importation and the PNA being
CC   delivered. The transport mediator is a peptide or protein able to pass
CC   through the plasma membrane, particularly derived from the penetratin
CC   family protein. The PNA is designed to hybridize to at least part of the
CC   tat or rev genes and is especially targeted to the long terminal repeat
CC   or the polypurine tract, the central DNA flap, Nef, NCp7 or the gag slice
CC   site, at the RNA level. The conjugate has the structure transport
CC   mediator-addressing protein-PNA, particularly with a spacer (e.g.
CC   polylysine or a synthetic polymer) between addressing protein and PNA.
CC   The conjugate of the invention has anti-HIV activity. The transport
CC   mediator/addressing protein combination provide rapid and efficient
CC   transport of PNA to the nucleus and PNA is resistant to proteases and
CC   nucleases. The conjugate can be used in both early and late stages of
CC   infection. This sequence represents a fragment of HIV-1 LTR region used
CC   to construct PNA's used in the method of the invention.
XX
SQ   Sequence 23 BP; 0 A; 8 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 23;
  Best Local Similarity   85.0%;  Pred. No. 3.5e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2181
```

```
                  | |||||| |||||||| ||
Db          4 CCCCTTTTCTTTTTTTTCTT 23


RESULT 3090
AAS18179
ID   AAS18179 standard; DNA; 24 BP.
XX
AC   AAS18179;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human proliferating cell nuclear antigen (PCNA) 13 RT-PCR primer #2.
XX
KW   Human; proliferating cell nuclear antigen 13; PCNA 13; malignant tumour;
KW   cancer; haemopathy; HIV infection; human immunodeficiency virus; ss;
KW   inflammation; transfusion reaction; graft immune rejection; gene chip;
KW   development disease; microarray; nucleic acid hybridisation; haemostatic;
KW   cytostatic; virucide; immunomodulatory; antiinflammatory; RT-PCR; primer;
KW   hereditary disease.
XX
OS   Homo sapiens.
XX
PN   WO200190169-A1.
XX
PD   29-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-CN000787.
XX
PR   19-MAY-2000; 2000CN-00115755.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-106182/14.
XX
PT   Human proliferating cell nuclear antigen 13 and encoded polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 3; Page 12; 35pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of human proliferating
CC   cell nuclear antigen (PCNA) 13. This polypeptide and its related
CC   polynucleotide are applicable in diagnosis and treatment of tumours,
CC   transfusion reaction, haemopathy, graft immune rejection, development
CC   disease, hereditary disease, HIV infection and inflammation. Regulators
CC   of the polypeptide activity or expression that can mimic, promote,
CC   antagonise or inhibit human PCNA 13 can be used for this purpose, and
CC   also an antibody that binds specifically to the polypeptide. A method for
CC   detecting diseases or disease susceptibility relating to the polypeptide
CC   involves measuring the expression dose of the polypeptide, determining
CC   the polypeptide activity, or detecting the polypeptide expression dose
CC   caused by the polynucleotide that has abnormal activity due to a
CC   polynucleotide mutation. The polynucleotide can be used to supply primers
CC   for nucleic acid amplification and probes for hybridisation reactions, or
CC   in producing gene chips or microarrays. This sequence represents a
CC   reverse-transcription PCR (RT-PCR) primer used for isolation of cDNA
CC   encoding human PCNA 13
XX
SQ   Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 24;
  Best Local Similarity   85.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                |||| |||| |||| |||||
Db          1 TTTTATTTTATTTTATTTTT 20


RESULT 3091
AAL57131
ID   AAL57131 standard; DNA; 24 BP.
XX
AC   AAL57131;
XX
DT   04-DEC-2003  (first entry)
XX
DE   RT-PCR primer 2 related to human zinc finger protein 61-82.
XX
KW   Human zinc finger protein 61.82; cancer; HIV infection; RT-PCR; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1381486-A.
XX
PD   27-NOV-2002.
XX
PF   18-APR-2001; 2001CN-00112634.
XX
PR   18-APR-2001; 2001CN-00112634.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-258239/26.
XX
PT   Polypeptide-human zinc finger protein-61.82 and polynucleotide for coding
PT   it.
XX
PS   Example 3; Page 20; 0pp; Chinese.
XX
CC   This invention relates to a novel human zinc finger protein 61.82 and the
CC   DNA sequence encoding it. The protein of the invention may be useful for
CC   the treatment of diseases such as cancer and HIV infection. The present
CC   sequence is that of RT-PCR primer 2 related to the human zinc finger
CC   protein 61.82 of the invention and used in example 3 of the specification
XX
SQ   Sequence 24 BP; 2 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 24;
  Best Local Similarity   85.0%;  Pred. No. 3.7e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                | ||||||||||||||  ||
Db          2 TGTTTTTTTTTTTTTTGGTT 21


RESULT 3092
AAT27193/c
ID   AAT27193 standard; DNA; 25 BP.
XX
AC   AAT27193;
XX
DT   20-NOV-1996  (first entry)
XX
DE   Stem loop oligonucleotide targeted to p53 chromosomal binding site.
XX
KW   Stem loop; target; secondary structure; parallel binding domain;
KW   antiparallel; replication inhibitor; cell growth inhibitor; p53;
KW   detection; stable; strong affinity; nuclease resistant;
KW   Watson-Crick bonding; Hoogsteen bonding; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .25
FT                   /*tag=  a
FT                   /note= "loop without stem structure"
FT   misc_binding    3. .10
```

```
FT                   /*tag=  b
FT                   /note= "target binding area"
FT   misc_binding    16. .23
FT                   /*tag=  c
FT                   /note= "target binding area"
XX
PN   US5514546-A.
XX
PD   07-MAY-1996.
XX
PF   01-SEP-1993;   93US-00115497.
XX
PR   01-SEP-1993;   93CA-02105364.
XX
PA   (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI   Kool ET;
XX
DR   WPI; 1995-162088/22.
XX
PT   Stem-loop oligo:nucleotide(s) contain parallel and antiparallel binding
PT   domains - for binding target nucleic acids, to regulate biosynthesis of
PT   nucleic acid or protein in a cell, for treating e.g. cancer.
XX
PS   Example 1; Col 30; 34pp; English.
XX
CC   AAT27193-T27198 and AAT27200 are stem loop oligonucleotides directed
CC   towards chromosomal sites normally bound by p53 (see AAT35519) The stem
CC   loop oligonucleotides bind with strong affinity and high selectivity to
CC   their target nucleic acids, they are also nuclease resistant. They are
CC   used to inhibit cell growth and DNA replication and other processes
CC   involving a nucleic acid template. In addition to this the
CC   oligonucleotides may be used for the detection and isolation of target
CC   nucleic acids and for cell type-specific drug delivery. The stem loops
CC   bind to their target via a system of co- operative Watson-Crick bonding
CC   and Hoogsteen bonding
XX
SQ   Sequence 25 BP; 0 A; 7 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
             ||||||||| | | ||||||
Db         24 GAAAAAAAAGAGAGAAAAAA 5


RESULT 3093
AAC96817
ID   AAC96817 standard; DNA; 25 BP.
XX
AC   AAC96817;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-C gene PCR primer #22.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
             |||||||||||| |||  ||
Db          1 TTTTTTTTTTTTCACTGCGA 20


RESULT 3094
AAC96075/c
ID   AAC96075 standard; DNA; 25 BP.
XX
AC   AAC96075;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #42.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
```

```
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              |||||   ||||||||||||
Db         20 TGAAAGCCAAAAAAAAAAAA 1


RESULT 3095
AAC96447/c
ID   AAC96447 standard; DNA; 25 BP.
XX
AC   AAC96447;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #49.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              ||  | ||||||||||||||
Db         20 TAAGACTGAAAAAAAAAAAA 1


RESULT 3096
AAC96434/c
ID   AAC96434 standard; DNA; 25 BP.
XX
AC   AAC96434;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #36.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 5 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAA 2798
              ||| ||  ||||||||||||
Db         20 AGAGTTATAAAAAAAAAAAA 1


RESULT 3097
AAC96448/c
ID   AAC96448 standard; DNA; 25 BP.
XX
AC   AAC96448;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #50.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
```

```
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              ||  | ||||||||||||||
Db         20 TAAGACTGAAAAAAAAAAAA 1


RESULT 3098
AAC96449/c
ID   AAC96449 standard; DNA; 25 BP.
XX
AC   AAC96449;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #1.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || || | ||||||||||||
Db         20 TGCAAGATAAAAAAAAAAAA 1


RESULT 3099
AAC95730/c
ID   AAC95730 standard; DNA; 25 BP.
XX
AC   AAC95730;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #1.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 25;
  Best Local Similarity   85.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || || | ||||||||||||
Db         20 TGCAAGATAAAAAAAAAAAA 1
```

```
RESULT 3100
AAX89364/c
ID   AAX89364 standard; DNA; 26 BP.
XX
AC   AAX89364;
XX
DT   24-SEP-1999  (first entry)
XX
DE   Chromosomal binding site for p53 protein (Seq ID No: 10 of US5936079).
XX
KW   Cell growth inhibition; chromosomal binding site; p53 protein;
KW   cellular replication; cancer; ss.
XX
OS   Synthetic.
XX
PN   US5936079-A.
XX
PD   10-AUG-1999.
XX
PF   15-AUG-1994;   94US-00291011.
XX
PR   06-APR-1992;   92US-00863661.
PR   01-MAY-1992;   92US-00879618.
XX
PA   (ALTO-) ALTON OCHSNER MEDICAL FOUND.
XX
PI   Cook J,  Re R;
XX
DR   WPI; 1999-457628/38.
XX
PT   New oligonucleotide useful for treating and preventing cancer.
XX
PS   Example 1; Col 12; 12pp; English.
XX
CC   The invention provides methods for inhibiting cell growth by providing a
CC   growing cell with an oligonucleotide capable of binding to a chromosomal
CC   binding site for p53 protein. Sequences AAX89362, AAX89363 and AAX89366
CC   represent oligonucleotides that are derived from the sequence AAX89355.
CC   The oligonucleotides are used for inhibiting mammalian cellular
CC   replication and the treatment and prevention of cancer in a human. The
CC   oligonucleotides can be used in vitro to inhibit the growth of cultured
CC   mammalian cells e.g. human, monkey, mouse, rat and hamster cells which
CC   have chromosomal DNA encoding a binding site for p53 protein. Sequences
CC   AAX89356-366 represent oligonucleotides that are based on chromosomal
CC   binding sites for p53 protein
XX
SQ   Sequence 26 BP; 0 A; 7 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 26;
  Best Local Similarity   85.0%;  Pred. No. 4.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||| |||||||  ||||
Db         25 GAAAAAGAAAAAAAGGAAAA 6


RESULT 3101
ABS54659/c
ID   ABS54659 standard; DNA; 26 BP.
XX
AC   ABS54659;
XX
DT   03-DEC-2002  (first entry)
XX
DE   Human p53 protein chromosomal binding region oligonucleotide Hoog3.
XX
KW   ss; p53; chromosomal binding region; cancer; carcinoma; sarcoma;
KW   breast cancer; adrenal cortex cancer; colon cancer; bladder cancer;
KW   prostate cancer; lung cancer; leukaemic cancer.
XX
OS   Synthetic.
XX
PN   US2002103153-A1.
XX
PD   01-AUG-2002.
XX
PF   22-AUG-2001; 2001US-00935247.
XX
PR   06-APR-1992;   92US-00863661.
PR   01-MAY-1992;   92US-00879618.
PR   15-AUG-1994;   94US-00291011.
PR   10-MAR-1999;   99US-00266065.
XX
PA   (RERR/) RE R.
PA   (COOK/) COOK J.
XX
PI   Re R,  Cook J;
XX
DR   WPI; 2002-674027/72.
XX
PT   Composition for treating cancer comprises an oligonucleotide that binds a
PT   chromosomal binding site for p53.
XX
PS   Example 1; Page 7; 13pp; English.
XX
CC   The invention relates to composition comprising an oligonucleotide that
CC   can bind a chromosomal binding site for p53 protein, and a
CC   pharmaceutically acceptable carrier. The composition is useful for
CC   inhibiting mammalian (e.g. human, ape, monkey, cow, mouse, rat, hamster,
CC   rabbit, cat, sheep or bull, dog, horse) cell growth and replication,
CC   especially cancer (e.g. carcinoma, sarcoma, breast cancer, adrenal cortex
CC   cancer, colon cancer, bladder cancer, prostate cancer, lung cancer or
CC   leukaemic cancer). The present sequence is human p53 protein chromosomal
CC   binding region scrambled control oligonucleotide Hoog3
XX
SQ   Sequence 26 BP; 0 A; 7 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15.2;  DB 1;  Length 26;
  Best Local Similarity   85.0%;  Pred. No. 4.1e+03;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              |||||| |||||||  ||||
Db         25 GAAAAAGAAAAAAAGGAAAA 6


RESULT 3102
AAQ79185
ID   AAQ79185 standard; DNA; 15 BP.
XX
AC   AAQ79185;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
XX
DE   Nuclease resistant oligonucleotide.
XX
KW   Nuclease resistant oligonucleotide; inhibition of gene expression;
KW   9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   13
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "9-methyl-acyclo-adenosine"
XX
PN   WO9422864-A1.
XX
PD   13-OCT-1994.
XX
PF   21-MAR-1994;   94WO-US002995.
```

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XX
PR   30-MAR-1993;   93US-00040326.
XX
PA   (STER ) STERLING WINTHROP INC.
XX
PI   Cook PD,  Delecki DJ,  Guinosso C;
XX
DR   WPI; 1994-333078/41.
XX
PT   New acyclic nucleoside analogues - used to prepare nuclease resistant
PT   oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS   Example 11; Page 20; 37pp; English.
XX
CC   AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic
CC   nucleoside analogues which inhibit nuclease degradation. The nuclease
CC   resistant oligonucleotides can themselves be used to inhibit gene
CC   expression as antisense agents, in nucleic acid sequencing and diagnostic
CC   assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3103
AAQ79185/c
ID   AAQ79185 standard; DNA; 15 BP.
XX
AC   AAQ79185;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
XX
DE   Nuclease resistant oligonucleotide.
XX
KW   Nuclease resistant oligonucleotide; inhibition of gene expression;
KW   9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    13
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "9-methyl-acyclo-adenosine"
XX
PN   WO9422864-A1.
XX
PD   13-OCT-1994.
XX
PF   21-MAR-1994;   94WO-US002995.
XX
PR   30-MAR-1993;   93US-00040326.
XX
PA   (STER ) STERLING WINTHROP INC.
XX
PI   Cook PD,  Delecki DJ,  Guinosso C;
XX
DR   WPI; 1994-333078/41.
XX
PT   New acyclic nucleoside analogues - used to prepare nuclease resistant
PT   oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS   Example 11; Page 20; 37pp; English.
XX
CC   AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic
CC   nucleoside analogues which inhibit nuclease degradation. The nuclease
CC   resistant oligonucleotides can themselves be used to inhibit gene
CC   expression as antisense agents, in nucleic acid sequencing and diagnostic
CC   assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3104
AAQ79184
ID   AAQ79184 standard; DNA; 15 BP.
XX
AC   AAQ79184;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
XX
DE   Nuclease resistant oligonucleotide.
XX
KW   Nuclease resistant oligonucleotide; inhibition of gene expression;
KW   9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    14
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "9-methyl-acyclo-adenosine"
XX
PN   WO9422864-A1.
XX
PD   13-OCT-1994.
XX
PF   21-MAR-1994;   94WO-US002995.
XX
PR   30-MAR-1993;   93US-00040326.
XX
PA   (STER ) STERLING WINTHROP INC.
XX
PI   Cook PD,  Delecki DJ,  Guinosso C;
XX
DR   WPI; 1994-333078/41.
XX
PT   New acyclic nucleoside analogues - used to prepare nuclease resistant
PT   oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS   Example 10; Page 20; 37pp; English.
XX
CC   AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic
CC   nucleoside analogues which inhibit nuclease degradation. The nuclease
CC   resistant oligonucleotides can themselves be used to inhibit gene
CC   expression as antisense agents, in nucleic acid sequencing and diagnostic
CC   assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15
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RESULT 3105
AAQ79184/c
ID   AAQ79184 standard; DNA; 15 BP.
XX
AC   AAQ79184;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1995  (first entry)
XX
DE   Nuclease resistant oligonucleotide.
XX
KW   Nuclease resistant oligonucleotide; inhibition of gene expression;
KW   9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    14
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "9-methyl-acyclo-adenosine"
XX
PN   WO9422864-A1.
XX
PD   13-OCT-1994.
XX
PF   21-MAR-1994;   94WO-US002995.
XX
PR   30-MAR-1993;   93US-00040326.
XX
PA   (STER ) STERLING WINTHROP INC.
XX
PI   Cook PD,  Delecki DJ,  Guinosso C;
XX
DR   WPI; 1994-333078/41.
XX
PT   New acyclic nucleoside analogues - used to prepare nuclease resistant
PT   oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS   Example 10; Page 20; 37pp; English.
XX
CC   AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic
CC   nucleoside analogues which inhibit nuclease degradation. The nuclease
CC   resistant oligonucleotides can themselves be used to inhibit gene
CC   expression as antisense agents, in nucleic acid sequencing and diagnostic
CC   assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3106
AAT52136
ID   AAT52136 standard; RNA; 15 BP.
XX
AC   AAT52136;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2910).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
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  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 3107
AAT52136/c
ID   AAT52136 standard; RNA; 15 BP.
XX
AC   AAT52136;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2910).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3108
AAT52138
ID   AAT52138 standard; RNA; 15 BP.
XX
AC   AAT52138;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2911).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
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PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 3109
AAT52138/c
ID   AAT52138 standard; RNA; 15 BP.
XX
AC   AAT52138;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2911).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3110
AAT52140/c
ID   AAT52140 standard; RNA; 15 BP.
XX
AC   AAT52140;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2912).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db         15 GAAAAAAAAAAAAAA 1


RESULT 3111
AAT52142/c
ID   AAT52142 standard; RNA; 15 BP.
XX
AC   AAT52142;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2913).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
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PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 1 A; 1 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
              |||||||||||||||
Db         15 TGAAAAAAAAAAAAA 1


RESULT 3112
AAV01604
ID   AAV01604 standard; DNA; 15 BP.
XX
AC   AAV01604;
XX
DT   25-MAR-2003  (revised)
DT   31-MAR-1998  (first entry)
XX
DE   Oligonucleotide containing phosphoramidate linkages.
XX
KW   phosphoramidate linkage; solid phase synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "these residues have N3'->P5' phosphoramidate
FT                   linkages"
XX
PN   WO9731009-A1.
XX
PD   28-AUG-1997.
XX
PF   14-JUN-1996;   96WO-US010418.
XX
PR   21-FEB-1996;   96US-00603566.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Hirschbein BL,  Fearon KL,  Gryaznov SM,  Mccurdy SN,  Nelson JS;
PI   Schultz RG;
XX
DR   WPI; 1997-435080/40.
XX
PT   Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT   immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT   phosphoramidite then oxidation, useful as research, diagnostic and
PT   therapeutic agents.
XX
PS   Disclosure; Page 28; 60pp; English.
XX
CC   A new method is provided for the synthesis of oligonucleotides having N3'
CC   ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC   protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC   amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC   phosphoramidite monomer to form an internucleoside N3'-> P5'
CC   phosphoramidite link; (d) oxidising this link to phosphoramidate; and
CC   optionally repeating steps (b)-(d) until the required oligonucleotide is
CC   completed. This method provides better yields with lower reagent
CC   consumption than known processes, and can be operated on a large scale.
CC   The obtained oligos, containing phosphoramidate linkages, have favourable
CC   binding properties, nuclease resistance and solubility, and are useful as
CC   research, diagnostic and therapeutic agents. The present sequence is an
CC   example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
CC   have been introduced by the new method. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3113
AAV01604/c
ID   AAV01604 standard; DNA; 15 BP.
XX
AC   AAV01604;
XX
DT   25-MAR-2003  (revised)
DT   31-MAR-1998  (first entry)
XX
DE   Oligonucleotide containing phosphoramidate linkages.
XX
KW   phosphoramidate linkage; solid phase synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "these residues have N3'->P5' phosphoramidate
FT                   linkages"
XX
PN   WO9731009-A1.
XX
PD   28-AUG-1997.
XX
```

```
PF   14-JUN-1996;   96WO-US010418.
XX
PR   21-FEB-1996;   96US-00603566.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Hirschbein BL,  Fearon KL,  Gryaznov SM,  Mccurdy SN,  Nelson JS;
PI   Schultz RG;
XX
DR   WPI; 1997-435080/40.
XX
PT   Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT   immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT   phosphoramidite then oxidation, useful as research, diagnostic and
PT   therapeutic agents.
XX
PS   Disclosure; Page 28; 60pp; English.
XX
CC   A new method is provided for the synthesis of oligonucleotides having N3'
CC   ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC   protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC   amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC   phosphoramidite monomer to form an internucleoside N3'-> P5'
CC   phosphoramidite link; (d) oxidising this link to phosphoramidate; and
CC   optionally repeating steps (b)-(d) until the required oligonucleotide is
CC   completed. This method provides better yields with lower reagent
CC   consumption than known processes, and can be operated on a large scale.
CC   The obtained oligos, containing phosphoramidate linkages, have favourable
CC   binding properties, nuclease resistance and solubility, and are useful as
CC   research, diagnostic and therapeutic agents. The present sequence is an
CC   example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
CC   have been introduced by the new method. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3114
AAV01603
ID   AAV01603 standard; DNA; 15 BP.
XX
AC   AAV01603;
XX
DT   25-MAR-2003  (revised)
DT   31-MAR-1998  (first entry)
XX
DE   Oligonucleotide containing phosphoramidate linkages.
XX
KW   phosphoramidate linkage; solid phase synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "these residues have N3'->P5' phosphoramidate
FT                   linkages"
XX
PN   WO9731009-A1.
XX
PD   28-AUG-1997.
XX
PF   14-JUN-1996;   96WO-US010418.
XX
PR   21-FEB-1996;   96US-00603566.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Hirschbein BL,  Fearon KL,  Gryaznov SM,  Mccurdy SN,  Nelson JS;
PI   Schultz RG;
XX
DR   WPI; 1997-435080/40.
XX
PT   Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT   immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT   phosphoramidite then oxidation, useful as research, diagnostic and
PT   therapeutic agents.
XX
PS   Disclosure; Page 28; 60pp; English.
XX
CC   A new method is provided for the synthesis of oligonucleotides having N3'
CC   ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC   protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC   amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC   phosphoramidite monomer to form an internucleoside N3'-> P5'
CC   phosphoramidite link; (d) oxidising this link to phosphoramidate; and
CC   optionally repeating steps (b)-(d) until the required oligonucleotide is
CC   completed. This method provides better yields with lower reagent
CC   consumption than known processes, and can be operated on a large scale.
CC   The obtained oligos, containing phosphoramidate linkages, have favourable
CC   binding properties, nuclease resistance and solubility, and are useful as
CC   research, diagnostic and therapeutic agents. The present sequence is an
CC   example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
CC   have been introduced by the new method. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3115
AAV01603/c
ID   AAV01603 standard; DNA; 15 BP.
XX
AC   AAV01603;
XX
DT   25-MAR-2003  (revised)
DT   31-MAR-1998  (first entry)
XX
DE   Oligonucleotide containing phosphoramidate linkages.
XX
KW   phosphoramidate linkage; solid phase synthesis; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "these residues have N3'->P5' phosphoramidate
FT                   linkages"
XX
PN   WO9731009-A1.
XX
PD   28-AUG-1997.
XX
PF   14-JUN-1996;   96WO-US010418.
XX
PR   21-FEB-1996;   96US-00603566.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
```

```
PI   Hirschbein BL,  Fearon KL,  Gryaznov SM,  Mccurdy SN,  Nelson JS;
PI   Schultz RG;
XX
DR   WPI; 1997-435080/40.
XX
PT   Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
PT   immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
PT   phosphoramidite then oxidation, useful as research, diagnostic and
PT   therapeutic agents.
XX
PS   Disclosure; Page 28; 60pp; English.
XX
CC   A new method is provided for the synthesis of oligonucleotides having N3'
CC   ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
CC   protected amino nucleoside to a solid support; (b) deprotecting the 3'-
CC   amino; (c) reacting with a 3'-protected aminonucleoside-5'-
CC   phosphoramidite monomer to form an internucleoside N3'-> P5'
CC   phosphoramidite link; (d) oxidising this link to phosphoramidate; and
CC   optionally repeating steps (b)-(d) until the required oligonucleotide is
CC   completed. This method provides better yields with lower reagent
CC   consumption than known processes, and can be operated on a large scale.
CC   The obtained oligos, containing phosphoramidate linkages, have favourable
CC   binding properties, nuclease resistance and solubility, and are useful as
CC   research, diagnostic and therapeutic agents. The present sequence is an
CC   example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
CC   have been introduced by the new method. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3116
AAV07431
ID   AAV07431 standard; DNA; 15 BP.
XX
AC   AAV07431;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Synthetic peptide-labeled oligonucleotide primer.
XX
KW   oligonucleotide; peptide; conjugate; release tag compound;
KW   mass spectrometry; detection; identification; diagnosis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9826095-A1.
XX
PD   18-JUN-1998.
XX
PF   10-DEC-1997;   97WO-US022639.
XX
PR   10-DEC-1996;   96US-0033037P.
PR   16-MAY-1997;   97US-0046719P.
XX
PA   (GENE-) GENETRACE SYSTEMS INC.
XX
PI   Montforte JA,  Becker CH,  Pollart DJ,  Shaler TA;
XX
DR   WPI; 1998-348547/30.
XX
PT   New release tag compounds for detecting target molecule(s) - comprising a
PT   reactive group, a release group and a releasable non-volatile mass label
PT   detectable by mass spectrometry.
XX
PS   Example 3; Page 92; 170pp; English.
XX
CC   The sequence is that of an oligonucleotide primer which was produced as
CC   part of an oligonucleotide peptide conjugate as an example of a release
CC   tag compound (RTC). These comprise a reactive group, a release group and
CC   a non-volatile mass label comprising a synthetic polymer or biopolymer
CC   detectable by mass spectrometry. The RTCs can be used as probes for the
CC   detection of TMs. They can be used for e.g. identification of gene
CC   sequences, identification of non-coding nucleotide sequences,
CC   identification of mutations within a gene or protein sequence, detection
CC   of metals, detection of toxins, detection of receptors on an organism or
CC   a cell, characterisation of antibody-antigen interactions, enzyme-
CC   substrate interactions and characterisation of ligand interactions.
CC   Multiplex applications include multiple pathogen diagnostics, multigene
CC   genetic polymorphism screening, single nucleotide polymorphism (SNP)
CC   genotyping, clone and gene mapping, and gene expression analysis. The
CC   RTCs permit the ready detection of releasable mass labels by mass
CC   spectroscopy. The releasable mass labels permit the multiplexing of tens,
CC   hundreds and perhaps even thousands of different mass labels that can be
CC   used to uniquely identify each desired target
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3117
AAV07431/c
ID   AAV07431 standard; DNA; 15 BP.
XX
AC   AAV07431;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Synthetic peptide-labeled oligonucleotide primer.
XX
KW   oligonucleotide; peptide; conjugate; release tag compound;
KW   mass spectrometry; detection; identification; diagnosis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9826095-A1.
XX
PD   18-JUN-1998.
XX
PF   10-DEC-1997;   97WO-US022639.
XX
PR   10-DEC-1996;   96US-0033037P.
PR   16-MAY-1997;   97US-0046719P.
XX
PA   (GENE-) GENETRACE SYSTEMS INC.
XX
PI   Montforte JA,  Becker CH,  Pollart DJ,  Shaler TA;
XX
DR   WPI; 1998-348547/30.
XX
PT   New release tag compounds for detecting target molecule(s) - comprising a
PT   reactive group, a release group and a releasable non-volatile mass label
PT   detectable by mass spectrometry.
XX
PS   Example 3; Page 92; 170pp; English.
XX
CC   The sequence is that of an oligonucleotide primer which was produced as
CC   part of an oligonucleotide peptide conjugate as an example of a release
CC   tag compound (RTC). These comprise a reactive group, a release group and
CC   a non-volatile mass label comprising a synthetic polymer or biopolymer
CC   detectable by mass spectrometry. The RTCs can be used as probes for the
```

```
CC   detection of TMs. They can be used for e.g. identification of gene
CC   sequences, identification of non-coding nucleotide sequences,
CC   identification of mutations within a gene or protein sequence, detection
CC   of metals, detection of toxins, detection of receptors on an organism or
CC   a cell, characterisation of antibody-antigen interactions, enzyme-
CC   substrate interactions and characterisation of ligand interactions.
CC   Multiplex applications include multiple pathogen diagnostics, multigene
CC   genetic polymorphism screening, single nucleotide polymorphism (SNP)
CC   genotyping, clone and gene mapping, and gene expression analysis. The
CC   RTCs permit the ready detection of releasable mass labels by mass
CC   spectroscopy. The releasable mass labels permit the multiplexing of tens,
CC   hundreds and perhaps even thousands of different mass labels that can be
CC   used to uniquely identify each desired target
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3118
AAT86675
ID   AAT86675 standard; DNA; 15 BP.
XX
AC   AAT86675;
XX
DT   04-JUN-1998  (first entry)
XX
DE   Oligonucleotide linked to polyacrylamide.
XX
KW   Capillary afinity gel electrophoresis; separation; polymer-gel;
KW   polyacrylamide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Thymine at 5' end attached to a polyacrylamide
FT                   gel via a linking group"
XX
PN   WO9745721-A1.
XX
PD   04-DEC-1997.
XX
PF   23-MAY-1997;   97WO-EP002647.
XX
PR   24-MAY-1996;   96CH-00001320.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Muscate A,  Paulus A,  Natt F;
XX
DR   WPI; 1998-041763/04.
XX
PT   Separation of electrically charged target molecules - by capillary
PT   affinity gel electrophoresis using polymer-gel to which receptors for
PT   target molecules are bound.
XX
PS   Example A1; Page 22; 41pp; English.
XX
CC   This sequence represents an oligonucleotide receptor molecule covalently
CC   bound to a polyacrylamide gel via a linking group. The invention relates
CC   to selective separation of electrically charged target molecules in an
CC   analytical mixture. It comprises capillary affinity gel electrophoresis
CC   using a capillary tube which is at least partly filled with a polymer
CC   gel. Receptors for target molecules are covalently bound to the polymer.
CC   An electric field of at least 50 volts/cm is applied. The capillary tube
CC   is charged with the analytical mixture. In a first separation stage, the
CC   target molecules in the mixture are bound to the receptors and the
CC   remaining components are eluted, optionally whilst splitting open. In a
CC   second stage, the elution conditions are changed, optionally in stages,
CC   so that the affinity of the target molecules for the receptor is
CC   eliminated and the target molecules are eluted and detected, optionally
CC   whilst splitting open. The process is useful for selective separation
CC   and/or determination of charged organic compounds, such as
CC   oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
CC   isolation of specific proteins and DNA molecules, purification of
CC   antibodies, analysis of antisense compounds or screening for enzyme
CC   inhibitors. The process achieves higher resolution and selectivity than
CC   prior art processes, especially in the case of complex biological
CC   analytical mixtures. It has high sensitivity, even with small amounts of
CC   samples. The derivatised polymers may be synthesised specifically using
CC   standard methods
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3119
AAT86675/c
ID   AAT86675 standard; DNA; 15 BP.
XX
AC   AAT86675;
XX
DT   04-JUN-1998  (first entry)
XX
DE   Oligonucleotide linked to polyacrylamide.
XX
KW   Capillary afinity gel electrophoresis; separation; polymer-gel;
KW   polyacrylamide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Thymine at 5' end attached to a polyacrylamide
FT                   gel via a linking group"
XX
PN   WO9745721-A1.
XX
PD   04-DEC-1997.
XX
PF   23-MAY-1997;   97WO-EP002647.
XX
PR   24-MAY-1996;   96CH-00001320.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Muscate A,  Paulus A,  Natt F;
XX
DR   WPI; 1998-041763/04.
XX
PT   Separation of electrically charged target molecules - by capillary
PT   affinity gel electrophoresis using polymer-gel to which receptors for
PT   target molecules are bound.
XX
PS   Example A1; Page 22; 41pp; English.
XX
CC   This sequence represents an oligonucleotide receptor molecule covalently
CC   bound to a polyacrylamide gel via a linking group. The invention relates
CC   to selective separation of electrically charged target molecules in an
CC   analytical mixture. It comprises capillary affinity gel electrophoresis
```

CC using a capillary tube which is at least partly filled with a polymer
CC gel. Receptors for target molecules are covalently bound to the polymer.
CC An electric field of at least 50 volts/cm is applied. The capillary tube
CC is charged with the analytical mixture. In a first separation stage, the
CC target molecules in the mixture are bound to the receptors and the
CC remaining components are eluted, optionally whilst splitting open. In a
CC second stage, the elution conditions are changed, optionally in stages,
CC so that the affinity of the target molecules for the receptor is
CC eliminated and the target molecules are eluted and detected, optionally
CC whilst splitting open. The process is useful for selective separation
CC and/or determination of charged organic compounds, such as
CC oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
CC isolation of specific proteins and DNA molecules, purification of
CC antibodies, analysis of antisense compounds or screening for enzyme
CC inhibitors. The process achieves higher resolution and selectivity than
CC prior art processes, especially in the case of complex biological
CC analytical mixtures. It has high sensitivity, even with small amounts of
CC samples. The derivatised polymers may be synthesised specifically using
CC standard methods
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3120
AAT86605
ID AAT86605 standard; DNA; 15 BP.
XX
AC AAT86605;
XX
DT 04-JUN-1998 (first entry)
XX
DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW Capillary afinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX
OS Synthetic.
XX
PN WO9745721-A1.
XX
PD 04-DEC-1997.
XX
PF 23-MAY-1997; 97WO-EP002647.
XX
PR 24-MAY-1996; 96CH-00001320.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Muscate A, Paulus A, Natt F;
XX
DR WPI; 1998-041763/04.
XX
PT Separation of electrically charged target molecules - by capillary
PT affinity gel electrophoresis using polymer-gel to which receptors for
PT target molecules are bound.
XX
PS Example D3; Page 25; 41pp; English.
XX
CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC process using capillary affinity gel electrophoresis. The invention
CC relates to selective separation of electrically charged target molecules
CC in an analytical mixture. It comprises capillary affinity gel
CC electrophoresis using a capillary tube which is at least partly filled
CC with a polymer gel. Receptors for target molecules are covalently bound
CC to the polymer. An electric field of at least 50 volts/cm is applied. The
CC capillary tube is charged with the analytical mixture. In a first
CC separation stage, the target molecules in the mixture are bound to the
CC receptors and the remaining components are eluted, optionally whilst
CC splitting open. In a second stage, the elution conditions are changed,
CC optionally in stages, so that the affinity of the target molecules for
CC the receptor is eliminated and the target molecules are eluted and
CC detected, optionally whilst splitting open. The process is useful for
CC selective separation and/or determination of charged organic compounds,
CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC for isolation of specific proteins and DNA molecules, purification of
CC antibodies, analysis of antisense compounds or screening for enzyme
CC inhibitors. The process achieves higher resolution and selectivity than
CC prior art processes, especially in the case of complex biological
CC analytical mixtures. It has high sensitivity, even with small amounts of
CC samples. The derivatised polymers may be synthesised specifically using
CC standard methods
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3121
AAT86605/c
ID AAT86605 standard; DNA; 15 BP.
XX
AC AAT86605;
XX
DT 04-JUN-1998 (first entry)
XX
DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW Capillary afinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX
OS Synthetic.
XX
PN WO9745721-A1.
XX
PD 04-DEC-1997.
XX
PF 23-MAY-1997; 97WO-EP002647.
XX
PR 24-MAY-1996; 96CH-00001320.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Muscate A, Paulus A, Natt F;
XX
DR WPI; 1998-041763/04.
XX
PT Separation of electrically charged target molecules - by capillary
PT affinity gel electrophoresis using polymer-gel to which receptors for
PT target molecules are bound.
XX
PS Example D3; Page 25; 41pp; English.
XX
CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC process using capillary affinity gel electrophoresis. The invention
CC relates to selective separation of electrically charged target molecules
CC in an analytical mixture. It comprises capillary affinity gel
CC electrophoresis using a capillary tube which is at least partly filled
CC with a polymer gel. Receptors for target molecules are covalently bound
CC to the polymer. An electric field of at least 50 volts/cm is applied. The
CC capillary tube is charged with the analytical mixture. In a first
CC separation stage, the target molecules in the mixture are bound to the
CC receptors and the remaining components are eluted, optionally whilst

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CC   splitting open. In a second stage, the elution conditions are changed,
CC   optionally in stages, so that the affinity of the target molecules for
CC   the receptor is eliminated and the target molecules are eluted and
CC   detected, optionally whilst splitting open. The process is useful for
CC   selective separation and/or determination of charged organic compounds,
CC   such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC   for isolation of specific proteins and DNA molecules, purification of
CC   antibodies, analysis of antisense compounds or screening for enzyme
CC   inhibitors. The process achieves higher resolution and selectivity than
CC   prior art processes, especially in the case of complex biological
CC   analytical mixtures. It has high sensitivity, even with small amounts of
CC   samples. The derivatised polymers may be synthesised specifically using
CC   standard methods
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3122
AAX00787
ID   AAX00787 standard; DNA; 15 BP.
XX
AC   AAX00787;
XX
DT   13-APR-1999  (first entry)
XX
DE   N3-P5 phosphoramidate oligonucleotide #3.
XX
KW   Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .15
FT                   /*tag=  a
FT                   /note= "contains internucleotide N3-P5 phosphoramidate
FT                   internucleotide linkages"
XX
PN   US5859233-A.
XX
PD   12-JAN-1999.
XX
PF   20-DEC-1996;   96US-00771789.
XX
PR   21-FEB-1996;   96US-00603566.
PR   14-JUN-1996;   96US-00663918.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Nelson JS,  Mccurdy SN,  Hirschbein BL,  Schultz RG;
PI   Fearon KL;
XX
DR   WPI; 1999-120007/10.
XX
PT   New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT   the synthesis of oligo-nucleotide(s).
XX
PS   Example 10; Col 33; 34pp; English.
XX
CC   This sequence represents an example of an oligonucleotide containing
CC   novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC   sequence is generated synthetically by using an amine-exchange reaction
CC   of phosphoramidites in which a deprotected 3'-amino group of an
CC   oligonucleotide chain is exchanged for the amino portion of a 5'-
CC   phosphoramidite with a protected 3' amino group. The resulting
CC   phosphoramidite internucleotide linkage is oxidised to form a stable
CC   protected phosphoramidate linkage
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3123
AAX00787/c
ID   AAX00787 standard; DNA; 15 BP.
XX
AC   AAX00787;
XX
DT   13-APR-1999  (first entry)
XX
DE   N3-P5 phosphoramidate oligonucleotide #3.
XX
KW   Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .15
FT                   /*tag=  a
FT                   /note= "contains internucleotide N3-P5 phosphoramidate
FT                   internucleotide linkages"
XX
PN   US5859233-A.
XX
PD   12-JAN-1999.
XX
PF   20-DEC-1996;   96US-00771789.
XX
PR   21-FEB-1996;   96US-00603566.
PR   14-JUN-1996;   96US-00663918.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Nelson JS,  Mccurdy SN,  Hirschbein BL,  Schultz RG;
PI   Fearon KL;
XX
DR   WPI; 1999-120007/10.
XX
PT   New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT   the synthesis of oligo-nucleotide(s).
XX
PS   Example 10; Col 33; 34pp; English.
XX
CC   This sequence represents an example of an oligonucleotide containing
CC   novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC   sequence is generated synthetically by using an amine-exchange reaction
CC   of phosphoramidites in which a deprotected 3'-amino group of an
CC   oligonucleotide chain is exchanged for the amino portion of a 5'-
CC   phosphoramidite with a protected 3' amino group. The resulting
CC   phosphoramidite internucleotide linkage is oxidised to form a stable
CC   protected phosphoramidate linkage
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
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RESULT 3124
AAX00788
ID   AAX00788 standard; DNA; 15 BP.
XX
AC   AAX00788;
XX
DT   13-APR-1999  (first entry)
XX
DE   N3-P5 phosphoramidate oligonucleotide #4.
XX
KW   Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .15
FT                   /*tag=  a
FT                   /note= "contains internucleotide N3-P5 phosphoramidate
FT                   internucleotide linkages"
XX
PN   US5859233-A.
XX
PD   12-JAN-1999.
XX
PF   20-DEC-1996;   96US-00771789.
XX
PR   21-FEB-1996;   96US-00603566.
PR   14-JUN-1996;   96US-00663918.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Nelson JS,  Mccurdy SN,  Hirschbein BL,  Schultz RG;
PI   Fearon KL;
XX
DR   WPI; 1999-120007/10.
XX
PT   New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT   the synthesis of oligo-nucleotide(s).
XX
PS   Example 10; Col 33; 34pp; English.
XX
CC   This sequence represents an example of an oligonucleotide containing
CC   novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC   sequence is generated synthetically by using an amine-exchange reaction
CC   of phosphoramidites in which a deprotected 3'-amino group of an
CC   oligonucleotide chain is exchanged for the amino portion of a 5'-
CC   phosphoramidite with a protected 3' amino group. The resulting
CC   phosphoramidite internucleotide linkage is oxidised to form a stable
CC   protected phosphoramidate linkage
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3125
AAX00788/c
ID   AAX00788 standard; DNA; 15 BP.
XX
AC   AAX00788;
XX
DT   13-APR-1999  (first entry)
XX
DE   N3-P5 phosphoramidate oligonucleotide #4.
XX
KW   Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .15
FT                   /*tag=  a
FT                   /note= "contains internucleotide N3-P5 phosphoramidate
FT                   internucleotide linkages"
XX
PN   US5859233-A.
XX
PD   12-JAN-1999.
XX
PF   20-DEC-1996;   96US-00771789.
XX
PR   21-FEB-1996;   96US-00603566.
PR   14-JUN-1996;   96US-00663918.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Nelson JS,  Mccurdy SN,  Hirschbein BL,  Schultz RG;
PI   Fearon KL;
XX
DR   WPI; 1999-120007/10.
XX
PT   New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT   the synthesis of oligo-nucleotide(s).
XX
PS   Example 10; Col 33; 34pp; English.
XX
CC   This sequence represents an example of an oligonucleotide containing
CC   novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC   sequence is generated synthetically by using an amine-exchange reaction
CC   of phosphoramidites in which a deprotected 3'-amino group of an
CC   oligonucleotide chain is exchanged for the amino portion of a 5'-
CC   phosphoramidite with a protected 3' amino group. The resulting
CC   phosphoramidite internucleotide linkage is oxidised to form a stable
CC   protected phosphoramidate linkage
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3126
AAX55056
ID   AAX55056 standard; DNA; 15 BP.
XX
AC   AAX55056;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
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PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 15 BP; 0 A; 4 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3127
AAA34503
ID   AAA34503 standard; DNA; 15 BP.
XX
AC   AAA34503;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2192.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 540; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 15 BP; 0 A; 4 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3128
AAZ61854
ID   AAZ61854 standard; RNA; 15 BP.
XX
AC   AAZ61854;
XX
DT   28-MAR-2000  (first entry)
XX
DE   HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
```

```
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 49; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC   HCV sequence was screened for optimal ribozyme target sites using a
CC   computer folding algorithm and regions of the mRNA which did not form
CC   secondary folding structures and contained potential ribozyme cleavage
CC   sites were identified. Ribozymes were synthesised to target these sites
CC   and their activities optimised by either varying the length of the
CC   binding arms or by modification to prevent degradation by nucleases. The
CC   ribozymes of the invention inhibit gene expression and/or viral
CC   replication, and are used to treat diseases associated with Hepatitis C
CC   virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC   carcinoma. The ribozymes may be used in combination with interferon to
CC   treat HCV infection, other infectious diseases, autoimmune diseases, and
CC   cancer
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative    15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2180
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 15


RESULT 3129
AAZ61854/c
ID   AAZ61854 standard; RNA; 15 BP.
XX
AC   AAZ61854;
XX
DT   28-MAR-2000  (first entry)
XX
DE   HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 49; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC   HCV sequence was screened for optimal ribozyme target sites using a
CC   computer folding algorithm and regions of the mRNA which did not form
CC   secondary folding structures and contained potential ribozyme cleavage
CC   sites were identified. Ribozymes were synthesised to target these sites
CC   and their activities optimised by either varying the length of the
CC   binding arms or by modification to prevent degradation by nucleases. The
CC   ribozymes of the invention inhibit gene expression and/or viral
CC   replication, and are used to treat diseases associated with Hepatitis C
CC   virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC   carcinoma. The ribozymes may be used in combination with interferon to
CC   treat HCV infection, other infectious diseases, autoimmune diseases, and
CC   cancer
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3130
AAZ64910
ID   AAZ64910 standard; RNA; 15 BP.
XX
AC   AAZ64910;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
```

DR WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 102; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.6e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15
```

RESULT 3131
AAZ64910/c
ID AAZ64910 standard; RNA; 15 BP.
XX
AC AAZ64910;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX
DR WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 102; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
```

RESULT 3132
AAA46502
ID AAA46502 standard; cDNA; 15 BP.
XX
AC AAA46502;
XX
DT 04-SEP-2000 (first entry)
XX
DE PCR primer used to amplify DNA encoding an endo-beta-mannanase.
XX
KW Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW PCR primer; ss.
XX
OS Coffea arabica.
XX
PN WO200028046-A1.
XX
PD 18-MAY-2000.
XX
PF 28-OCT-1999; 99WO-EP008314.
XX
PR 11-NOV-1998; 98EP-00203742.
XX
PA (NEST) SOC PROD NESTLE SA.
XX
PI Marraccini P, Rogers J;
XX
DR WPI; 2000-399535/34.
XX
PT New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
XX
PS Disclosure; Page 32; 41pp; French.
XX
CC PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides
CC that consist of molecules of mannan, either simple or branched, linked
CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is
CC used for in vivo modification of the coffee endo-beta-mannanase gene. It
CC is also used to produce transgenic plant cells (especially coffee cells)
CC which have modified properties of mannan polysaccharide, and thus altered
CC flavour or structure. The enzyme is used for modification, degradation or
CC synthesis of mannan polysaccharides in vitro, particularly to treat
CC coffee beans to increase the percentage of dry matter extraction, and
CC thus reduce the quantity of sediment
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3133
AAA46502/c
ID   AAA46502 standard; cDNA; 15 BP.
XX
AC   AAA46502;
XX
DT   04-SEP-2000  (first entry)
XX
DE   PCR primer used to amplify DNA encoding an endo-beta-mannanase.
XX
KW   Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW   PCR primer; ss.
XX
OS   Coffea arabica.
XX
PN   WO200028046-A1.
XX
PD   18-MAY-2000.
XX
PF   28-OCT-1999;   99WO-EP008314.
XX
PR   11-NOV-1998;   98EP-00203742.
XX
PA   (NEST ) SOC PROD NESTLE SA.
XX
PI   Marraccini P,  Rogers J;
XX
DR   WPI; 2000-399535/34.
XX
PT   New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT   pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
XX
PS   Disclosure; Page 32; 41pp; French.
XX
CC   PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
CC   mannanase enzyme, which is involved in the hydrolysis of polysaccharides
CC   that consist of molecules of mannan, either simple or branched, linked
CC   together by beta(1-4) bonds. The mannanase polynucleotide sequence is
CC   used for in vivo modification of the coffee endo-beta-mannanase gene. It
CC   is also used to produce transgenic plant cells (especially coffee cells)
CC   which have modified properties of mannan polysaccharide, and thus altered
CC   flavour or structure. The enzyme is used for modification, degradation or
CC   synthesis of mannan polysaccharides in vitro, particularly to treat
CC   coffee beans to increase the percentage of dry matter extraction, and
CC   thus reduce the quantity of sediment
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3134
AAA75048
ID   AAA75048 standard; DNA; 15 BP.
XX
AC   AAA75048;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Primer used to reverse transcribe human RNA.
XX
KW   Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW   heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW   wound healing; infection; burn; angiogenesis; restenosis;
KW   atherosclerosis; inflammation; neurodegenerative disease;
KW   Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200052178-A1.
XX
PD   08-SEP-2000.
XX
PF   14-FEB-2000; 2000WO-US003542.
XX
PR   01-MAR-1999;   99US-00258892.
XX
PA   (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA   (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA   (FRIE/) FRIEDMAN M M.
XX
PI   Pecker I,  Vlodavsky I,  Feinstein E;
XX
DR   WPI; 2000-579289/54.
XX
PT   New polynucleotides encoding a polypeptide having heparanase activity,
PT   useful in wound healing and in gene therapy, particularly in treating
PT   tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS   Disclosure; Page 44; 152pp; English.
XX
CC   The present primer was used to reverse transcribe human RNA, from which a
CC   cDNA sequence encoding a protein with heparanase catalytic activity was
CC   amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC   particularly in treating tumour, inflammation or autoimmunity.
CC   Particularly, the polynucleotide is useful in modulating the
CC   bioavailability of heparin-binding growth factors, cellular responses to
CC   heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC   interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC   susceptibility to certain viral and some bacterial and protozoa
CC   infections, or disintegration of neurodegenerative plaques. The
CC   polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC   radiation burns), and in the treatment of angiogenesis, restenosis,
CC   atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC   Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC   bacterial or protozoa infections
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3135
AAA75048/c
ID   AAA75048 standard; DNA; 15 BP.
XX
AC   AAA75048;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Primer used to reverse transcribe human RNA.
XX
KW   Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW   heparin-binding growth factor; cytokine; neurodegenerative plaque;
```

KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200052178-A1.
XX
PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000WO-US003542.
XX
PR 01-MAR-1999; 99US-00258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2000-579289/54.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS Disclosure; Page 44; 152pp; English.
XX
CC The present primer was used to reverse transcribe human RNA, from which a
CC cDNA sequence encoding a protein with heparanase catalytic activity was
CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3136
AAA07792
ID AAA07792 standard; DNA; 15 BP.
XX
AC AAA07792;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-e.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
:|||||||||||||:
Db 1 UTTTTTTTTTTTTTU 15

RESULT 3137
AAA07792/c
ID AAA07792 standard; DNA; 15 BP.
XX
AC AAA07792;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-e.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX

```
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3138
AAA07794
ID   AAA07794 standard; DNA; 15 BP.
XX
AC   AAA07794;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-g.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
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CC   The invention provides modified nucleomonomers of specified formula and
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CC   infected cells. They are used in oligomers for gene regulation, antisense
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CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
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CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 3139
AAA07794/c
ID   AAA07794 standard; DNA; 15 BP.
XX
AC   AAA07794;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-g.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
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XX
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CC   fidelity for target DNA sequences. The oligomers demonstrate significant
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CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3140
AAA07828
ID   AAA07828 standard; DNA; 15 BP.
XX
AC   AAA07828;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 15.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 1.6e+03;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15


RESULT 3141
AAA07828/c
ID   AAA07828 standard; DNA; 15 BP.
XX
AC   AAA07828;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 15.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
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CC infected cells. They are used in oligomers for gene regulation, antisense
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CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
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CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07820-834 represent sequences forming triplex oligomers
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3142
AAA07790
ID AAA07790 standard; DNA; 15 BP.
XX
AC AAA07790;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-c.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
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CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||:|||:|||||
Db 1 TTTTTUTTTUTTTTT 15

RESULT 3143
AAA07790/c
ID AAA07790 standard; DNA; 15 BP.
XX
AC AAA07790;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-c.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
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XX
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CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3144
AAA07789
ID AAA07789 standard; DNA; 15 BP.
XX
AC AAA07789;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-b.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
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SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||:|||||||
Db 1 TTTTTTTUTTTTTTT 15

RESULT 3145
AAA07789/c
ID AAA07789 standard; DNA; 15 BP.
XX
AC AAA07789;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-b.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
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PD 02-MAR-2000.
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  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3146
AAA07795
ID   AAA07795 standard; DNA; 15 BP.
XX
AC   AAA07795;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-h.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
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  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15


RESULT 3147
AAA07795/c
ID   AAA07795 standard; DNA; 15 BP.
XX
AC   AAA07795;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-h.
XX
KW   Nucleomonomer, cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
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SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3148
AAA07797
ID   AAA07797 standard; DNA; 15 BP.
XX
AC   AAA07797;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-j.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 1.6e+03;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :|||||||||||||:
Db          1 UTTTTTTTTTTTTTU 15


RESULT 3149
AAA07797/c
ID   AAA07797 standard; DNA; 15 BP.
XX
AC   AAA07797;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-j.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
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CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
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CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3150
AAA07799
ID   AAA07799 standard; DNA; 15 BP.
XX
AC   AAA07799;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-1.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
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CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 3151
AAA07799/c
ID   AAA07799 standard; DNA; 15 BP.
XX
AC   AAA07799;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-1.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
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CC   infected cells. They are used in oligomers for gene regulation, antisense
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CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
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CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3152
AAA07802
ID   AAA07802 standard; DNA; 15 BP.
XX
AC   AAA07802;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-0.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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XX
PS   Disclosure; Page 20; 42pp; English.
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CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 1.6e+03;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :|||||||||||||:
Db          1 UTTTTTTTTTTTTTU 15


RESULT 3153
AAA07802/c
ID   AAA07802 standard; DNA; 15 BP.
XX
AC   AAA07802;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-0.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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XX
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CC   technology, diagnostic applications to detect target sequences in
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CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   interleukins associated with pathological conditions such as inflammatory
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CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
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CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3154
AAA07825
ID   AAA07825 standard; DNA; 15 BP.
XX
AC   AAA07825;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 14.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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XX
PS   Disclosure; Page 30; 42pp; English.
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 3155
AAA07825/c
ID   AAA07825 standard; DNA; 15 BP.
XX
AC   AAA07825;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 14.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
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```
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3156
AAA07831
ID   AAA07831 standard; DNA; 15 BP.
XX
AC   AAA07831;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 16.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
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XX
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CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||:|||||||
Db          1 TTTTTTTUTTTTTTT 15


RESULT 3157
AAA07831/c
ID   AAA07831 standard; DNA; 15 BP.
XX
AC   AAA07831;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 16.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
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CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
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CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
```

RESULT 3158
AAA07803
ID AAA07803 standard; DNA; 15 BP.
XX
AC AAA07803;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-p.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15
```

RESULT 3159
AAA07803/c
ID AAA07803 standard; DNA; 15 BP.
XX
AC AAA07803;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-p.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
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PS Disclosure; Page 20; 42pp; English.
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CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1
```

```
RESULT 3160
AAA07834
ID   AAA07834 standard; DNA; 15 BP.
XX
AC   AAA07834;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 17.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 30; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 1.6e+03;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15


RESULT 3161
AAA07834/c
ID   AAA07834 standard; DNA; 15 BP.
XX
AC   AAA07834;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of a strand of triplex oligomer 17.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; triplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 30; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07820-834 represent sequences forming triplex oligomers
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3162
AAA07796
ID   AAA07796 standard; DNA; 15 BP.
XX
AC   AAA07796;
```

```
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-i.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 1.6e+03;
  Matches   11;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :||||:|||:||||:
Db          1 UTTTTUTTTUTTTTU 15


RESULT 3163
AAA07796/c
ID   AAA07796 standard; DNA; 15 BP.
XX
AC   AAA07796;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-i.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3164
AAA07800
ID   AAA07800 standard; DNA; 15 BP.
XX
AC   AAA07800;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-m.
```

```
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
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CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 1.6e+03;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||:|||:|||||
Db          1 TTTTTUTTTUTTTTT 15


RESULT 3165
AAA07800/c
ID   AAA07800 standard; DNA; 15 BP.
XX
AC   AAA07800;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-m.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
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CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
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CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3166
AAA07793
ID   AAA07793 standard; DNA; 15 BP.
XX
AC   AAA07793;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-f.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
```

```
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
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CC   monomers in oligomers, which are used in pharmaceutical compositions to
CC   inhibit expression of nucleic acid molecules including DNA and RNA in
CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
CC   nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 3167
AAA07793/c
ID   AAA07793 standard; DNA; 15 BP.
XX
AC   AAA07793;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-f.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
CC   their pharmaceutically acceptable salts. The nucleomonomers are used as
CC   monomers in oligomers, which are used in pharmaceutical compositions to
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CC   cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC   infected cells. They are used in oligomers for gene regulation, antisense
CC   technology, diagnostic applications to detect target sequences in
CC   biological samples such as those containing pathogenic bacteria, fungi
CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC   molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
CC   uses for which the oligomers are suitable for). Oligomers comprising the
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CC   target nucleic acid sequences, are physiologically stable, non-toxic and
CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3168
AAA07798
ID   AAA07798 standard; DNA; 15 BP.
XX
AC   AAA07798;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-k.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
```

XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
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CC their pharmaceutically acceptable salts. The nucleomonomers are used as
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CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
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CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 1.6e+03;
Matches 0; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
:::::::::::::::
Db 1 UUUUUUUUUUUUUUU 15

RESULT 3169
AAA07798/c
ID AAA07798 standard; DNA; 15 BP.
XX
AC AAA07798;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-k.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
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XX
PS Disclosure; Page 20; 42pp; English.
XX
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CC infected cells. They are used in oligomers for gene regulation, antisense
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CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
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CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3170
AAA07788
ID AAA07788 standard; DNA; 15 BP.
XX
AC AAA07788;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-a.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.

XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3171
AAA07788/c
ID AAA07788 standard; DNA; 15 BP.
XX
AC AAA07788;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-a.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
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CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
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CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3172
AAA07791
ID AAA07791 standard; DNA; 15 BP.
XX
AC AAA07791;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-d.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.

```
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
PT   regulation, antisense technology and diagnostics.
XX
PS   Disclosure; Page 20; 42pp; English.
XX
CC   The invention provides modified nucleomonomers of specified formula and
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CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   infections and bacterial infections (see AAA07786 for details of other
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CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 1.6e+03;
  Matches   11;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :||||:|||:||||:
Db          1 UTTTTUTTTUTTTTU 15


RESULT 3173
AAA07791/c
ID   AAA07791 standard; DNA; 15 BP.
XX
AC   AAA07791;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-d.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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XX
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CC   interleukins associated with pathological conditions such as inflammatory
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CC   AAA07788-803 represent oligonucleotides forming a third strand along with
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XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3174
AAA07801
ID   AAA07801 standard; DNA; 15 BP.
XX
AC   AAA07801;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-n.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
```

```
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
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CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 1.6e+03;
  Matches   11;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :||||:|||:||||:
Db          1 UTTTTUTTTUTTTTU 15


RESULT 3175
AAA07801/c
ID   AAA07801 standard; DNA; 15 BP.
XX
AC   AAA07801;
XX
DT   23-JUN-2000  (first entry)
XX
DE   Nucleic acid sequence of ODN-n.
XX
KW   Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW   viral infection; inflammatory response; cellular proliferation;
KW   psoriasis; duplex; ss.
XX
OS   Synthetic.
XX
PN   WO200011013-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US019029.
XX
PR   22-AUG-1998;   98US-0097712P.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Gold B;
XX
DR   WPI; 2000-246530/21.
XX
PT   Modified nucleomonomers, used in physiologically stable, non-toxic
PT   oligomers used to inhibit expression of nucleic acids and in gene
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XX
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CC   inhibit expression of nucleic acid molecules including DNA and RNA in
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CC   and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC   encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
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CC   interleukins associated with pathological conditions such as inflammatory
CC   conditions, cardiovascular disorders, immune reactions, cancer, viral
CC   infections and bacterial infections (see AAA07786 for details of other
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CC   able to penetrate into cells while maintaining stringent base pair
CC   fidelity for target DNA sequences. The oligomers demonstrate significant
CC   single- or double-stranded target nucleic acid binding activity to form
CC   duplexes, triplexes or other forms of stable association. Sequences
CC   AAA07788-803 represent oligonucleotides forming a third strand along with
CC   the duplex sequences
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3176
AAF20625
ID   AAF20625 standard; DNA; 15 BP.
XX
AC   AAF20625;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2192.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
```

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XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 264; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 15 BP; 0 A; 4 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3177
AAA62350
ID   AAA62350 standard; DNA; 15 BP.
XX
AC   AAA62350;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    7
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base    9
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 16; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3178
AAA62350/c
ID   AAA62350 standard; DNA; 15 BP.
XX
AC   AAA62350;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    7
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base    9
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
```

```
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 16; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3179
AAA62347
ID   AAA62347 standard; DNA; 15 BP.
XX
AC   AAA62347;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   11
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   13
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   15
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 15; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3180
AAA62347/c
ID   AAA62347 standard; DNA; 15 BP.
XX
AC   AAA62347;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

```
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   11
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   13
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
FT   modified_base   15
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 15; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3181
AAA62348
ID   AAA62348 standard; DNA; 15 BP.
XX
AC   AAA62348;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   7
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 15; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3182
AAA62348/c
ID   AAA62348 standard; DNA; 15 BP.
XX
AC   AAA62348;
XX
```

```
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   7
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 15; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3183
AAH20308
ID   AAH20308 standard; DNA; 15 BP.
XX
AC   AAH20308;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Oligo dT15 EDTA labelled probe.
XX
KW   Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
FT   modified_base   5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
FT   modified_base   8
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
XX
PN   US2001002314-A1.
XX
PD   31-MAY-2001.
XX
PF   04-AUG-1998;   98US-00128732.
XX
PR   30-OCT-1987;   87US-00115922.
PR   16-NOV-1990;   90US-00614205.
PR   12-NOV-1993;   93US-00152250.
XX
PA   (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
PI   Dervan PB,  Moser HE;
XX
DR   WPI; 2001-342909/36.
XX
PT   New hybridization probe for specific triplex formation with large double
PT   helices, useful e.g. for site-specific diagnostic cleavage, contains
PT   attached functional residue.
XX
PS   Example 1; Fig 3B; 20pp; English.
XX
CC   This invention relates to hybridisation probes which target a specific
CC   sequence within a large double-helical nucleic acid. The probe is
CC   complementary to the target sequence and contains at least one nucleotide
CC   with an attached molecule that is able to cleave double-helical DNA e.g.
CC   EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC   where the attached molecule is a label or compound that alters gene
CC   expression, are used for specific detection and/or cleavage of double-
CC   helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC   caused by viruses, genetic defects or oncogenes), for chromosomal
CC   analysis, and for the isolation and mapping of genes. The present
CC   sequence represents probe of the invention used in an example
CC   illustrating how the probe binds to and cleaves double stranded DNA
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3184
AAH20308/c
ID   AAH20308 standard; DNA; 15 BP.
XX
AC   AAH20308;
XX
DT   31-JUL-2001  (first entry)
```

```
XX
DE   Oligo dT15 EDTA labelled probe.
XX
KW   Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
FT   modified_base   5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
FT   modified_base   8
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally thymidine has EDTA covalently attached
FT                   at C-5"
XX
PN   US2001002314-A1.
XX
PD   31-MAY-2001.
XX
PF   04-AUG-1998;   98US-00128732.
XX
PR   30-OCT-1987;   87US-00115922.
PR   16-NOV-1990;   90US-00614205.
PR   12-NOV-1993;   93US-00152250.
XX
PA   (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
XX
PI   Dervan PB,  Moser HE;
XX
DR   WPI; 2001-342909/36.
XX
PT   New hybridization probe for specific triplex formation with large double
PT   helices, useful e.g. for site-specific diagnostic cleavage, contains
PT   attached functional residue.
XX
PS   Example 1; Fig 3B; 20pp; English.
XX
CC   This invention relates to hybridisation probes which target a specific
CC   sequence within a large double-helical nucleic acid. The probe is
CC   complementary to the target sequence and contains at least one nucleotide
CC   with an attached molecule that is able to cleave double-helical DNA e.g.
CC   EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC   where the attached molecule is a label or compound that alters gene
CC   expression, are used for specific detection and/or cleavage of double-
CC   helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC   caused by viruses, genetic defects or oncogenes), for chromosomal
CC   analysis, and for the isolation and mapping of genes. The present
CC   sequence represents probe of the invention used in an example
CC   illustrating how the probe binds to and cleaves double stranded DNA
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3185
AAF30882
ID   AAF30882 standard; DNA; 15 BP.
XX
AC   AAF30882;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 58; 105pp; English.
XX
CC   The present sequence is that of the oligonucleotide (ODN) component of an
CC   ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC   invention. MGBs bind in a non-intercalating manner to the minor groove of
CC   non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC   but in an intercalating manner, or lies in the minor groove, or is
CC   oriented in some other way to the DNA molecule by MGB, such that it
CC   becomes fluorescent (or its fluorescent properties change detectably).
CC   The conjugates are used as hybridisation probes and amplification primers
CC   for fluorescent detection of specifically hybridising sequences, for
CC   analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC   mismatch discrimination, target or signal amplification, array-based
CC   assays and sequencing, including detection of double-stranded DNA by
CC   triplex formation. Many different targets can be detected a single
CC   reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC   hybridisation-triggered fluorescence. Upon hybridisation to the
CC   complementary target sequence there was an increase in fluorescence
CC   yield, measured as the ratio of the fluorescence emitted by the hybrid
CC   between the ODN-MGB-LF conjugate and its target sequence to the
CC   fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC   of 8.3
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3186
AAF30882/c
ID   AAF30882 standard; DNA; 15 BP.
XX
AC   AAF30882;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Oligonucleotide portion of ODN-MGB-LF conjugate.
```

```
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Disclosure; Page 58; 105pp; English.
XX
CC   The present sequence is that of the oligonucleotide (ODN) component of an
CC   ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC   invention. MGBs bind in a non-intercalating manner to the minor groove of
CC   non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC   but in an intercalating manner, or lies in the minor groove, or is
CC   oriented in some other way to the DNA molecule by MGB, such that it
CC   becomes fluorescent (or its fluorescent properties change detectably).
CC   The conjugates are used as hybridisation probes and amplification primers
CC   for fluorescent detection of specifically hybridising sequences, for
CC   analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC   mismatch discrimination, target or signal amplification, array-based
CC   assays and sequencing, including detection of double-stranded DNA by
CC   triplex formation. Many different targets can be detected a single
CC   reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC   hybridisation-triggered fluorescence. Upon hybridisation to the
CC   complementary target sequence there was an increase in fluorescence
CC   yield, measured as the ratio of the fluorescence emitted by the hybrid
CC   between the ODN-MGB-LF conjugate and its target sequence to the
CC   fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC   of 8.3
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3187
AAH20511
ID   AAH20511 standard; DNA; 15 BP.
XX
AC   AAH20511;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX
KW   Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
KW   phosphorothioate; solid phase synthesis; modified oligonucleotide;
KW   clinical diagnostic; cancer treatment; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .14
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate deoxynucleotides"
XX
PN   DE10051726-A1.
XX
PD   10-MAY-2001.
XX
PF   18-OCT-2000; 2000DE-01051726.
XX
PR   30-OCT-1999;   99DE-01052376.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Seliger H,  Sobkowski M,  Hinz M;
XX
DR   WPI; 2001-336414/36.
XX
PT   Intermediate for oligonucleotide synthesis comprises partially hydrolysed
PT   cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
XX
PS   Example 2; Page 5; 8pp; German.
XX
CC   This invention describes a novel chemical product comprising a partially
CC   hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
CC   with nucleotide derivative(s). The product is an intermediate for the
CC   large (gram) scale solid phase synthesis of modified oligonucleotides
CC   useful e.g. as clinical diagnostics and therapeutics, e.g. for the
CC   treatment of AIDS and cancers. The presence of the partially hydrolysed
CC   copolymer facilitates the synthesis of larger amounts of oligonucleotides
CC   compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
CC   described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
CC   Oligonucleotides are obtained in very good quality and high yields, Also,
CC   the nucleosides do not display the reduced activity seen in some prior
CC   art procedures, less carrier material, reagents and solvent are required.
CC   Further, the carrier material is biodegradable and thus does not present
CC   disposal problems. It also swells uniformly in a range of solvents, which
CC   obviates expansion or contraction during use or solvent exchange.
CC   AAH20510-AAH20513 represent oligonucleotides containing modified
CC   deoxynucleotides which are used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3188
AAH20511/c
ID   AAH20511 standard; DNA; 15 BP.
XX
AC   AAH20511;
XX
DT   31-JUL-2001  (first entry)
XX
DE   Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX
KW   Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
KW   phosphorothioate; solid phase synthesis; modified oligonucleotide;
KW   clinical diagnostic; cancer treatment; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .14
```

```
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate deoxynucleotides"
XX
PN   DE10051726-A1.
XX
PD   10-MAY-2001.
XX
PF   18-OCT-2000; 2000DE-01051726.
XX
PR   30-OCT-1999;   99DE-01052376.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Seliger H,  Sobkowski M,  Hinz M;
XX
DR   WPI; 2001-336414/36.
XX
PT   Intermediate for oligonucleotide synthesis comprises partially hydrolysed
PT   cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
XX
PS   Example 2; Page 5; 8pp; German.
XX
CC   This invention describes a novel chemical product comprising a partially
CC   hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
CC   with nucleotide derivative(s). The product is an intermediate for the
CC   large (gram) scale solid phase synthesis of modified oligonucleotides
CC   useful e.g. as clinical diagnostics and therapeutics, e.g. for the
CC   treatment of AIDS and cancers. The presence of the partially hydrolysed
CC   copolymer facilitates the synthesis of larger amounts of oligonucleotides
CC   compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
CC   described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
CC   Oligonucleotides are obtained in very good quality and high yields, Also,
CC   the nucleosides do not display the reduced activity seen in some prior
CC   art procedures, less carrier material, reagents and solvent are required.
CC   Further, the carrier material is biodegradable and thus does not present
CC   disposal problems. It also swells uniformly in a range of solvents, which
CC   obviates expansion or contraction during use or solvent exchange.
CC   AAH20510-AAH20513 represent oligonucleotides containing modified
CC   deoxynucleotides which are used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3189
AAF16603/c
ID   AAF16603 standard; DNA; 15 BP.
XX
AC   AAF16603;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.
XX
KW   Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW   stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW   DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
XX
PN   WO200071164-A1.
XX
PD   30-NOV-2000.
XX
PF   24-MAY-2000; 2000WO-AU000498.
XX
PR   24-MAY-1999;   99AU-00000510.
XX
PA   (TACH/) TACHAS G.
XX
PI   Tachas G;
XX
DR   WPI; 2001-025093/03.
XX
PT   Treating gastric acid disturbance by administering an oligonucleotide
PT   which modulates the activity of a polypeptide involved in gastric acid
PT   production or secretion.
XX
PS   Example 3; Page 148; 164pp; English.
XX
CC   The present invention provides oligonucleotides, and methods for their
CC   use, which are useful in modulating the action of proteins involved in
CC   gastric acid production. The target protein is preferably the histamine
CC   H2 receptor or one of the proteins which form part of the gastric proton
CC   pump. The sequences and methods of the invention are useful in the
CC   treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC   duodenal ulcers and other gastric acid disturbances, most of which are
CC   caused by Helicobacter pylori
XX
SQ   Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTA 1


RESULT 3190
AAH49243
ID   AAH49243 standard; DNA; 15 BP.
XX
AC   AAH49243;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #7.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   9
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "t-but"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "t-hex"
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
```

```
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 26; Page 40; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3191
AAH49243/c
ID   AAH49243 standard; DNA; 15 BP.
XX
AC   AAH49243;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #7.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   9
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "t-but"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "t-hex"
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 26; Page 40; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
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                    ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3192
ABL40743
ID   ABL40743 standard; DNA; 15 BP.
XX
AC   ABL40743;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.
XX
KW   Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;
KW   anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
XX
OS   Gallus gallus.
XX
PN   US2002034810-A1.
XX
PD   21-MAR-2002.
XX
PF   16-AUG-2001; 2001US-00930218.
XX
PR   20-SEP-2000; 2000US-00666390.
XX
PA   (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX
PI   Goldshmidt O,  Pecker I,  Vlodavsky I,  Michal I,  Zcharia E;
XX
DR   WPI; 2002-338926/37.
XX
PT   Nucleic acid encoding avian and reptile heparanase polypeptide is useful
PT   to treat various heparin-related disorders and the signal peptide is
PT   useful in production of membrane-targeted or secreted recombinant
PT   proteins.
XX
PS   Disclosure; Page 13; 39pp; English.
XX
CC   The invention relates to an isolated avian and reptile nucleic acid,
CC   encoding a polypeptide with heparanase catalytic activity. The signal
CC   peptide of the nucleic acid can be used to express membrane-associated or
CC   secreted proteins in heterologous expression systems. The encoded
CC   polypeptides can be used to prevent tumour angiogenesis, metastasis and
CC   invasion, and to intervene with pathologies associated with impaired
CC   heparin-binding growth factors, cellular responses to heparin-binding
CC   growth factors and cytokines, cell interaction with plasma lipoproteins,
CC   cellular susceptibility to viral, protozoa and bacterial infections or
CC   disintegration of neurodegenerative plaques. The present sequence
CC   represents a chicken heparanase (hpa) cDNA cloning oligo dT(15) primer
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3193
ABL40743/c
ID   ABL40743 standard; DNA; 15 BP.
XX
AC   ABL40743;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.
XX
KW   Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;
KW   anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
XX
OS   Gallus gallus.
XX
PN   US2002034810-A1.
XX
PD   21-MAR-2002.
XX
PF   16-AUG-2001; 2001US-00930218.
XX
PR   20-SEP-2000; 2000US-00666390.
XX
PA   (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX
PI   Goldshmidt O,  Pecker I,  Vlodavsky I,  Michal I,  Zcharia E;
XX
DR   WPI; 2002-338926/37.
XX
PT   Nucleic acid encoding avian and reptile heparanase polypeptide is useful
PT   to treat various heparin-related disorders and the signal peptide is
PT   useful in production of membrane-targeted or secreted recombinant
PT   proteins.
XX
PS   Disclosure; Page 13; 39pp; English.
XX
CC   The invention relates to an isolated avian and reptile nucleic acid,
CC   encoding a polypeptide with heparanase catalytic activity. The signal
CC   peptide of the nucleic acid can be used to express membrane-associated or
CC   secreted proteins in heterologous expression systems. The encoded
CC   polypeptides can be used to prevent tumour angiogenesis, metastasis and
CC   invasion, and to intervene with pathologies associated with impaired
CC   heparin-binding growth factors, cellular responses to heparin-binding
CC   growth factors and cytokines, cell interaction with plasma lipoproteins,
CC   cellular susceptibility to viral, protozoa and bacterial infections or
CC   disintegration of neurodegenerative plaques. The present sequence
CC   represents a chicken heparanase (hpa) cDNA cloning oligo dT(15) primer
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3194
ABA97403
ID   ABA97403 standard; DNA; 15 BP.
XX
AC   ABA97403;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Nucleotide sequence of oligomer # 10 used to compare mismatches.
XX
KW   Protein nucleic acid molecule; PNA; ds.
XX
OS   Synthetic.
XX
PN   WO200168673-A1.
XX
PD   20-SEP-2001.
XX
PF   13-MAR-2001; 2001WO-US008111.
XX
PR   14-MAR-2000; 2000US-0189190P.
PR   30-NOV-2000; 2000US-0250334P.
XX
PA   (ACTI-) ACTIVE MOTIF.
```

```
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeacon J;
PI   Chakhmakhcheau O,  Buryakova A,  Choob M,  Hondorp K;
XX
DR   WPI; 2002-041177/05.
XX
PT   Oligonucleotides analogs useful in detection, separation and purification
PT   of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS   Example 20; Page 123; 197pp; English.
XX
CC   This invention relates to oligonucleotide analogues comprising a protein
CC   nucleic acid molecule (PNA) monomer. They are used in the detection and
CC   separation of nucleic acid molecules and as probes, primers, linkers,
CC   adapters and antisense agents on solid supports. Modifications enhance
CC   their use as capture and detection probes e.g. by the incorporation of
CC   biotin, digoxigenen, radioisotopes, fluorescent labels such as
CC   fluorescein and reporter molecules such as alkaline phosphatase. They are
CC   also used for enhancing or inhibiting the activity of an enzyme or
CC   cellular activity. The compounds are stable to nucleases and proteases,
CC   have high affinity, binding specificity and solubility. The polyamide
CC   backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC   nucleic acid molecules with greater affinity than DNA or RNA
CC   concentration. The compounds are relatively simple to synthesize and are
CC   used in a wide variety of applications. This sequence represents a DNA
CC   oligomer which is used to represent the effect of single base mismatches
CC   on oligonucleotides
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3195
ABA97403/c
ID   ABA97403 standard; DNA; 15 BP.
XX
AC   ABA97403;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Nucleotide sequence of oligomer # 10 used to compare mismatches.
XX
KW   Protein nucleic acid molecule; PNA; ds.
XX
OS   Synthetic.
XX
PN   WO200168673-A1.
XX
PD   20-SEP-2001.
XX
PF   13-MAR-2001; 2001WO-US008111.
XX
PR   14-MAR-2000; 2000US-0189190P.
PR   30-NOV-2000; 2000US-0250334P.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeacon J;
PI   Chakhmakhcheau O,  Buryakova A,  Choob M,  Hondorp K;
XX
DR   WPI; 2002-041177/05.
XX
PT   Oligonucleotides analogs useful in detection, separation and purification
PT   of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS   Example 20; Page 123; 197pp; English.
XX
CC   This invention relates to oligonucleotide analogues comprising a protein
CC   nucleic acid molecule (PNA) monomer. They are used in the detection and
CC   separation of nucleic acid molecules and as probes, primers, linkers,
CC   adapters and antisense agents on solid supports. Modifications enhance
CC   their use as capture and detection probes e.g. by the incorporation of
CC   biotin, digoxigenen, radioisotopes, fluorescent labels such as
CC   fluorescein and reporter molecules such as alkaline phosphatase. They are
CC   also used for enhancing or inhibiting the activity of an enzyme or
CC   cellular activity. The compounds are stable to nucleases and proteases,
CC   have high affinity, binding specificity and solubility. The polyamide
CC   backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC   nucleic acid molecules with greater affinity than DNA or RNA
CC   concentration. The compounds are relatively simple to synthesize and are
CC   used in a wide variety of applications. This sequence represents a DNA
CC   oligomer which is used to represent the effect of single base mismatches
CC   on oligonucleotides
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3196
AAL49453
ID   AAL49453 standard; DNA; 15 BP.
XX
AC   AAL49453;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
XX
KW   Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW   protein production; cancer; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15
FT                   /*tag=  a
FT                   /product= "tag peptide"
FT                   /partial
FT                   /note= "no start or stop"
XX
PN   WO200266675-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-EP001651.
XX
PR   16-FEB-2001; 2001DE-01007317.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Kahmann S,  Mueller O;
XX
DR   WPI; 2002-674959/72.
DR   P-PSDB; AAO19054.
XX
PT   Detecting mutations in nucleic acid, useful for diagnosis and
PT   characterization of tumors, by amplification, in vitro transcription and
PT   translation, then protein detection.
XX
PS   Claim 11; Fig 5; 62pp; German.
XX
CC   The present invention relates to a method of detecting mutations in a
```

```
CC   nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC   amplicon, in vitro transcription and translation of this amplicon, and
CC   detection of the translated protein. The primers used for amplification
CC   are designed to produce an amplicon that is translatable and allows
CC   differentiation between translation products of wild-type and mutated
CC   nucleic acids. The method is used to detect mutations in tumour
CC   suppressor genes, for (early) diagnosis, monitoring and characterisation
CC   of tumours (especially of bladder and intestines) and in the germ line
CC   (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC   is used to detect or verify the reading frame of a nucleic acid cloned in
CC   it, and to determine the suitability of detectable peptides for analysis
CC   and/or purification of a recombinant protein, expressed from a sequence
CC   cloned in the vector. The present sequence encodes a tag peptide and was
CC   used in the invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3197
AAL49453/c
ID   AAL49453 standard; DNA; 15 BP.
XX
AC   AAL49453;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
XX
KW   Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW   protein production; cancer; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15
FT                   /*tag=  a
FT                   /product= "tag peptide"
FT                   /partial
FT                   /note= "no start or stop"
XX
PN   WO200266675-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-EP001651.
XX
PR   16-FEB-2001; 2001DE-01007317.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Kahmann S,  Mueller O;
XX
DR   WPI; 2002-674959/72.
DR   P-PSDB; AAO19054.
XX
PT   Detecting mutations in nucleic acid, useful for diagnosis and
PT   characterization of tumors, by amplification, in vitro transcription and
PT   translation, then protein detection.
XX
PS   Claim 11; Fig 5; 62pp; German.
XX
CC   The present invention relates to a method of detecting mutations in a
CC   nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC   amplicon, in vitro transcription and translation of this amplicon, and
CC   detection of the translated protein. The primers used for amplification
CC   are designed to produce an amplicon that is translatable and allows
CC   differentiation between translation products of wild-type and mutated
CC   nucleic acids. The method is used to detect mutations in tumour
CC   suppressor genes, for (early) diagnosis, monitoring and characterisation
CC   of tumours (especially of bladder and intestines) and in the germ line
CC   (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC   is used to detect or verify the reading frame of a nucleic acid cloned in
CC   it, and to determine the suitability of detectable peptides for analysis
CC   and/or purification of a recombinant protein, expressed from a sequence
CC   cloned in the vector. The present sequence encodes a tag peptide and was
CC   used in the invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3198
AAL49455
ID   AAL49455 standard; DNA; 15 BP.
XX
AC   AAL49455;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
XX
KW   Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW   protein production; cancer; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15
FT                   /*tag=  a
FT                   /product= "tag peptide"
FT                   /partial
FT                   /note= "no start or stop"
XX
PN   WO200266675-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-EP001651.
XX
PR   16-FEB-2001; 2001DE-01007317.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Kahmann S,  Mueller O;
XX
DR   WPI; 2002-674959/72.
DR   P-PSDB; AAO19056.
XX
PT   Detecting mutations in nucleic acid, useful for diagnosis and
PT   characterization of tumors, by amplification, in vitro transcription and
PT   translation, then protein detection.
XX
PS   Claim 11; Fig 5; 62pp; German.
XX
CC   The present invention relates to a method of detecting mutations in a
CC   nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC   amplicon, in vitro transcription and translation of this amplicon, and
CC   detection of the translated protein. The primers used for amplification
CC   are designed to produce an amplicon that is translatable and allows
CC   differentiation between translation products of wild-type and mutated
CC   nucleic acids. The method is used to detect mutations in tumour
```

```
CC   suppressor genes, for (early) diagnosis, monitoring and characterisation
CC   of tumours (especially of bladder and intestines) and in the germ line
CC   (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC   is used to detect or verify the reading frame of a nucleic acid cloned in
CC   it, and to determine the suitability of detectable peptides for analysis
CC   and/or purification of a recombinant protein, expressed from a sequence
CC   cloned in the vector. The present sequence encodes a tag peptide and was
CC   used in the invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3199
AAL49455/c
ID   AAL49455 standard; DNA; 15 BP.
XX
AC   AAL49455;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
XX
KW   Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW   protein production; cancer; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15
FT                   /*tag=  a
FT                   /product= "tag peptide"
FT                   /partial
FT                   /note= "no start or stop"
XX
PN   WO200266675-A2.
XX
PD   29-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-EP001651.
XX
PR   16-FEB-2001; 2001DE-01007317.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Kahmann S,  Mueller O;
XX
DR   WPI; 2002-674959/72.
DR   P-PSDB; AAO19056.
XX
PT   Detecting mutations in nucleic acid, useful for diagnosis and
PT   characterization of tumors, by amplification, in vitro transcription and
PT   translation, then protein detection.
XX
PS   Claim 11; Fig 5; 62pp; German.
XX
CC   The present invention relates to a method of detecting mutations in a
CC   nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC   amplicon, in vitro transcription and translation of this amplicon, and
CC   detection of the translated protein. The primers used for amplification
CC   are designed to produce an amplicon that is translatable and allows
CC   differentiation between translation products of wild-type and mutated
CC   nucleic acids. The method is used to detect mutations in tumour
CC   suppressor genes, for (early) diagnosis, monitoring and characterisation
CC   of tumours (especially of bladder and intestines) and in the germ line
CC   (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC   is used to detect or verify the reading frame of a nucleic acid cloned in
CC   it, and to determine the suitability of detectable peptides for analysis
CC   and/or purification of a recombinant protein, expressed from a sequence
CC   cloned in the vector. The present sequence encodes a tag peptide and was
CC   used in the invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3200
AAD29506
ID   AAD29506 standard; DNA; 15 BP.
XX
AC   AAD29506;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Primer used for the expression of adipocytes in human preadipose cells.
XX
KW   Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
KW   diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200206450-A1.
XX
PD   24-JAN-2002.
XX
PF   13-JUL-2001; 2001WO-EP008165.
XX
PR   18-JUL-2000; 2000EP-00115489.
XX
PA   (NEST ) SOC PROD NESTLE SA.
XX
PI   Darimont C,  Mace K,  Pfeifer A;
XX
DR   WPI; 2002-188539/24.
XX
PT   New human pre-adipose cell line capable of differentiating to adipose
PT   cells, useful in developing drug, food ingredients, and supplements
PT   against obesity, diabetes and cardiovascular diseases.
XX
PS   Example 5; Page 10; 30pp; English.
XX
CC   The present invention relates to new human pre-adipose cell lines capable
CC   to differentiate to white adipose cells, exhibiting essentially the same
CC   cellular properties of normal white adipose cells. The human pre-adipose
CC   cell lines are useful for the identification of substances controlling
CC   the regulation of lipid uptake and release by human white adipocytes, and
CC   substances controlling the differentiation of preadipocytes into mature
CC   adipocytes. They are useful for screening compounds capable to regulate
CC   the secretion of any metabolites or hormones from human white adipocytes.
CC   Sequences of the invention are useful for developing drugs, food
CC   ingredients and supplements against obesity, diabetes and cardio-
CC   vascular diseases. The present DNA sequence is a reverse transcription
CC   (RT)-PCR primer which is used for the expression of adipocytes in
CC   differentiated immortalised human preadipose cells. This primer is used
CC   in the exemplification of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3201
AAD29506/c
ID   AAD29506 standard; DNA; 15 BP.
XX
AC   AAD29506;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Primer used for the expression of adipocytes in human preadipose cells.
XX
KW   Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
KW   diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200206450-A1.
XX
PD   24-JAN-2002.
XX
PF   13-JUL-2001; 2001WO-EP008165.
XX
PR   18-JUL-2000; 2000EP-00115489.
XX
PA   (NEST ) SOC PROD NESTLE SA.
XX
PI   Darimont C,  Mace K,  Pfeifer A;
XX
DR   WPI; 2002-188539/24.
XX
PT   New human pre-adipose cell line capable of differentiating to adipose
PT   cells, useful in developing drug, food ingredients, and supplements
PT   against obesity, diabetes and cardiovascular diseases.
XX
PS   Example 5; Page 10; 30pp; English.
XX
CC   The present invention relates to new human pre-adipose cell lines capable
CC   to differentiate to white adipose cells, exhibiting essentially the same
CC   cellular properties of normal white adipose cells. The human pre-adipose
CC   cell lines are useful for the identification of substances controlling
CC   the regulation of lipid uptake and release by human white adipocytes, and
CC   substances controlling the differentiation of preadipocytes into mature
CC   adipocytes. They are useful for screening compounds capable to regulate
CC   the secretion of any metabolites or hormones from human white adipocytes.
CC   Sequences of the invention are useful for developing drugs, food
CC   ingredients and supplements against obesity, diabetes and cardio-
CC   vascular diseases. The present DNA sequence is a reverse transcription
CC   (RT)-PCR primer which is used for the expression of adipocytes in
CC   differentiated immortalised human preadipose cells. This primer is used
CC   in the exemplification of the invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3202
AAD22531
ID   AAD22531 standard; RNA; 15 BP.
XX
AC   AAD22531;
XX
DT   29-AUG-2003  (revised)
DT   07-AUG-2003  (revised)
DT   12-FEB-2002  (first entry)
XX
DE   Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
XX
KW   RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
KW   virucide; oncogene; cancer; transcription; translation; leukaemia virus;
KW   hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
KW   poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
XX
OS   unidentified retrovirus.
OS   Unidentified.
XX
PN   US6291438-B1.
XX
PD   18-SEP-2001.
XX
PF   06-OCT-1998;   98US-00167375.
XX
PR   24-FEB-1993;   93US-00022055.
PR   23-FEB-1994;   94US-00200650.
PR   22-FEB-1996;   96US-00604871.
XX
PA   (WANG/) WANG J H.
XX
PI   Wang JH;
XX
DR   WPI; 2002-009339/01.
XX
PT   Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
PT   reverse transcriptase comprises at the 2'-O position of the
PT   oligoribonucleotide, a hydrophobic carrier reagent containing a poly
PT   substituted phenyl compound.
XX
PS   Example 3; Col 24; 56pp; English.
XX
CC   The invention relates to derivatised antisense oligoribonucleotides with
CC   enhanced membrane permeability and stability. The derivatised antisense
CC   oligoribonucleotide complementary to a sequence of nucleotides found in a
CC   virus or a cell is useful for inhibiting e.g., viral reverse
CC   transcriptase. Derivatised antisense oligoribonucleotide is conjugated at
CC   the 2'-O position with a hydrophobic carrier reagent containing a poly
CC   substituted phenyl compound. The derivatised oligoribonucleotides are
CC   used to decrease the expression of oncogenes and thereby decrease the
CC   expression of cancer cells which rely upon oncogene expression for their
CC   phenotypic and pathological properties. The oligoribonucleotides are also
CC   used for increasing the effectiveness of antisense oligonucleotide
CC   targetted to a gene associated with a disease or a condition in an
CC   animal. To alter gene transcription and/or translation for any gene or
CC   gene segment responsible for expression, to inhibit viral reverse
CC   transcriptase, to inhibit the expression of leukaemia virus, hepatitis
CC   virus, oncogenes and human immunodeficiency virus. The present sequence
CC   is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
CC   which is used in the treatment of moloney murine leukaemia virus (MuLV)
CC   in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-
CC   AUG-2003 to standardise OS field)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3203
AAD22531/c
ID   AAD22531 standard; RNA; 15 BP.
```

```
XX
AC   AAD22531;
XX
DT   29-AUG-2003  (revised)
DT   07-AUG-2003  (revised)
DT   12-FEB-2002  (first entry)
XX
DE   Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
XX
KW   RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
KW   virucide; oncogene; cancer; transcription; translation; leukaemia virus;
KW   hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A];
KW   poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
XX
OS   unidentified retrovirus.
OS   Unidentified.
XX
PN   US6291438-B1.
XX
PD   18-SEP-2001.
XX
PF   06-OCT-1998;   98US-00167375.
XX
PR   24-FEB-1993;   93US-00022055.
PR   23-FEB-1994;   94US-00200650.
PR   22-FEB-1996;   96US-00604871.
XX
PA   (WANG/) WANG J H.
XX
PI   Wang JH;
XX
DR   WPI; 2002-009339/01.
XX
PT   Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
PT   reverse transcriptase comprises at the 2'-O position of the
PT   oligoribonucleotide, a hydrophobic carrier reagent containing a poly
PT   substituted phenyl compound.
XX
PS   Example 3; Col 24; 56pp; English.
XX
CC   The invention relates to derivatised antisense oligoribonucleotides with
CC   enhanced membrane permeability and stability. The derivatised antisense
CC   oligoribonucleotide complementary to a sequence of nucleotides found in a
CC   virus or a cell is useful for inhibiting e.g., viral reverse
CC   transcriptase. Derivatised antisense oligoribonucleotide is conjugated at
CC   the 2'-O position with a hydrophobic carrier reagent containing a poly
CC   substituted phenyl compound. The derivatised oligoribonucleotides are
CC   used to decrease the expression of oncogenes and thereby decrease the
CC   expression of cancer cells which rely upon oncogene expression for their
CC   phenotypic and pathological properties. The oligoribonucleotides are also
CC   used for increasing the effectiveness of antisense oligonucleotide
CC   targetted to a gene associated with a disease or a condition in an
CC   animal. To alter gene transcription and/or translation for any gene or
CC   gene segment responsible for expression, to inhibit viral reverse
CC   transcriptase, to inhibit the expression of leukaemia virus, hepatitis
CC   virus, oncogenes and human immunodeficiency virus. The present sequence
CC   is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
CC   which is used in the treatment of moloney murine leukaemia virus (MuLV)
CC   in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-
CC   AUG-2003 to standardise OS field)
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3204
ABQ82140
ID   ABQ82140 standard; DNA; 15 BP.
XX
AC   ABQ82140;
XX
DT   11-DEC-2002  (first entry)
XX
DE   Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.
XX
KW   Chimeric nucleic acid construct; recombinational cloning; silencing;
KW   recombination site; double stranded RNA; plant; ds.
XX
OS   Synthetic.
XX
PN   WO200259294-A1.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-AU000073.
XX
PR   26-JAN-2001; 2001US-0264067P.
PR   29-NOV-2001; 2001US-0333743P.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Wesley S,  Waterhouse P,  Helliwell C;
XX
DR   WPI; 2002-682669/73.
XX
PT   New vectors comprising operably linked DNA fragments having an origin of
PT   replication, a selectable marker and a chimeric DNA construct, useful for
PT   silencing target nucleic acids and for producing large amounts of double-
PT   stranded RNA.
XX
PS   Claim 14; Page 74; 104pp; English.
XX
CC   The present invention describes a vector (I) comprising operably linked
CC   DNA fragments having: (a) origin of replication allowing replication in a
CC   recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC   selectable marker region capable of being expressed in the recipient cell
CC   ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC   region capable of being recognized by RNA polymerases of a eukaryotic
CC   cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC   fourth recombination sites; (iii) 3' transcription terminating and
CC   polyadenylation region functional in the eukaryotic cell. The first and
CC   fourth recombination sites, or the second and third recombination sites
CC   are capable of reacting with a same recombination site, and preferably
CC   are identical. The first and second recombination sites, or the third and
CC   fourth recombination sites, do not recombine with each other or with a
CC   same recombination site. The vector is useful for producing large amounts
CC   of double-stranded RNA which can be used for silencing target nucleic
CC   acid sequences. The vectors can also be used to convert a DNA fragment
CC   into an inverted repeat structure. Plants transformed with a vector from
CC   the present invention can be used in a conventional breeding scheme to
CC   produce more plants with the same characteristics or to introduce a
CC   chimeric gene for reduction of the phenotypic expression of nucleic
CC   acids. The present sequence represents an acceptor vector nucleotide
CC   sequence from the present invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
             |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3205
ABQ82140/c
ID   ABQ82140 standard; DNA; 15 BP.
```

```
XX
AC   ABQ82140;
XX
DT   11-DEC-2002  (first entry)
XX
DE   Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.
XX
KW   Chimeric nucleic acid construct; recombinational cloning; silencing;
KW   recombination site; double stranded RNA; plant; ds.
XX
OS   Synthetic.
XX
PN   WO200259294-A1.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-AU000073.
XX
PR   26-JAN-2001; 2001US-0264067P.
PR   29-NOV-2001; 2001US-0333743P.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Wesley S,  Waterhouse P,  Helliwell C;
XX
DR   WPI; 2002-682669/73.
XX
PT   New vectors comprising operably linked DNA fragments having an origin of
PT   replication, a selectable marker and a chimeric DNA construct, useful for
PT   silencing target nucleic acids and for producing large amounts of double-
PT   stranded RNA.
XX
PS   Claim 14; Page 74; 104pp; English.
XX
CC   The present invention describes a vector (I) comprising operably linked
CC   DNA fragments having: (a) origin of replication allowing replication in a
CC   recipient cell, preferably in bacteria such as Escherichia coli; (b)
CC   selectable marker region capable of being expressed in the recipient cell
CC   ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
CC   region capable of being recognized by RNA polymerases of a eukaryotic
CC   cell or by prokaryotic RNA polymerase; (ii) first, second, third and
CC   fourth recombination sites; (iii) 3' transcription terminating and
CC   polyadenylation region functional in the eukaryotic cell. The first and
CC   fourth recombination sites, or the second and third recombination sites
CC   are capable of reacting with a same recombination site, and preferably
CC   are identical. The first and second recombination sites, or the third and
CC   fourth recombination sites, do not recombine with each other or with a
CC   same recombination site. The vector is useful for producing large amounts
CC   of double-stranded RNA which can be used for silencing target nucleic
CC   acid sequences. The vectors can also be used to convert a DNA fragment
CC   into an inverted repeat structure. Plants transformed with a vector from
CC   the present invention can be used in a conventional breeding scheme to
CC   produce more plants with the same characteristics or to introduce a
CC   chimeric gene for reduction of the phenotypic expression of nucleic
CC   acids. The present sequence represents an acceptor vector nucleotide
CC   sequence from the present invention
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3206
ABX00240
ID   ABX00240 standard; RNA; 15 BP.
XX
AC   ABX00240;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 21; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 3207
ABX00240/c
ID   ABX00240 standard; RNA; 15 BP.
XX
AC   ABX00240;
XX
DT   23-DEC-2002  (first entry)
```

```
XX
DE   Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 21; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3208
ABX03406
ID   ABX03406 standard; RNA; 15 BP.
XX
AC   ABX03406;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 64; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 1.6e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              :::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 3209
ABX03406/c
ID   ABX03406 standard; RNA; 15 BP.
XX
AC   ABX03406;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
```

```
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 64; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3210
ABL57064
ID   ABL57064 standard; DNA; 15 BP.
XX
AC   ABL57064;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)methyl)isophthalate, synthetic branching
FT                   amidite"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 4; Page 44; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O35, which was produced in an
CC   example from the invention and which includes a synthetic branching
CC   amidite compound. The invention describes an improved process for
CC   immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3211
ABL57064/c
ID   ABL57064 standard; DNA; 15 BP.
XX
AC   ABL57064;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O35.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)methyl)isophthalate, synthetic branching
FT                   amidite"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 4; Page 44; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O35, which was produced in an
CC   example from the invention and which includes a synthetic branching
CC   amidite compound. The invention describes an improved process for
CC   immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3212
ABL57054
ID   ABL57054 standard; DNA; 15 BP.
XX
AC   ABL57054;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide phosphoramidite oligonucleotide O9.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)-N'-tritylhexanohydrazide"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 2; Page 40; 120pp; English.
XX
CC   The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC   15-mer, designated oligo O9, which was produced in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3213
ABL57054/c
ID   ABL57054 standard; DNA; 15 BP.
XX
AC   ABL57054;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide phosphoramidite oligonucleotide O9.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
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```
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)-N'-tritylhexanohydrazide"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
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PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 2; Page 40; 120pp; English.
XX
CC   The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC   15-mer, designated oligo O9, which was produced in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3214
ABL57063
ID   ABL57063 standard; DNA; 15 BP.
XX
AC   ABL57063;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O39.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
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FT                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzyloxy)-5
FT                   -((2'-cyanoethyl)(diisopropylamino) phosphanyloxymethyl)-
FT                   benzene"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O39, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3215
ABL57063/c
ID   ABL57063 standard; DNA; 15 BP.
XX
AC   ABL57063;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O39.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
```

```
FT                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzyloxy)-5
FT                   -((2'-cyanoethyl)(diisopropylamino) phosphanyloxymethyl)-
FT                   benzene"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo 039, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3216
ABL57066
ID   ABL57066 standard; DNA; 15 BP.
XX
AC   ABL57066;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Amino-C6 modification"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 12; Page 57; 120pp; English.
XX
CC   The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
CC   oligonucleotide that was used in a comparison of hydrazine and amine
CC   attachment moieties on active ester surfaces in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3217
ABL57066/c
ID   ABL57066 standard; DNA; 15 BP.
XX
AC   ABL57066;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Amino-C6 modification"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
```

```
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 12; Page 57; 120pp; English.
XX
CC   The present sequence is of an amino-C6-modified and Cy3 dye labeled T15
CC   oligonucleotide that was used in a comparison of hydrazine and amine
CC   attachment moieties on active ester surfaces in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3218
ABL57059
ID   ABL57059 standard; DNA; 15 BP.
XX
AC   ABL57059;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O33.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "4-((2-cyanoethyl)(diisopropylamino)
FT                   phosphanyloxymethyl)-benzoic acid methyl ester"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
```

```
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O33, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3219
ABL57059/c
ID   ABL57059 standard; DNA; 15 BP.
XX
AC   ABL57059;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O33.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "4-((2-cyanoethyl)(diisopropylamino)
FT                   phosphanyloxymethyl)-benzoic acid methyl ester"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
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PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O33, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3220
ABL57061
ID   ABL57061 standard; DNA; 15 BP.
XX
AC   ABL57061;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT                   phenylcarbonylamido)-2-((2''-cyanoethyloxy)
FT                   (diisopropyl)amino)-phosphanyloxy)-propane"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
```

```
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O37, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3221
ABL57061/c
ID   ABL57061 standard; DNA; 15 BP.
XX
AC   ABL57061;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O37.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT                   phenylcarbonylamido)-2-((2''-cyanoethyloxy)
FT                   (diisopropyl)amino)-phosphanyloxy)-propane"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
```

```
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O37, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3222
ABL57056
ID   ABL57056 standard; DNA; 15 BP.
XX
AC   ABL57056;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide phosphoramidite oligonucleotide O31.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)-N'-tritylhexanohydrazide"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 2; Page 40; 120pp; English.
XX
CC   The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC   15-mer, designated oligo O31, which was produced in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3223
ABL57056/c
ID   ABL57056 standard; DNA; 15 BP.
XX
AC   ABL57056;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide phosphoramidite oligonucleotide O31.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "6-((2Cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)-N'-tritylhexanohydrazide"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
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PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 2; Page 40; 120pp; English.
XX
CC   The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC   15-mer, designated oligo O31, which was produced in an example from the
CC   invention. The invention describes an improved process for immobilisation
CC   of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC   RNA and peptides, especially macromolecules containing multiple reactive
CC   sites, to a substrate surface or other conjugation target. It also
CC   describes the preparation of oligos containing one or more hydrazides,
CC   which can be used for conjugation to surface binding moieties, or for
CC   other conjugation reactions. The process is useful e.g. in nucleic acid
CC   hybridisation based assays, DNA chip technology and biosensor
CC   applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3224
ABL57060
ID   ABL57060 standard; DNA; 15 BP.
XX
AC   ABL57060;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O34.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)methyl)isophthalate"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O34, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3225
ABL57060/c
ID   ABL57060 standard; DNA; 15 BP.
XX
AC   ABL57060;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Hydrazide precursor phosphoramidite oligonucleotide O34.
XX
KW   Macromolecule; hydrazide; immobilisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  b
FT                   /note= "phosphoramidite linkage"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Diethyl 5-(((2-cyanoethoxy)(diisopropylamino)
FT                   phosphanyloxy)methyl)isophthalate"
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3' Cy3 dye"
XX
PN   WO200214558-A2.
XX
PD   21-FEB-2002.
XX
PF   10-AUG-2001; 2001WO-US041663.
XX
```

```
PR   11-AUG-2000; 2000WO-US022205.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Raddatz S,  Mueller-Ibeler J,  Schweitzer M,  Bruecher C,  Windhab N;
PI   Havens JR,  Onofrey TJ,  Greef CH,  Wang D;
XX
DR   WPI; 2002-404476/43.
XX
PT   Compound for binding macromolecule to substrate surface or conjugation
PT   targets, contains phosphorous containing reactive group, hydrazide
PT   protecting group and benzene ring, and has predefined formula.
XX
PS   Example 3; Page 43; 120pp; English.
XX
CC   The present sequence is of a hydrazine treated hydrazide precursor
CC   phosphoramidite 15-mer, designated oligo O34, which was produced in an
CC   example from the invention. The invention describes an improved process
CC   for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC   acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC   multiple reactive sites, to a substrate surface or other conjugation
CC   target. It also describes the preparation of oligos containing one or
CC   more hydrazides, which can be used for conjugation to surface binding
CC   moieties, or for other conjugation reactions. The process is useful e.g.
CC   in nucleic acid hybridisation based assays, DNA chip technology and
CC   biosensor applications
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3226
ABK98141
ID   ABK98141 standard; DNA; 15 BP.
XX
AC   ABK98141;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Triple helix forming associated oligonucleotide #26.
XX
KW   Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW   gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW   pathogenic bacteria; virus; replication; virulence; cancer;
KW   oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS   Synthetic.
XX
PN   US6403302-B1.
XX
PD   11-JUN-2002.
XX
PF   16-DEC-1993;   93US-00168920.
XX
PR   17-SEP-1992;   92US-00946976.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Dervan PB,  Beal PA;
XX
DR   WPI; 2002-536030/57.
XX
PT   A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT   oligonucleotide which binds in parallel and antiparallel orientation,
PT   respectively, for targetting sequences on alternate strands of DHNA to
PT   control gene expression.
XX
PS   Example 1; Fig 3B; 108pp; English.
XX
CC   The present invention relates to methods and oligonucleotides for forming
CC   a triple-helix comprising a double helical nucleic acid comprising first
CC   and second substantially complementary strands, and an oligonucleotide
CC   bound to a purine-rich target sequence within the double helical nucleic
CC   acid, where the oligonucleotide binds in a parallel and antiparallel
CC   orientation, respectively, to target sequences on alternate strands of
CC   the double helical nucleic acid. The method has therapeutic applications,
CC   where gene expression is controlled by selective triple-helix formation
CC   within expression regulatory sequences of a target gene. The
CC   oligonucleotides can be used to form triple-helices, and are useful to
CC   detect the presence or absence of specific sequences within genomic DNA
CC   for diagnostic and therapeutic purposes. The oligonucleotides can be
CC   selected to specifically bind to pathogenic double-stranded DNA including
CC   specific sequences required by pathogenic bacteria or viruses for
CC   replication or virulence, reducing their pathogenicity. Alternatively,
CC   the oligonucleotide can be chosen to target a unique sequence of the
CC   pathogen which is not found in the genome of pathogen's host. The
CC   oligonucleotides can be used in cancer treatment by way of triple-helix
CC   suppression of specific oncogenes including those of endogenous or viral
CC   origin. Such therapeutic oligonucleotides are capable of forming triple-
CC   helices with such sequences in cancerous cells containing the activated
CC   oncogene, so preferentially killing or repressing the cancer causing
CC   cell. The present sequence represents an oligonucleotide used in the
CC   methods of the present invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3227
ABK98141/c
ID   ABK98141 standard; DNA; 15 BP.
XX
AC   ABK98141;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Triple helix forming associated oligonucleotide #26.
XX
KW   Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW   gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW   pathogenic bacteria; virus; replication; virulence; cancer;
KW   oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS   Synthetic.
XX
PN   US6403302-B1.
XX
PD   11-JUN-2002.
XX
PF   16-DEC-1993;   93US-00168920.
XX
PR   17-SEP-1992;   92US-00946976.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Dervan PB,  Beal PA;
XX
DR   WPI; 2002-536030/57.
XX
PT   A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT   oligonucleotide which binds in parallel and antiparallel orientation,
PT   respectively, for targetting sequences on alternate strands of DHNA to
```

PT control gene expression.
XX
PS Example 1; Fig 3B; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3228
ABK98184
ID ABK98184 standard; DNA; 15 BP.
XX
AC ABK98184;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #48.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3229
ABK98184/c
ID ABK98184 standard; DNA; 15 BP.
XX
AC ABK98184;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #48.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an

PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3230
ABZ96319
ID ABZ96319 standard; DNA; 15 BP.
XX
AC ABZ96319;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human C/EBP antisense fragment no.2179.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11561; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 15 BP; 0 A; 4 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3231
ABZ37501
ID ABZ37501 standard; DNA; 15 BP.
XX
AC ABZ37501;
XX
DT 18-FEB-2003 (first entry)
XX
DE Oligonucleotide SEQ ID NO:622.
XX
KW Library; cleavage; display; diverse family; ss.
XX
OS Synthetic.
XX
PN WO200283872-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012405.
XX
PR 17-APR-2001; 2001US-00837306.
PR 24-OCT-2001; 2001US-00000516.
PR 25-OCT-2001; 2001US-00045674.
XX
PA (LADN/) LADNER R C.
PA (COHE/) COHEN E H.
PA (NAST/) NASTRI H G.
PA (ROOK/) ROOKEY K L.
PA (HOET/) HOET R.
PA (HOOG/) HOOGENBOOM H R J M.
XX

PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
PI Hoogenboom HRJM;
XX
DR WPI; 2003-093015/08.
XX
PT Cleaving single-stranded nucleic acid sequences at a desired location by
PT contacting the nucleic acid with an single strand oligonucleotide
PT complementary to a nucleic acid region where cleavage is desired.
XX
PS Disclosure; Page 481; 485pp; English.
XX
CC The present invention describes a method for cleaving single-stranded
CC nucleic acid sequences at a desired location. Also described: (1) methods
CC for displaying or expressing a member of a diverse family of peptides,
CC polypeptides or proteins on the surface of a genetic package and
CC collectively displaying at least a part of the diversity of the family,
CC where the displayed or expressed peptide, polypeptide or protein is
CC encoded at least in part by a nucleic acid that has been cleaved at a
CC desired location; (2) a method for preparing single-stranded nucleic
CC acids; (3) a method for preparing a library comprising a collection of
CC genetic packages that display a member of a diverse family of peptides,
CC polypeptides or proteins and that collectively display at least a portion
CC of the family; (4) a vector comprising a DNA sequence encoding an
CC antibody variable region linked to a version of PIII anchor which does
CC not mediate infection of phage particles, and wild-type gene III; (5) a
CC method for producing a population or a library of immunoglobulin genes;
CC and (6) a library of immunoglobulins that comprise members having at
CC least one variable domain in which at least one of CDR1 and CDR2 contain
CC synthetic diversity and CDR3 diversity is captured from B cells. The
CC method is useful for cleaving single-stranded nucleic acid sequences at a
CC desired location, which can be subsequently used to produce libraries or
CC genetic packages that display and/or express a diverse family of
CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to
CC ABP55499 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3232
ABZ37501/c
ID ABZ37501 standard; DNA; 15 BP.
XX
AC ABZ37501;
XX
DT 18-FEB-2003 (first entry)
XX
DE Oligonucleotide SEQ ID NO:622.
XX
KW Library; cleavage; display; diverse family; ss.
XX
OS Synthetic.
XX
PN WO200283872-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012405.
XX
PR 17-APR-2001; 2001US-00837306.
PR 24-OCT-2001; 2001US-00000516.
PR 25-OCT-2001; 2001US-00045674.
XX
PA (LADN/) LADNER R C.
PA (COHE/) COHEN E H.
PA (NAST/) NASTRI H G.
PA (ROOK/) ROOKEY K L.
PA (HOET/) HOET R.
PA (HOOG/) HOOGENBOOM H R J M.
XX
PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
PI Hoogenboom HRJM;
XX
DR WPI; 2003-093015/08.
XX
PT Cleaving single-stranded nucleic acid sequences at a desired location by
PT contacting the nucleic acid with an single strand oligonucleotide
PT complementary to a nucleic acid region where cleavage is desired.
XX
PS Disclosure; Page 481; 485pp; English.
XX
CC The present invention describes a method for cleaving single-stranded
CC nucleic acid sequences at a desired location. Also described: (1) methods
CC for displaying or expressing a member of a diverse family of peptides,
CC polypeptides or proteins on the surface of a genetic package and
CC collectively displaying at least a part of the diversity of the family,
CC where the displayed or expressed peptide, polypeptide or protein is
CC encoded at least in part by a nucleic acid that has been cleaved at a
CC desired location; (2) a method for preparing single-stranded nucleic
CC acids; (3) a method for preparing a library comprising a collection of
CC genetic packages that display a member of a diverse family of peptides,
CC polypeptides or proteins and that collectively display at least a portion
CC of the family; (4) a vector comprising a DNA sequence encoding an
CC antibody variable region linked to a version of PIII anchor which does
CC not mediate infection of phage particles, and wild-type gene III; (5) a
CC method for producing a population or a library of immunoglobulin genes;
CC and (6) a library of immunoglobulins that comprise members having at
CC least one variable domain in which at least one of CDR1 and CDR2 contain
CC synthetic diversity and CDR3 diversity is captured from B cells. The
CC method is useful for cleaving single-stranded nucleic acid sequences at a
CC desired location, which can be subsequently used to produce libraries or
CC genetic packages that display and/or express a diverse family of
CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to
CC ABP55499 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3233
ABV74142
ID ABV74142 standard; DNA; 15 BP.
XX
AC ABV74142;
XX
DT 23-JAN-2003 (first entry)
XX
DE 5' End of cDNA library clone.
XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KW microarray; anosmia; attractant; aromatic; pesticide; ss.
XX
OS Synthetic.
XX
PN WO200277200-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009559.
XX

```
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of the 5' end of a cDNA clone isolated from
CC   a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC   using a method designed to rapidly array and normalize a complex cDNA
CC   library obtained from a target species. Clones are arrayed into multi-
CC   well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC   5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC   and a unique 3' sequence, which allows an anchored oligonucleotide in
CC   each well to selectively hybridise only to those cDNA clones with a
CC   complementary 5' end. The unique 3' key sequences are designed to give a
CC   comprehensive level of degeneracy since they are diverse and numerous
CC   enough to ensure that every possible cDNA sequence can be bound by an
CC   individual, specific oligonucleotide in a single well. The cDNA library
CC   is heated to denature the clones into single stranded DNA, and an aliquot
CC   is added to every well. The anchored oligonucleotide serves as the 3'
CC   primer in PCR, and the common 5' region present in every cDNA clone
CC   serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC   in each well. The library is now arrayed and normalised. The method was
CC   used to identify and isolate clones encoding G-protein coupled receptors,
CC   especially odourant receptors, and active effectors involved in the
CC   olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
CC   proteins, or other olfactory or neuronal proteins. The identified
CC   receptors and proteins are useful for identifying compounds that reduce a
CC   target animal's sensitivity to odours, for manufacturing compounds or
CC   devices that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3234
ABV74142/c
ID   ABV74142 standard; DNA; 15 BP.
XX
AC   ABV74142;
XX
DT   23-JAN-2003  (first entry)
XX
DE   5' End of cDNA library clone.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; ss.
XX
OS   Synthetic.
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of the 5' end of a cDNA clone isolated from
CC   a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC   using a method designed to rapidly array and normalize a complex cDNA
CC   library obtained from a target species. Clones are arrayed into multi-
CC   well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC   5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC   and a unique 3' sequence, which allows an anchored oligonucleotide in
CC   each well to selectively hybridise only to those cDNA clones with a
CC   complementary 5' end. The unique 3' key sequences are designed to give a
CC   comprehensive level of degeneracy since they are diverse and numerous
CC   enough to ensure that every possible cDNA sequence can be bound by an
CC   individual, specific oligonucleotide in a single well. The cDNA library
CC   is heated to denature the clones into single stranded DNA, and an aliquot
CC   is added to every well. The anchored oligonucleotide serves as the 3'
CC   primer in PCR, and the common 5' region present in every cDNA clone
CC   serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC   in each well. The library is now arrayed and normalised. The method was
CC   used to identify and isolate clones encoding G-protein coupled receptors,
CC   especially odourant receptors, and active effectors involved in the
CC   olfactory pathway of invertebrates and vertebrates, e.g. odourant binding
CC   proteins, or other olfactory or neuronal proteins. The identified
CC   receptors and proteins are useful for identifying compounds that reduce a
CC   target animal's sensitivity to odours, for manufacturing compounds or
CC   devices that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3235
ABV74141
ID   ABV74141 standard; DNA; 15 BP.
XX
AC   ABV74141;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
```

```
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of a poly-T oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db             1 TTTTTTTTTTTTTTT 15

RESULT 3236
```

```
ABV74141/c
ID   ABV74141 standard; DNA; 15 BP.
XX
AC   ABV74141;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' polylinker"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of a poly-T oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
```

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3237
ABV75865
ID   ABV75865 standard; DNA; 15 BP.
XX
AC   ABV75865;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Oligonucleotide T15-Q-CDPI3.
XX
KW   Deprotection; phosphoramidite; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphoramidite linkage"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3' Q-CDPI3"
XX
PN   WO200272864-A2.
XX
PD   19-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US006739.
XX
PR   08-MAR-2001; 2001US-0274309P.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Nelson J;
XX
DR   WPI; 2003-046740/04.
XX
PT   New oligonucleotide deprotection reagent useful for deprotecting
PT   oligonucleotide comprises an active methylene compound and an amine
PT   reagent.
XX
PS   Example 2; Page 25; 46pp; English.
XX
CC   The present invention provides a method for deprotection of an
CC   oligonucleotide. This involves reacting a protected oligonucleotide,
CC   which is preferably covalently attached to a solid support through a
CC   linkage, with a deprotection reagent comprising an active methylene
CC   compound and an amine reagent. The process and reagent minimise side-
CC   reactions leading to certain impurities that contaminate synthetic
CC   oligonucleotides. The present sequence is a T15 phosphoramidite
CC   oligonucleotide having a quencher moiety (Q) and minor groove binder
CC   (CDPI3) at the 3' end, which was synthesised in an example of the
CC   invention. This protected oligonucleotide was treated either with 15%
CC   ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%
CC   ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that
CC   deprotection without DEM yielded a complex mixture of products containing
CC   only 26.5% of the desired product. When DEM was used, 76.8% of the
CC   desired product was obtained
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3238
ABV75865/c
ID   ABV75865 standard; DNA; 15 BP.
XX
AC   ABV75865;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Oligonucleotide T15-Q-CDPI3.
XX
KW   Deprotection; phosphoramidite; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .15
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphoramidite linkage"
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3' Q-CDPI3"
XX
PN   WO200272864-A2.
XX
PD   19-SEP-2002.
XX
PF   04-MAR-2002; 2002WO-US006739.
XX
PR   08-MAR-2001; 2001US-0274309P.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Nelson J;
XX
DR   WPI; 2003-046740/04.
XX
PT   New oligonucleotide deprotection reagent useful for deprotecting
PT   oligonucleotide comprises an active methylene compound and an amine
PT   reagent.
XX
PS   Example 2; Page 25; 46pp; English.
XX
CC   The present invention provides a method for deprotection of an
CC   oligonucleotide. This involves reacting a protected oligonucleotide,
CC   which is preferably covalently attached to a solid support through a
CC   linkage, with a deprotection reagent comprising an active methylene
CC   compound and an amine reagent. The process and reagent minimise side-
CC   reactions leading to certain impurities that contaminate synthetic
CC   oligonucleotides. The present sequence is a T15 phosphoramidite
CC   oligonucleotide having a quencher moiety (Q) and minor groove binder
CC   (CDPI3) at the 3' end, which was synthesised in an example of the
CC   invention. This protected oligonucleotide was treated either with 15%
CC   ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%
CC   ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that
CC   deprotection without DEM yielded a complex mixture of products containing
CC   only 26.5% of the desired product. When DEM was used, 76.8% of the
CC   desired product was obtained
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3239
ADA14836
ID   ADA14836 standard; DNA; 15 BP.
XX
AC   ADA14836;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin target sequence, #1, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .15
FT                   /*tag=  a
FT                   /bound_moiety= "Hairpin oligonucleotide #1"
FT                   /note= "Forms a doube-stranded region with the hairpin
FT                   oligonucleotide shown in example 2"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 2; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
CC   complementary probe. Also claimed is a microarray comprising the hairpin
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide target
CC   sequence, #1, used in an example of the invention.
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3240
ADA14836/c
ID   ADA14836 standard; DNA; 15 BP.
XX
AC   ADA14836;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin target sequence, #1, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .15
FT                   /*tag=  a
FT                   /bound_moiety= "Hairpin oligonucleotide #1"
FT                   /note= "Forms a doube-stranded region with the hairpin
FT                   oligonucleotide shown in example 2"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 2; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
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```
CC   complementary probe. Also claimed is a microarray comprising the hairpin
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide target
CC   sequence, #1, used in an example of the invention.
XX
SQ   Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3241
ADB68520
ID   ADB68520 standard; DNA; 15 BP.
XX
AC   ADB68520;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Single-base mismatch oligonucleotide SEQ ID 10 DNA.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; single-base mismatch; ss;
KW   phosphono-peptide nucleic acid; pPNA.
XX
OS   Synthetic.
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 20; Page 234; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the
CC   invention. This sequence may also comprise a peptide nucleic acid (PNA),
CC   a phosphono-PNA (pPNA) or a HypNA.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3242
ADB68520/c
ID   ADB68520 standard; DNA; 15 BP.
XX
AC   ADB68520;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Single-base mismatch oligonucleotide SEQ ID 10 DNA.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; single-base mismatch; ss;
KW   phosphono-peptide nucleic acid; pPNA.
XX
OS   Synthetic.
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 20; Page 234; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
```

CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the
CC invention. This sequence may also comprise a peptide nucleic acid (PNA),
CC a phosphono-PNA (pPNA) or a HypNA.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 15 AAAAAAAAAAAAAAA 1

RESULT 3243
ADC18592
ID ADC18592 standard; DNA; 15 BP.
XX
AC ADC18592;
XX
DT 18-DEC-2003 (first entry)
XX
DE Annealing control primer Oligo-dT15 SEQ ID NO:54.
XX
KW annealing control primer; ACP; annealing specificity;
KW nucleic acid amplification; hybridisation; DNA fingerprinting;
KW genomic DNA; RNA fingerprint; primer; ss.
XX
OS Synthetic.
XX
PN WO2003050305-A1.
XX
PD 19-JUN-2003.
XX
PF 19-SEP-2002; 2002WO-KR001781.
XX
PR 08-DEC-2001; 2001WO-KR002133.
PR 01-MAY-2002; 2002WO-KR000816.
XX
PA (SEEG-) SEEGENE INC.
XX
PI Chun J;
XX
DR WPI; 2003-627256/59.
XX
PT Annealing control primer to improve annealing specificity in nucleic acid
PT amplification, has region complementary to target, arbitrary nucleotide
PT sequence, regulator with universal base/non-discriminatory base analog.
XX
PS Example 2; SEQ ID NO 54; 190pp; English.
XX
CC The present invention describes an annealing control primer (ACP) (I) for
CC improving the annealing specificity in nucleic acid amplification. (I)
CC has a 3'-end portion with a nucleotide sequence complementary to a site
CC on a template nucleic acid for hybridisation, a 5'-end portion having a
CC pre-selected arbitrary nucleotide sequence, and a regulator portion
CC between the 3' and 5'-end portions, comprising a universal or non-
CC discriminatory base analogue, where the regulator portion is capable of
CC regulating an annealing portion of the primer in association with
CC annealing temperature. (I) is useful for improving annealing specificity
CC in nucleic acid amplification. (I) is useful for amplifying a nucleic
CC acid sequence from a DNA or a mixture of nucleic acids, for selectively
CC amplifying a target nucleic acid sequence from a DNA, and for selectively
CC amplifying a target nucleic acid sequence from a mRNA, by reverse
CC transcribing the mRNA and performing an amplification reaction using (I).
CC (I) is also useful for detecting DNA complementary to differentially
CC expressed mRNA in two or more nucleic acid samples, by reverse
CC transcribing the mRNA and performing an amplification reaction using (I).
CC (I) is also useful for rapidly amplifying a target cDNA fragment
CC comprising a cDNA region corresponding to the 3'-end or 5'-end region of
CC an mRNA, for amplifying a population of full-length double-stranded cDNAs
CC complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs
CC complementary to mRNA. (I) is also useful for amplifying more than one
CC target nucleotide sequence simultaneously using more than one pair of
CC primers in the same reaction, where the primers are derived from (I), for
CC producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
CC fingerprint of an mRNA sample, identifying conserved homology segments in
CC a multigene family from an mRNA sample, and for identifying conserved
CC homology segments in a multigene family from gDNA. (I) is also useful for
CC identifying a nucleotide variation in a target nucleic acid, and for
CC mutagenesis in a target nucleic acid. The present sequence represents a
CC primer which is used in the exemplification of the present invention.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3244
ADC18592/c
ID ADC18592 standard; DNA; 15 BP.
XX
AC ADC18592;
XX
DT 18-DEC-2003 (first entry)
XX
DE Annealing control primer Oligo-dT15 SEQ ID NO:54.
XX
KW annealing control primer; ACP; annealing specificity;
KW nucleic acid amplification; hybridisation; DNA fingerprinting;
KW genomic DNA; RNA fingerprint; primer; ss.
XX
OS Synthetic.
XX
PN WO2003050305-A1.
XX
PD 19-JUN-2003.
XX
PF 19-SEP-2002; 2002WO-KR001781.
XX
PR 08-DEC-2001; 2001WO-KR002133.
PR 01-MAY-2002; 2002WO-KR000816.
XX
PA (SEEG-) SEEGENE INC.
XX
PI Chun J;
XX
DR WPI; 2003-627256/59.
XX
PT Annealing control primer to improve annealing specificity in nucleic acid
PT amplification, has region complementary to target, arbitrary nucleotide
PT sequence, regulator with universal base/non-discriminatory base analog.
XX
PS Example 2; SEQ ID NO 54; 190pp; English.
XX
CC The present invention describes an annealing control primer (ACP) (I) for
CC improving the annealing specificity in nucleic acid amplification. (I)
CC has a 3'-end portion with a nucleotide sequence complementary to a site
CC on a template nucleic acid for hybridisation, a 5'-end portion having a
CC pre-selected arbitrary nucleotide sequence, and a regulator portion
CC between the 3' and 5'-end portions, comprising a universal or non-

```
CC   discriminatory base analogue, where the regulator portion is capable of
CC   regulating an annealing portion of the primer in association with
CC   annealing temperature. (I) is useful for improving annealing specificity
CC   in nucleic acid amplification. (I) is useful for amplifying a nucleic
CC   acid sequence from a DNA or a mixture of nucleic acids, for selectively
CC   amplifying a target nucleic acid sequence from a DNA, and for selectively
CC   amplifying a target nucleic acid sequence from a mRNA, by reverse
CC   transcribing the mRNA and performing an amplification reaction using (I).
CC   (I) is also useful for detecting DNA complementary to differentially
CC   expressed mRNA in two or more nucleic acid samples, by reverse
CC   transcribing the mRNA and performing an amplification reaction using (I).
CC   (I) is also useful for rapidly amplifying a target cDNA fragment
CC   comprising a cDNA region corresponding to the 3'-end or 5'-end region of
CC   an mRNA, for amplifying a population of full-length double-stranded cDNAs
CC   complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs
CC   complementary to mRNA. (I) is also useful for amplifying more than one
CC   target nucleotide sequence simultaneously using more than one pair of
CC   primers in the same reaction, where the primers are derived from (I), for
CC   producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
CC   fingerprint of an mRNA sample, identifying conserved homology segments in
CC   a multigene family from an mRNA sample, and for identifying conserved
CC   homology segments in a multigene family from gDNA. (I) is also useful for
CC   identifying a nucleotide variation in a target nucleic acid, and for
CC   mutagenesis in a target nucleic acid. The present sequence represents a
CC   primer which is used in the exemplification of the present invention.
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3245
ABL57075/c
ID   ABL57075 standard; DNA; 16 BP.
XX
AC   ABL57075;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .16
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 5-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 3246
AAD57845/c
ID   AAD57845 standard; DNA; 16 BP.
XX
AC   AAD57845;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20-B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
```

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CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2166 TTTTTTTTTTTTTTT 2180
             |||||||||||||||
Db        16 TTTTTTTTTTTTTTT 2

RESULT 3247
AAT75138
ID   AAT75138 standard; DNA; 16 BP.
XX
AC   AAT75138;
XX
DT   03-MAR-1998  (first entry)
XX
DE   Arbitrary anchor primer HC.
XX
KW   dhc-1; homocysteine; hypohomocysteinaemia; atherosclerosis; diagnosis;
KW   serum; Dami cell; PCR; arbitrary primer; messenger RNA pool; ss.
XX
OS   Synthetic.
XX
PN   WO9725440-A2.
XX
PD   17-JUL-1997.
XX
PF   02-JAN-1997;   97WO-CA000001.
XX
PR   03-JAN-1996;   96US-00582261.
XX
PA   (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
XX
PI   Austin RC,  Hirsh J,  Weitz J;
XX
DR   WPI; 1997-372877/34.
XX
PT   Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -
PT   and/or predisposition to develop premature atherosclerosis by detecting
PT   increased levels of serum homocysteine.
XX
PS   Disclosure; Page 22; 84pp; English.
XX
CC   Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from
CC   cells exposed to hyperphysiological, normal or subphysiological levels of
CC   homocysteine. PCR products were separated on a sequencing gel and
CC   discrete fractions which were increased or decreased were identified.
CC   This method was used to identify mRNA and the corresponding cDNA which
CC   are increased in the cells of a patient having hyperhomocysteinaemia or a
CC   predisposition to homocysteine mediated atherosclerosis. These
CC   polynucleotides can be used for the diagnosis and treatment of
CC   atherosclerotic diseases and diseases of metabolism of sulphur containing
CC   amino acids (e.g. homocysteinaemia), which are associated with vascular
CC   damage and atherosclerotic disease, specifically unstable angina, acute
CC   myocardial infarction (heart attack), cerebrovascular accidents (stroke),
CC   hypertension, renal artery stenosis, aortic stenosis and deep vein
CC   occlusive disease
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db         1 AAGCTTTTTTTTTTT 15

RESULT 3248
AAX89227
ID   AAX89227 standard; DNA; 16 BP.
XX
AC   AAX89227;
XX
DT   15-SEP-1999  (first entry)
XX
DE   PCR primer H-T11A.
XX
KW   ST2L; extracellular domain; mouse; epitope; antibody; T-helper cell; Th1;
KW   Th2; medicament; therapy; allergic reaction; asthma; Leishmania;
KW   intracellular pathogen; inflammatory disease; arthritis; immunoglobulin;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9934217-A1.
XX
PD   08-JUL-1999.
XX
PF   24-DEC-1998;   98WO-GB003913.
XX
PR   24-DEC-1997;   97GB-00027172.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Liew FY,  Xu D;
XX
DR   WPI; 1999-430265/36.
XX
PT   Novel antibody to ST2L, an epitope found on the extracellular surfaces of
PT   T helper 1 cells.
XX
PS   Disclosure; Page 12; 44pp; English.
XX
CC   The invention provides an antibody specific for epitopes (AAY27164-175)
CC   located on the extracellular domain of ST2L protein. The antibody is
CC   used: (a) in a binding assay to identify and/or distinguish T-helper 1
CC   (Th1) or Th2 and evaluate the abundance of Th2 in a sample of body fluid
CC   or tissue; (b) to lyse Th2 cells in preference to Th1 cells or otherwise
CC   inhibit Th2 cell function; and (c) as a medicament for use in therapy as
CC   a mediator of an allergic reaction, e.g. asthma; diseases mediated by
CC   intracellular pathogens, especially Leishmania, or against an
CC   inflammatory disease, especially arthritis. The antibody is targeted to
CC   an epitope (ST2L) which is a member of the immunoglobulin superfamily and
CC   is found on Th2 cells and not Th1 cells
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db         1 AAGCTTTTTTTTTTT 15

RESULT 3249
AAX55055
ID   AAX55055 standard; DNA; 16 BP.
XX
AC   AAX55055;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
```

```
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3250
AAX19464
ID   AAX19464 standard; DNA; 16 BP.
XX
AC   AAX19464;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human senescence factor p23 H-T11 primer SEQ ID NO:6.
XX
KW   Human; senescence factor; p23; cancer; persistent inflammation;
KW   proliferative disorder; degenerative disorder; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9907893-A1.
XX
PD   18-FEB-1999.
XX
PF   05-AUG-1998;   98WO-US016343.
XX
PR   08-AUG-1997;   97US-00908873.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Swisshelm K,  Hosier S,  Kubbies M;
XX
DR   WPI; 1999-167454/14.
XX
PT   Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT   polypeptide - useful for inducing a senescence phenotype in a cell.
XX
PS   Example 1; Page 18; 44pp; English.
XX
CC   The present invention describes human senescence factor p23. An
CC   expression vector for p23 is useful for inducing a senescent phenotype in
CC   a cell (preferably eukaryotic). This may help in regulating diseases,
CC   including cancer, persistent inflammation, and various proliferative and
CC   degenerative disorders. These transgenic cells are useful in gene therapy
CC   for treating cancer, particularly where antisense oligonucleotides are
CC   useful for blocking normal or mutant p23 expression in cancer cells or
CC   other proliferating cells. Transgenic cells are also useful for producing
CC   the p23 polypeptide in large quantities. The antibodies are useful for
CC   raising antiserum against p23, and for identifying senescent cells in
CC   culture and tissue biopsies. The p23 polynucleotides are useful for
CC   modulating or altering p23 activity in a cell, and for identifying and
CC   isolating the whole gene encoding p23, and variants of p23. Assays based
CC   on p23 elements, which detect p23 levels and activity are useful as
CC   diagnostic markers for staging tumours, determining prognosis, and/or
CC   predicting therapeutic success. These elements also provide an assay for
CC   detecting chromosomal rearrangements in chromosome 3 in a human cell. The
CC   isolation of the p23 polynucleotide permits the manipulation of malignant
CC   growth in cancer. The present sequence represents a primer used in an
CC   example from the present invention
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3251
AAX19463
ID   AAX19463 standard; DNA; 16 BP.
XX
AC   AAX19463;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human senescence factor p23 H-T11 primer SEQ ID NO:5.
XX
KW   Human; senescence factor; p23; cancer; persistent inflammation;
KW   proliferative disorder; degenerative disorder; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
```

PN WO9907893-A1.
XX
PD 18-FEB-1999.
XX
PF 05-AUG-1998; 98WO-US016343.
XX
PR 08-AUG-1997; 97US-00908873.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Swisshelm K, Hosier S, Kubbies M;
XX
DR WPI; 1999-167454/14.
XX
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT polypeptide - useful for inducing a senescence phenotype in a cell.
XX
PS Example 1; Page 18; 44pp; English.
XX
CC The present invention describes human senescence factor p23. An
CC expression vector for p23 is useful for inducing a senescent phenotype in
CC a cell (preferably eukaryotic). This may help in regulating diseases,
CC including cancer, persistent inflammation, and various proliferative and
CC degenerative disorders. These transgenic cells are useful in gene therapy
CC for treating cancer, particularly where antisense oligonucleotides are
CC useful for blocking normal or mutant p23 expression in cancer cells or
CC other proliferating cells. Transgenic cells are also useful for producing
CC the p23 polypeptide in large quantities. The antibodies are useful for
CC raising antiserum against p23, and for identifying senescent cells in
CC culture and tissue biopsies. The p23 polynucleotides are useful for
CC modulating or altering p23 activity in a cell, and for identifying and
CC isolating the whole gene encoding p23, and variants of p23. Assays based
CC on p23 elements, which detect p23 levels and activity are useful as
CC diagnostic markers for staging tumours, determining prognosis, and/or
CC predicting therapeutic success. These elements also provide an assay for
CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The
CC isolation of the p23 polynucleotide permits the manipulation of malignant
CC growth in cancer. The present sequence represents a primer used in an
CC example from the present invention
XX
SQ Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3252
AAX18360/c
ID AAX18360 standard; DNA; 16 BP.
XX
AC AAX18360;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 1.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 10; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAA 2799
|||||||||||||||
Db 15 GAAAAAAAAAAAAAA 1

RESULT 3253
AAX18369
ID AAX18369 standard; DNA; 16 BP.
XX
AC AAX18369;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 10.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX
PS Disclosure; Page 10; 19pp; Japanese.
XX
CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

```
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTA 15


RESULT 3254
AAX18368
ID   AAX18368 standard; DNA; 16 BP.
XX
AC   AAX18368;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 9.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTA 15


RESULT 3255
AAX18363/c
ID   AAX18363 standard; DNA; 16 BP.
XX
AC   AAX18363;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 4.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db         15 GAAAAAAAAAAAAAA 1


RESULT 3256
AAA99205
ID   AAA99205 standard; DNA; 16 BP.
XX
AC   AAA99205;
XX
DT   23-JAN-2001  (first entry)
XX
DE   Human apoptosis related protein CCR9 related primer #1.
XX
KW   Human; apoptosis; CCR9; anti-tumour; tumour; cancer; diagnosis; primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2000210089-A.
XX
PD   02-AUG-2000.
XX
PF   18-NOV-1999;   99JP-00327885.
XX
```

PR 20-NOV-1998; 98JP-00330302.
XX
PA (ASAK) ASAHI BREWERIES LTD.
XX
DR WPI; 2000-614556/59.
XX
PT Gene and its encoded protein that induce apoptosis, useful for producing
PT a malignant tumor gene treating agent and for the diagnosis on the
PT resistance of cancer cells against an anticancer agent.
XX
PS Example 1; Page 4; 13pp; Japanese.
XX
CC The present invention describes the human CRR9 protein, which is an
CC apoptosis related protein having apoptosis-inducing activity. Human CCR9
CC has anti-tumour activity, and can be used to produce a malignant tumour
CC gene treating agent. The CCR9 gene and protein can be used for the
CC diagnosis of the resistance of cancer cells against an anticancer agent.
CC The present sequence represents a primer which is used in an example from
CC the present invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3257
AAA99206
ID AAA99206 standard; DNA; 16 BP.
XX
AC AAA99206;
XX
DT 23-JAN-2001 (first entry)
XX
DE Human apoptosis related protein CCR9 related primer #2.
XX
KW Human; apoptosis; CCR9; anti-tumour; tumour; cancer; diagnosis; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN JP2000210089-A.
XX
PD 02-AUG-2000.
XX
PF 18-NOV-1999; 99JP-00327885.
XX
PR 20-NOV-1998; 98JP-00330302.
XX
PA (ASAK) ASAHI BREWERIES LTD.
XX
DR WPI; 2000-614556/59.
XX
PT Gene and its encoded protein that induce apoptosis, useful for producing
PT a malignant tumor gene treating agent and for the diagnosis on the
PT resistance of cancer cells against an anticancer agent.
XX
PS Example 1; Page 4; 13pp; Japanese.
XX
CC The present invention describes the human CRR9 protein, which is an
CC apoptosis related protein having apoptosis-inducing activity. Human CCR9
CC has anti-tumour activity, and can be used to produce a malignant tumour
CC gene treating agent. The CCR9 gene and protein can be used for the
CC diagnosis of the resistance of cancer cells against an anticancer agent.
CC The present sequence represents a primer which is used in an example from
CC the present invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3258
AAA34502
ID AAA34502 standard; DNA; 16 BP.
XX
AC AAA34502;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2191.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 539; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to

```
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3259
AAA97561
ID   AAA97561 standard; DNA; 16 BP.
XX
AC   AAA97561;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Reverse transcription primer used to isolate human mtHSP75.
XX
KW   Human mitochondria-localised heat shock protein 75; mitochondrial HSP75;
KW   mtHSP75; quantitative detection; expression level; cancer; tumour;
KW   anticancer drug selection; prognosis; platinum complex compound;
KW   cisplatin; reverse transcription primer; ss.
XX
OS   Synthetic.
XX
PN   JP2000224989-A.
XX
PD   15-AUG-2000.
XX
PF   20-NOV-1998;   98JP-00330309.
XX
PR   20-NOV-1998;   98JP-00330309.
XX
PA   (ASAK ) ASAHI BREWERIES LTD.
XX
DR   WPI; 2000-605127/58.
XX
PT   A method for sensitivity test to anti-cancer agents.
XX
PS   Example 1; Page 3; 7pp; Japanese.
XX
CC   The invention relates to a novel method for testing the sensitivity of
CC   cancer cells to anti-cancer agents. The method comprises quantitative
CC   detection of a mitochondria-localised heat shock protein 75 (mtHSP75)
CC   gene (mtHSP75 cDNA given in AAA97560). Cancer cells expressing high
CC   levels of mtHSP75 are more likely to be resistant to anti-cancer agents,
CC   while those expressing low levels are more likely to be susceptible to
CC   such agents. The invention also relates to the use of RNA complementary
CC   to mtHSP75 or an mtHSP75 gene fragment in the method of the invention,
CC   the use of Northern blotting to detect mtHSP75 RNA, and the use of
CC   Western blotting to detect the mtHSP75 gene product. The method of the
CC   invention may particularly be used to test the sensitivity of cancer
CC   cells to platinum complex compounds, especially cisplatin. The invention
CC   provides for the selection of anti-cancer agents likely to be effective
CC   against a tumour in a particular individual. The present sequence
CC   represents a reverse transcription primer used to generate human mtHSP75
CC   cDNA in an exemplification of the invention
XX
SQ   Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
                |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3260
AAA60992
ID   AAA60992 standard; DNA; 16 BP.
XX
AC   AAA60992;
XX
DT   09-NOV-2000  (first entry)
XX
DE   Rapid analysis of differential expression oligonucleotide.
XX
KW   Oestrogen receptor; ER-alpha; ER-beta; identification; screening;
KW   selective modulator; metallothionein; ss.
XX
OS   Synthetic.
XX
PN   WO200037681-A1.
XX
PD   29-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US029856.
XX
PR   18-DEC-1998;   98US-0112790P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Harris H,  Bhat RA;
XX
DR   WPI; 2000-442693/38.
XX
PT   Screening for a test compound that binds to an estrogen receptor in a
PT   receptor binding assay comprising detecting estrogen receptor polypeptide
PT   mediated transcription.
XX
PS   Example 3; Page 28; 77pp; English.
XX
CC   The present invention describes a method for screening a test compound
CC   that binds to an ER (oestrogen receptor) in a receptor binding assay. The
CC   method comprises: (a) providing a cell which comprises at least one
CC   oestrogen-regulated DNA sequence encoding MT-II (metallothionein) and at
CC   least one DNA sequence encoding ER-beta polypeptide; (b) contacting the
CC   cell with either the test compound; and (c) detecting the expression of
CC   the MT-II. The method is useful for screening a test compound that binds
CC   to an ER in a receptor binding assay by detecting (the inhibition of) ER-
CC   beta polypeptide mediated transcription and identifying drug candidates
CC   which mimic or inhibit oestrogen's effects on ER-beta or ER-alpha
CC   mediated transcription. The screening method is also useful for
CC   identifying tissue specific oestrogens. The method is adapted to a high
CC   throughput screen, allowing multiplicity of compounds to be tested in a
CC   single assay. The ER-beta binding assays are advantageous in
CC   accommodating many different types of solvents and therefore allowing the
CC   testing of compounds from many sources. The present sequence represents
CC   an oligonucleotide which is used in an example from the present
CC   invention, for RADE (rapid analysis of differential expression)
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
                |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3261
AAA29747
ID   AAA29747 standard; DNA; 16 BP.
XX
```

AC AAA29747;
XX
DT 15-AUG-2000 (first entry)
XX
DE Rabbit KKIAMRE kinase differential display PCR primer SEQ ID NO:1.
XX
KW Rabbit; KKIAMRE kinase; learning-induced kinase; learning; memory;
KW cdc2-related kinase; brain; gene therapy; genetic disorder; detection;
KW identification; PCR primer; ss.
XX
OS Oryctolagus cuniculus.
XX
PN WO200020567-A2.
XX
PD 13-APR-2000.
XX
PF 01-OCT-1999; 99WO-US023010.
XX
PR 02-OCT-1998; 98US-0102906P.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Thompson RF, Gomi H, Sun W;
XX
DR WPI; 2000-328932/28.
XX
PT Novel learning induced kinase polynucleotides and polypeptides, useful
PT for the analysis of learning and memory, and for gene therapy.
XX
PS Example 2; Page 4; 64pp; English.
XX
CC The present sequence represents a differential display PCR primer used in
CC the isolated of a learning-induced kinase, designated KKIAMRE kinase,
CC from rabbit brain tissue in an example from the present invention.
CC KKIAMRE kinase is a cdc2-related kinase. The KKIAMRE kinase
CC polynucleotides can be used to express recombinant protein for analysis,
CC characterisation or therapeutic use, as markers for tissues in which the
CC protein is preferentially expressed, as molecular weight markers on
CC Southern gels, as chromosome markers or tags, to compare endogenous DNA
CC sequences in patients to identify potential genetic disorders, as probes
CC to hybridise and discover novel related sequences, as a source of PCR
CC primers, and as an antigen to induce anti-DNA antibodies. The
CC polypeptides can be used in assay to discover biological activity, to
CC raise antibodies, as tissue markers, and to isolate correlative receptors
CC or ligands. The polynucleotides may also be used for gene therapy for the
CC treatment of disorders which are mediated by KKIAMRE kinase
XX
SQ Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3262
AAF20624
ID AAF20624 standard; DNA; 16 BP.
XX
AC AAF20624;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2191.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3263
AAA94103
ID AAA94103 standard; DNA; 16 BP.

```
XX
AC   AAA94103;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Fruit-associated banana TRX gene PCR primer H-T11C.
XX
KW   Banana; fruit-associated TRX gene; promoter; G1A; transgenic plant;
KW   fruit ripening; nutrition; PCR primer; ss.
XX
OS   Musa acuminata.
XX
PN   WO200056863-A1.
XX
PD   28-SEP-2000.
XX
PF   17-MAR-2000; 2000WO-US007293.
XX
PR   19-MAR-1999;   99US-0125310P.
XX
PA   (AGRI-) AGRITOPE INC.
XX
PI   Clendennen SK,  Kellogg JA,  Phan CB,  Mathews HV,  Webb NM;
XX
DR   WPI; 2000-628259/60.
XX
PT   Nucleic acid molecule encoding banana fruit associated promoter and melon
PT   actin promoter, useful for producing transgenic fruit-bearing plants.
XX
PS   Example 1; Page 35; 72pp; English.
XX
CC   The present sequence is a PCR primer which was used to isolate and
CC   amplify the promoter of the banana fruit-associated TRX (also known as
CC   the G1A) gene. This was isolated from a banana library using differential
CC   display analysis for banana-specific transcripts. The promoters of the
CC   invention can be used to produce transgenic fruit, with altered or
CC   improved characteristics, in particular their ripening, their nutritional
CC   content and the expression of useful proteins
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3264
AAA94102
ID   AAA94102 standard; DNA; 16 BP.
XX
AC   AAA94102;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Fruit-associated banana TRX gene PCR primer H-T11A.
XX
KW   Banana; fruit-associated TRX gene; promoter; G1A; transgenic plant;
KW   fruit ripening; nutrition; PCR primer; ss.
XX
OS   Musa acuminata.
XX
PN   WO200056863-A1.
XX
PD   28-SEP-2000.
XX
PF   17-MAR-2000; 2000WO-US007293.
XX
PR   19-MAR-1999;   99US-0125310P.
XX
PA   (AGRI-) AGRITOPE INC.
XX
PI   Clendennen SK,  Kellogg JA,  Phan CB,  Mathews HV,  Webb NM;
XX
DR   WPI; 2000-628259/60.
XX
PT   Nucleic acid molecule encoding banana fruit associated promoter and melon
PT   actin promoter, useful for producing transgenic fruit-bearing plants.
XX
PS   Example 1; Page 35; 72pp; English.
XX
CC   The present sequence is a PCR primer which was used to isolate and
CC   amplify the promoter of the banana fruit-associated TRX (also known as
CC   the G1A) gene. This was isolated from a banana library using differential
CC   display analysis for banana-specific transcripts. The promoters of the
CC   invention can be used to produce transgenic fruit, with altered or
CC   improved characteristics, in particular their ripening, their nutritional
CC   content and the expression of useful proteins
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3265
AAF82230
ID   AAF82230 standard; DNA; 16 BP.
XX
AC   AAF82230;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Human SFRP-1 gene reverse primer HT11A.
XX
KW   Human; hOB-SFRP-1; secreted frizzled related protein 1; SFRP-1;
KW   human osteoblast; hOB; osteopathic; antiarthritic; nootropic;
KW   bone formation; Wnt-mediated signalling; gene therapy; bone disorder;
KW   rapid analysis of differential expression; RADE; bone density;
KW   degenerative bone disorder; bone resorption; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200119855-A2.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US025035.
XX
PR   13-SEP-1999;   99US-00394832.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Bodine PVN;
XX
DR   WPI; 2001-273419/28.
XX
PT   Novel pharmaceutical composition for regulating bone formation in
PT   mammals, comprising secreted frizzled related protein, antibody formed
PT   from SFRP, nucleic acid encoding SFRP or antibody or its antisense
PT   sequence.
XX
PS   Example 1; Page 45; 88pp; English.
XX
CC   The present sequence was used to identify a fragment of the human
CC   osteoblast secreted frizzled related protein 1 (hOB-SFRP-1) gene. The
CC   fragment was obtained using rapid analysis of differential expression
CC   (RADE). The gene fragment was used in the production of a pharmaceutical
```

```
CC   composition for regulating bone-forming activity in a mammal. The
CC   composition comprises at least one of: SFRP or its regulating portion, an
CC   antibody formed from such proteins or its portion, a nucleic acid that
CC   encodes either SFRP or the antibody, and an antisense sequence of the
CC   nucleic acid. The composition is useful for treating human bone disorders
CC   such as bone formation disorders, degenerative bone disorders e.g.,
CC   neurodegeneration, myodegeneration, and osteodegeneration disorders, bone
CC   resorption disorders and bone density disorders. The osteodegeneration
CC   disorders that may be treated are osteopaenia, osteoarthritis and
CC   osteoporosis. SFRP is useful for modulating Wnt-mediated signalling in a
CC   cell. A recombinant construct expressing an antisense sequence to an SFRP
CC   nucleic acid is useful for facilitating bone formation or repair in a
CC   bone cell culture
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3266
AAF83581
ID   AAF83581 standard; DNA; 16 BP.
XX
AC   AAF83581;
XX
DT   23-JUL-2001  (first entry)
XX
DE   B. gymnorrhiza salt-tolerance cDNA amplifying primer H-T11A.
XX
KW   Salt-stress; genetic modification; salt tolerance; PCR primer; ss.
XX
OS   Bruguiera gymnorrhiza.
XX
PN   WO200130999-A1.
XX
PD   03-MAY-2001.
XX
PF   28-JUL-2000; 2000WO-JP005102.
XX
PR   22-OCT-1999;   99JP-00301621.
PR   20-DEC-1999;   99JP-00361107.
XX
PA   (EBAR ) EBARA CORP.
XX
PI   Karube I,  Hanagata N;
XX
DR   WPI; 2001-308636/32.
XX
PT   Nucleotide sequences, useful for generating salt-tolerant transgenic
PT   plants, obtained from the leaves of Bruguiera gymnorrhiza subjected to
PT   500 mM NaCl.
XX
PS   Example 2; Page 15; 49pp; English.
XX
CC   The invention provides nucleotide sequences highly expressed in salt-
CC   stressed leaves of Bruguiera gymnorrhiza. The invention is useful to
CC   provide salt tolerant plants by genetic modification. Plants transformed
CC   with the DNA sequences have improved salt tolerance. Sequences AAF83580 -
CC   592 represent PCR primers for amplifying B. gymnorrhiza salt tolerance
CC   gene associated cDNA fragments
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3267
AAF83582
ID   AAF83582 standard; DNA; 16 BP.
XX
AC   AAF83582;
XX
DT   23-JUL-2001  (first entry)
XX
DE   B. gymnorrhiza salt-tolerance cDNA amplifying primer H-T11C.
XX
KW   Salt-stress; genetic modification; salt tolerance; PCR primer; ss.
XX
OS   Bruguiera gymnorrhiza.
XX
PN   WO200130999-A1.
XX
PD   03-MAY-2001.
XX
PF   28-JUL-2000; 2000WO-JP005102.
XX
PR   22-OCT-1999;   99JP-00301621.
PR   20-DEC-1999;   99JP-00361107.
XX
PA   (EBAR ) EBARA CORP.
XX
PI   Karube I,  Hanagata N;
XX
DR   WPI; 2001-308636/32.
XX
PT   Nucleotide sequences, useful for generating salt-tolerant transgenic
PT   plants, obtained from the leaves of Bruguiera gymnorrhiza subjected to
PT   500 mM NaCl.
XX
PS   Example 2; Page 15; 49pp; English.
XX
CC   The invention provides nucleotide sequences highly expressed in salt-
CC   stressed leaves of Bruguiera gymnorrhiza. The invention is useful to
CC   provide salt tolerant plants by genetic modification. Plants transformed
CC   with the DNA sequences have improved salt tolerance. Sequences AAF83580 -
CC   592 represent PCR primers for amplifying B. gymnorrhiza salt tolerance
CC   gene associated cDNA fragments
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3268
AAS06650
ID   AAS06650 standard; DNA; 16 BP.
XX
AC   AAS06650;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human cDNA synthesis and differential display primer, HT11C.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11C.
```

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200134834-A2.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-DK000628.
XX
PR 11-NOV-1999; 99DK-00001626.
XX
PA (RIGS-) RIGSHOSPITALET.
XX
PI Leffers H, Jorgensen M, Skakkebaek NE;
XX
DR WPI; 2001-335941/35.
XX
PT Evaluating a cellular response to an environmental compound, for use in
PT toxicological analysis, involves determining or comparing the expression
PT levels of at least one endogenous gene.
XX
PS Example 3; Page 27; 77pp; English.
XX
CC The sequence represents a downstream PCR primer used in a DDRT-PCR
CC experiment (and in cDNA synthesis), demonstrating the method of the
CC invention. The method relates to evaluating a cellular response to an
CC environmental compound, comprising determining or comparing the
CC expression levels of at least one endogenous gene e.g by differential
CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC adapted to identify compounds that act on the level of endogenous gene
CC expression through activating nuclear receptors. The method is useful in
CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC testicular, breast, prostate and endometrium), asthma, hypospadia,
CC cryptorchism and/or allergy, and for evaluating the efficiency of a
CC treatment for hormonal deficiency or hormonal replacement therapy, in a
CC human such as a post-menopausal female. The method is also useful for
CC identifying environmental chemicals or pharmaceutical compositions that
CC interact with endocrine systems, and for detecting chemicals that pose a
CC health threat. Expression levels of endogenous genes are determined
CC rapidly using a sensitive technique, and the expression of any gene can
CC be monitored. The assays are far more informative than the currently used
CC assays, and significantly reduces the number of animals required for the
CC testing, as it is expected that essentially all the animals in a test
CC group will respond to the compound
XX
SQ Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3269
AAS06649
ID AAS06649 standard; DNA; 16 BP.
XX
AC AAS06649;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human cDNA synthesis and differential display primer, HT11A.
XX
KW Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW differential display of reverse transcribed mRNAs by PCR;
KW testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW HRT; endocrine system; HT11A.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200134834-A2.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-DK000628.
XX
PR 11-NOV-1999; 99DK-00001626.
XX
PA (RIGS-) RIGSHOSPITALET.
XX
PI Leffers H, Jorgensen M, Skakkebaek NE;
XX
DR WPI; 2001-335941/35.
XX
PT Evaluating a cellular response to an environmental compound, for use in
PT toxicological analysis, involves determining or comparing the expression
PT levels of at least one endogenous gene.
XX
PS Example 3; Page 27; 77pp; English.
XX
CC The sequence represents a downstream PCR primer used in a DDRT-PCR
CC experiment (and in cDNA synthesis), demonstrating the method of the
CC invention. The method relates to evaluating a cellular response to an
CC environmental compound, comprising determining or comparing the
CC expression levels of at least one endogenous gene e.g by differential
CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC adapted to identify compounds that act on the level of endogenous gene
CC expression through activating nuclear receptors. The method is useful in
CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC testicular, breast, prostate and endometrium), asthma, hypospadia,
CC cryptorchism and/or allergy, and for evaluating the efficiency of a
CC treatment for hormonal deficiency or hormonal replacement therapy, in a
CC human such as a post-menopausal female. The method is also useful for
CC identifying environmental chemicals or pharmaceutical compositions that
CC interact with endocrine systems, and for detecting chemicals that pose a
CC health threat. Expression levels of endogenous genes are determined
CC rapidly using a sensitive technique, and the expression of any gene can
CC be monitored. The assays are far more informative than the currently used
CC assays, and significantly reduces the number of animals required for the
CC testing, as it is expected that essentially all the animals in a test
CC group will respond to the compound
XX
SQ Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3270
ABK87149
ID ABK87149 standard; DNA; 16 BP.
XX
AC ABK87149;
XX
DT 07-OCT-2002 (first entry)
XX
DE Scarlet runner bean anchor/reverse RT-PCR primer C.
XX
KW Expression cassette; promoter activity; suspensor cell; plant embryo;
KW modulation of gene transcription; Scarlet runner bean; RT-PCR;
KW reverse transcriptase-PCR; primer; transgenic; ss.
XX
OS Phaseolus coccineus.
OS Synthetic.
XX

PN WO200244333-A2.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-US044737.
XX
PR 28-NOV-2000; 2000US-00724857.
PR 28-NOV-2000; 2000US-0253672P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (CERE-) CERES INC.
XX
PI Weterings K, Apuya NR, Tatarinova T, Goldberg RB;
XX
DR WPI; 2002-508506/54.
XX
PT Expression cassette comprises promoters with basal promoter activity
PT operably linked to a heterologous polynucleotide, useful for expression
PT genes in suspensor cells in plants and/or basal region of plant embryo.
XX
PS Example; Page 54; 114pp; English.
XX
CC The present invention relates to expression cassettes comprising a
CC promoter sequence and a promoter polynucleotide with basal promoter
CC activity, where the promoter sequence is operably linked to a
CC heterologous polynucleotide, and when the expression cassette is inserted
CC into a plant, the heterologous polynucleotide is specifically expressed
CC in a suspensor cell and/or basal region of a plant embryo. The invention
CC also provides polynucleotide sequences encoding Scarlet runner bean
CC (Phaseolus coccineus) G564 and C541 proteins for use in the expression
CC cassettes of the invention. The expression cassettes comprising promoters
CC and promoter control elements are useful for modulating transcription of
CC genes in a plant suspensor cell and/or basal region of a plant embryo.
CC The present sequence represents an anchor/reverse reverse transcriptase
CC (RT)-PCR primer used in the examples of the present invention
XX
SQ Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||| |
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3271
AAD34283
ID AAD34283 standard; DNA; 16 BP.
XX
AC AAD34283;
XX
DT 16-JUL-2002 (first entry)
XX
DE Mouse E2 cDNA amplifying PCR primer, H-T11-A.
XX
KW Mouse; metabolism; E2 gene; insulin resistance syndrome; dyslipidaemia;
KW therapy; non-insulin dependent diabetes mellitus; NIDDM; antilipaemic;
KW obesity; atherosclerosis; antiarteriosclerotic; anorectic; PCR; primer;
KW ss.
XX
OS Mus sp.
XX
PN WO200218421-A2.
XX
PD 07-MAR-2002.
XX
PF 23-AUG-2001; 2001WO-GB003807.
XX
PR 28-AUG-2000; 2000US-0228118P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
XX
PI Brodin P, Thelin A;
XX
DR WPI; 2002-329753/36.
XX
PT New E2 genes and proteins, useful for identifying or manufacturing agents
PT for controlling insulin resistance syndrome or related disorders, e.g.
PT non-insulin dependent diabetes mellitus, dyslipidemia or atherosclerosis.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC The invention relates to the regulation of metabolism and in particular
CC to a gene named E2 involved in insulin resistance syndrome. E2 gene and
CC protein are useful for identifying therapeutic agents for controlling
CC insulin resistance syndrome and other related disorders. They are
CC particularly useful in manufacturing compositions or pharmaceutical for
CC controlling the disorders. Particularly, the chemical compound or
CC composition is useful for controlling insulin resistance syndrome and
CC other related disorders, e.g. non-insulin dependent diabetes mellitus
CC (NIDDM), dyslipidaemia, obesity or atherosclerosis. The present sequence
CC is a PCR primer used to amplify mouse E2 cDNA
XX
SQ Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||| |
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3272
AAD34284
ID AAD34284 standard; DNA; 16 BP.
XX
AC AAD34284;
XX
DT 16-JUL-2002 (first entry)
XX
DE Mouse E2 cDNA amplifying PCR primer, H-T11-C.
XX
KW Mouse; metabolism; E2 gene; insulin resistance syndrome; dyslipidaemia;
KW therapy; non-insulin dependent diabetes mellitus; NIDDM; antilipaemic;
KW obesity; atherosclerosis; antiarteriosclerotic; anorectic; PCR; primer;
KW ss.
XX
OS Mus sp.
XX
PN WO200218421-A2.
XX
PD 07-MAR-2002.
XX
PF 23-AUG-2001; 2001WO-GB003807.
XX
PR 28-AUG-2000; 2000US-0228118P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
XX
PI Brodin P, Thelin A;
XX
DR WPI; 2002-329753/36.
XX
PT New E2 genes and proteins, useful for identifying or manufacturing agents
PT for controlling insulin resistance syndrome or related disorders, e.g.
PT non-insulin dependent diabetes mellitus, dyslipidemia or atherosclerosis.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC The invention relates to the regulation of metabolism and in particular

```
CC   to a gene named E2 involved in insulin resistance syndrome. E2 gene and
CC   protein are useful for identifying therapeutic agents for controlling
CC   insulin resistance syndrome and other related disorders. They are
CC   particularly useful in manufacturing compositions or pharmaceutical for
CC   controlling the disorders. Particularly, the chemical compound or
CC   composition is useful for controlling insulin resistance syndrome and
CC   other related disorders, e.g. non-insulin dependent diabetes mellitus
CC   (NIDDM), dyslipidaemia, obesity or atherosclerosis. The present sequence
CC   is a PCR primer used to amplify mouse E2 cDNA
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3273
AAD32156
ID   AAD32156 standard; DNA; 16 BP.
XX
AC   AAD32156;
XX
DT   18-JUN-2002  (first entry)
XX
DE   H-T11-C PCR primer, to determine ADAMTS-1 role in IRS and obesity.
XX
KW   A disintegrin and metalloproteinase with thrombospondin type 1 motif;
KW   ADAMTS-1; non-insulin dependent diabetes mellitus; ADAM; obesity; IRS;
KW   insulin resistance syndrome; NIDDM; atherosclerosis; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200216632-A1.
XX
PD   28-FEB-2002.
XX
PF   16-AUG-2001; 2001WO-GB003650.
XX
PR   22-AUG-2000; 2000SE-00002973.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Brodin P,  Thelin A;
XX
DR   WPI; 2002-269365/31.
XX
PT   Use of a modulator of ADAMTS-1 ( a disintegrin and metalloproteinase) for
PT   the treatment of obesity, insulin resistance syndrome (IRS), non-insulin
PT   dependent diabetes mellitus (NIDDM) or atherosclerosis.
XX
PS   Example 1; Page 39; 47pp; English.
XX
CC   The invention relates to the use of modulators of A Disintegrin And
CC   Metalloproteinase (ADAM) with Thrombospondin type 1 motif (ADAMTS-1)
CC   which are used in the preparation of a medicament for the treatment of
CC   obesity, insulin resistance syndrome (IRS), non-insulin dependent
CC   diabetes mellitus (NIDDM) and atherosclerosis. The invention also relates
CC   to methods for screening specific modulators of ADAMTS-1 activity. The
CC   present sequence is a PCR primer used to determine the role of ADAMTS-1
CC   in IRS, obesity, NIDDM and atherosclerosis
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3274
AAD32155
ID   AAD32155 standard; DNA; 16 BP.
XX
AC   AAD32155;
XX
DT   18-JUN-2002  (first entry)
XX
DE   H-T11-A PCR primer, to determine ADAMTS-1 role in IRS and obesity.
XX
KW   A disintegrin and metalloproteinase with thrombospondin type 1 motif;
KW   ADAMTS-1; non-insulin dependent diabetes mellitus; ADAM; obesity; IRS;
KW   insulin resistance syndrome; NIDDM; atherosclerosis; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200216632-A1.
XX
PD   28-FEB-2002.
XX
PF   16-AUG-2001; 2001WO-GB003650.
XX
PR   22-AUG-2000; 2000SE-00002973.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Brodin P,  Thelin A;
XX
DR   WPI; 2002-269365/31.
XX
PT   Use of a modulator of ADAMTS-1 ( a disintegrin and metalloproteinase) for
PT   the treatment of obesity, insulin resistance syndrome (IRS), non-insulin
PT   dependent diabetes mellitus (NIDDM) or atherosclerosis.
XX
PS   Example 1; Page 39; 47pp; English.
XX
CC   The invention relates to the use of modulators of A Disintegrin And
CC   Metalloproteinase (ADAM) with Thrombospondin type 1 motif (ADAMTS-1)
CC   which are used in the preparation of a medicament for the treatment of
CC   obesity, insulin resistance syndrome (IRS), non-insulin dependent
CC   diabetes mellitus (NIDDM) and atherosclerosis. The invention also relates
CC   to methods for screening specific modulators of ADAMTS-1 activity. The
CC   present sequence is a PCR primer used to determine the role of ADAMTS-1
CC   in IRS, obesity, NIDDM and atherosclerosis
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3275
ABK12621
ID   ABK12621 standard; DNA; 16 BP.
XX
AC   ABK12621;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Mouse E4 protein, PCR primer H-T11-A.
XX
KW   Mouse; E4; insulin resistance syndrome; NIDDM; dyslipidaemia; obesity;
```

```
KW   non-insulin dependent diabetes mellitus; atherosclerosis; primer; ss.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO200218568-A2.
XX
PD   07-MAR-2002.
XX
PF   23-AUG-2001; 2001WO-GB003828.
XX
PR   28-AUG-2000; 2000US-0228117P.
PR   10-APR-2001; 2001US-0282496P.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Brodin P,  Thelin A;
XX
DR   WPI; 2002-304254/34.
XX
PT   New isolated polynucleotide encoding E4 gene involved in insulin
PT   resistance syndrome, useful for identifying chemical compound useful for
PT   controlling e.g. non-insulin dependent diabetes mellitus.
XX
PS   Example 3; Page 19; 46pp; English.
XX
CC   The invention relates to an isolated polynucleotide (I) molecule
CC   comprising a nucleotide sequence which encodes an E4 polypeptide (II) or
CC   its fragment of at least 10 amino acids. (II) is useful for identifying a
CC   chemical compound capable of modulating the activity of E4 by contacting
CC   the chemical compound with (II) or a transgenic non-human mammal and
CC   measuring any effect of chemical compound on the activity of (II) or
CC   transgenic non-human mammal, where the identifying method is useful for
CC   making a pharmaceutical composition, which comprises mixing the compound
CC   thus identified with a carrier, and the compound is preferably an
CC   antibody that is useful for controlling insulin resistance syndrome and
CC   other related disorders such as non-insulin dependent diabetes mellitus
CC   (NIDDM), dyslipidaemia, obesity, and atherosclerosis. The present
CC   sequence represents a PCR primer used to isolate the coding sequence of
CC   mouse E4 protein
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3276
ABK12622
ID   ABK12622 standard; DNA; 16 BP.
XX
AC   ABK12622;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Mouse E4 protein, PCR primer H-T11-C.
XX
KW   Mouse; E4; insulin resistance syndrome; NIDDM; dyslipidaemia; obesity;
KW   non-insulin dependent diabetes mellitus; atherosclerosis; primer; ss.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO200218568-A2.
XX
PD   07-MAR-2002.
XX
PF   23-AUG-2001; 2001WO-GB003828.
XX
PR   28-AUG-2000; 2000US-0228117P.
PR   10-APR-2001; 2001US-0282496P.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Brodin P,  Thelin A;
XX
DR   WPI; 2002-304254/34.
XX
PT   New isolated polynucleotide encoding E4 gene involved in insulin
PT   resistance syndrome, useful for identifying chemical compound useful for
PT   controlling e.g. non-insulin dependent diabetes mellitus.
XX
PS   Example 3; Page 19; 46pp; English.
XX
CC   The invention relates to an isolated polynucleotide (I) molecule
CC   comprising a nucleotide sequence which encodes an E4 polypeptide (II) or
CC   its fragment of at least 10 amino acids. (II) is useful for identifying a
CC   chemical compound capable of modulating the activity of E4 by contacting
CC   the chemical compound with (II) or a transgenic non-human mammal and
CC   measuring any effect of chemical compound on the activity of (II) or
CC   transgenic non-human mammal, where the identifying method is useful for
CC   making a pharmaceutical composition, which comprises mixing the compound
CC   thus identified with a carrier, and the compound is preferably an
CC   antibody that is useful for controlling insulin resistance syndrome and
CC   other related disorders such as non-insulin dependent diabetes mellitus
CC   (NIDDM), dyslipidaemia, obesity, and atherosclerosis. The present
CC   sequence represents a PCR primer used to isolate the coding sequence of
CC   mouse E4 protein
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3277
ABK87933
ID   ABK87933 standard; DNA; 16 BP.
XX
AC   ABK87933;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Anchored oligo-dT primer, H-T11A, used for differential display.
XX
KW   Human; PCR; primer; H-T11A; ss; CC214; cervical cancer 2; HCCR-2;
KW   protooncogene; cytostatic; tumourigenesis; cervical cancer; cancer;
KW   leukaemia; lymphoma; antisense; gene therapy; carcinogen; anticancer;
KW   antioxidant.
XX
OS   Synthetic.
XX
PN   WO200244370-A1.
XX
PD   06-JUN-2002.
XX
PF   09-JUL-2001; 2001WO-KR001172.
XX
PR   28-NOV-2000; 2000KR-00071202.
XX
PA   (KIMJ/) KIM J W.
XX
PI   Kim JW;
XX
```

```
DR   WPI; 2002-557542/59.
XX
PT   Novel human cervical cancer 2 protooncogene protein and polynucleotide
PT   encoding it useful for diagnosing various cancers e.g. leukemia, lymphoma
PT   or uterine cervix cancer, and for producing transformed animals.
XX
PS   Disclosure; Page 47; 49pp; English.
XX
CC   The invention discloses a human cervical cancer 2 (HCCR-2) protooncogene
CC   and encoded protein. The protooncogene was discovered using mRNA
CC   differential display, identifying it as being amplified in cancer cells
CC   and, more specifically, involved in the tumourigenesis of cervical
CC   cancer. HCCR-2 is useful for preventing, diagnosing or treating cancer,
CC   including leukaemia, lymphoma, colon, breast, kidney, stomach, lung,
CC   ovary or uterine cervix cancer. HCCR-2 is also useful for producing
CC   antibodies which are useful as diagnostic tools. HCCR-2 protooncogene is
CC   useful in the diagnosis of various cancers, in antisense gene therapy and
CC   for producing transformed animals which are useful in screening for
CC   carcinogens or anticancer agents, such as antioxidants. The protooncogene
CC   is also useful for establishing a continuous viable cancer cell line
CC   which is useful in searching for anticancer agents. The sequence
CC   presented is the anchored oligo-dT primer, H-T11A, which was used to
CC   amplify cDNA for differential display. This technique identified a cDNA
CC   fragment, designated CC214, which was then used as a probe to isolate the
CC   full length cDNA (cervical cancer 2 (HCCR-2) protooncogene) from a human
CC   lung embryonic fibroblast cDNA library
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3278
ABK87932
ID   ABK87932 standard; DNA; 16 BP.
XX
AC   ABK87932;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Anchored oligo-dT primer, H-T11C, used for differential display.
XX
KW   Human; PCR; primer; H-T11C; ss; CC214; cervical cancer 2; HCCR-2;
KW   protooncogene; cytostatic; tumourigenesis; cervical cancer; cancer;
KW   leukaemia; lymphoma; antisense; gene therapy; carcinogen; anticancer;
KW   antioxidant.
XX
OS   Synthetic.
XX
PN   WO200244370-A1.
XX
PD   06-JUN-2002.
XX
PF   09-JUL-2001; 2001WO-KR001172.
XX
PR   28-NOV-2000; 2000KR-00071202.
XX
PA   (KIMJ/) KIM J W.
XX
PI   Kim JW;
XX
DR   WPI; 2002-557542/59.
XX
PT   Novel human cervical cancer 2 protooncogene protein and polynucleotide
PT   encoding it useful for diagnosing various cancers e.g. leukemia, lymphoma
PT   or uterine cervix cancer, and for producing transformed animals.
XX
PS   Example 1; Page 47; 49pp; English.
XX
CC   The invention discloses a human cervical cancer 2 (HCCR-2) protooncogene
CC   and encoded protein. The protooncogene was discovered using mRNA
CC   differential display, identifying it as being amplified in cancer cells
CC   and, more specifically, involved in the tumourigenesis of cervical
CC   cancer. HCCR-2 is useful for preventing, diagnosing or treating cancer,
CC   including leukaemia, lymphoma, colon, breast, kidney, stomach, lung,
CC   ovary or uterine cervix cancer. HCCR-2 is also useful for producing
CC   antibodies which are useful as diagnostic tools. HCCR-2 protooncogene is
CC   useful in the diagnosis of various cancers, in antisense gene therapy and
CC   for producing transformed animals which are useful in screening for
CC   carcinogens or anticancer agents, such as antioxidants. The protooncogene
CC   is also useful for establishing a continuous viable cancer cell line
CC   which is useful in searching for anticancer agents. The sequence
CC   presented is the anchored oligo-dT primer, H-T11C, which was used to
CC   amplify cDNA for differential display. This technique identified a cDNA
CC   fragment, designated CC214, which was then used as a probe to isolate the
CC   full length cDNA (cervical cancer 2 (HCCR-2) protooncogene) from a human
CC   lung embryonic fibroblast cDNA library
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3279
AAD30092
ID   AAD30092 standard; DNA; 16 BP.
XX
AC   AAD30092;
XX
DT   17-MAY-2002  (first entry)
XX
DE   PTTG cDNA isolating anchored PCR primer #2.
XX
KW   Pituitary tumour transforming gene; PTTG1; vulnerary; cytostatic;
KW   ophthalmological; antiangiogenic; antisense gene therapy; angiogenesis;
KW   wound healing; tissue regeneration; scar formation; malignant tumour;
KW   retinopathy; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200187935-A2.
XX
PD   22-NOV-2001.
XX
PF   12-MAY-2001; 2001WO-US015437.
XX
PR   12-MAY-2000; 2000US-00569956.
PR   13-OCT-2000; 2000US-00687911.
PR   04-DEC-2000; 2000US-00730469.
PR   05-FEB-2001; 2001US-00777422.
PR   11-MAY-2001; 2001US-00854326.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Heaney AP,  Ishikawa H,  Yu R,  Horwitz GA,  Zhang X,  Melmed S;
XX
DR   WPI; 2002-188148/24.
XX
PT   Modulating angiogenesis in a tissue comprising mammalian cells by
PT   modulating pituitary tumor transforming gene (PTTG1) expression and/or
PT   endogenous PTTG1 protein function.
XX
PS   Example 1; Page 62; 183pp; English.
XX
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CC   The invention relates to a method of modulating angiogenesis in a tissue
CC   comprising mammalian cells by modulating pituitary tumour transforming
CC   gene (PTTG) expression and/or endogenous PTTG1 protein function in at
CC   least one of the cells. The method is useful for enhancing or inhibiting
CC   angiogenesis. Specifically, enhancing wound healing and/or tissue
CC   regeneration and limiting scar formation. The method is also useful in
CC   treating malignant tumours and retinopathy. The present sequence is a PCR
CC   primer used for isolating PTTG1 cDNA
XX
SQ   Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3280
AAD30916
ID   AAD30916 standard; DNA; 16 BP.
XX
AC   AAD30916;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Rat PTTG1 cDNA amplifying PCR primer #3.
XX
KW   Rat; pituitary tumour transforming gene 1; cellular transformation;
KW   PTTG1; inhibition; immunogen; neoplastic cellular proliferation;
KW   T-lymphocyte; PCR primer; ss.
XX
OS   Rattus rattus.
XX
PN   WO200187934-A2.
XX
PD   22-NOV-2001.
XX
PF   12-MAY-2001; 2001WO-US015254.
XX
PR   12-MAY-2000; 2000US-00569956.
PR   13-OCT-2000; 2000US-00687911.
PR   04-DEC-2000; 2000US-00730469.
PR   05-FEB-2001; 2001US-00777422.
XX
PA   (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI   Horwitz GA,  Zhang X,  Heaney AP,  Melmed S;
XX
DR   WPI; 2002-226703/28.
XX
PT   Inhibiting neoplastic cellular proliferation and/or transformation of a
PT   mammalian cell, by using Pituitary tumor transforming gene carboxy-
PT   terminal peptides.
XX
PS   Example 1; Page 64; 190pp; English.
XX
CC   The patent discloses pituitary tumour transforming gene (PTTG) carboxy
CC   terminal peptides. The invention also relates to methods for inhibiting
CC   neoplastic cellular proliferation and transformation (NP/T) of mammalian
CC   cells. The method involves delivering a composition comprising a PTTG
CC   carboxy-terminal-related polynucleotide, an expression vector comprising
CC   a polynucleotide encoding PTTG C-terminal (PTTG-C) peptide, PTTG-C
CC   peptide to a mammalian cell that overexpresses PTTG. The compositions
CC   comprising PTTG-C peptides are useful for inhibiting neoplastic cellular
CC   proliferation and/or transformation of a mammalian cell. PTTG-C peptides
CC   are useful in bioassays, as immunogens to produce anti-PTTG-C antibodies
CC   and in therapeutic compositions. PTTG antibodies are also useful for
CC   inhibiting the activation of mammalian T-lymphocytes. Sequences of the
CC   invention are used as vaccines and in gene therapy. The present sequence
CC   is a PCR primer which is used for amplifying rat PTTG1 cDNA
XX
SQ   Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3281
ABZ21815
ID   ABZ21815 standard; DNA; 16 BP.
XX
AC   ABZ21815;
XX
DT   03-MAR-2003  (first entry)
XX
DE   Anti-cancer drug resistance related oligonucleotide #2.
XX
KW   Anti-cancer; drug resistance; lung cancer; head and neck cancer; ss.
XX
OS   Synthetic.
XX
PN   KR2002031530-A.
XX
PD   02-MAY-2002.
XX
PF   20-OCT-2000; 2000KR-00062030.
XX
PR   20-OCT-2000; 2000KR-00062030.
XX
PA   (PHAR-) PHARMGENIA CO LTD.
XX
PI   Jun SH;
XX
DR   WPI; 2002-737801/80.
XX
PT   DNA sequences relating to anti-cancer drug resistance and the use
PT   thereof.
XX
PS   Disclosure; Page 4; 34pp; Korean.
XX
CC   The present invention describes DNA sequences relating to anti-cancer
CC   drug resistance. The DNA sequences can be used as a component of a kit or
CC   a DNA chip for detecting the presence of anti-cancer resistance. The
CC   method for identifying and sequencing the DNA sequences comprises
CC   obtaining an anti-cancer sensitive cancer tissue and an anti-cancer drug
CC   resistant cancer tissue from patients suffering from lung cancer and head
CC   and neck cancer, isolating mRNAs from the tissues, preparing cDNAs of the
CC   tissues from mRNAs using reverse transcriptase; finding genes showing the
CC   increase or decrease of gene expression in the cancer tissues before and
CC   after the anti-cancer drug treatment using differential display of
CC   polymerase chain reaction (PCR), subjecting the genes to electrophoresis,
CC   amplifying the cDNAs by using PCR, sub-cloning the amplified cDNAs into
CC   pGEM-Teasy plasmid, and sequencing the cDNA using an auto-sequencing
CC   machine. The present sequence represents an oligonucleotide which is used
CC   in the exemplification of the present invention
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3282
```

ABZ21816
ID ABZ21816 standard; DNA; 16 BP.
XX
AC ABZ21816;
XX
DT 03-MAR-2003 (first entry)
XX
DE Anti-cancer drug resistance related oligonucleotide #3.
XX
KW Anti-cancer; drug resistance; lung cancer; head and neck cancer; ss.
XX
OS Synthetic.
XX
PN KR2002031530-A.
XX
PD 02-MAY-2002.
XX
PF 20-OCT-2000; 2000KR-00062030.
XX
PR 20-OCT-2000; 2000KR-00062030.
XX
PA (PHAR-) PHARMGENIA CO LTD.
XX
PI Jun SH;
XX
DR WPI; 2002-737801/80.
XX
PT DNA sequences relating to anti-cancer drug resistance and the use
PT thereof.
XX
PS Disclosure; Page 4; 34pp; Korean.
XX
CC The present invention describes DNA sequences relating to anti-cancer
CC drug resistance. The DNA sequences can be used as a component of a kit or
CC a DNA chip for detecting the presence of anti-cancer resistance. The
CC method for identifying and sequencing the DNA sequences comprises
CC obtaining an anti-cancer sensitive cancer tissue and an anti-cancer drug
CC resistant cancer tissue from patients suffering from lung cancer and head
CC and neck cancer, isolating mRNAs from the tissues, preparing cDNAs of the
CC tissues from mRNAs using reverse transcriptase; finding genes showing the
CC increase or decrease of gene expression in the cancer tissues before and
CC after the anti-cancer drug treatment using differential display of
CC polymerase chain reaction (PCR), subjecting the genes to electrophoresis,
CC amplifying the cDNAs by using PCR, sub-cloning the amplified cDNAs into
CC pGEM-Teasy plasmid, and sequencing the cDNA using an auto-sequencing
CC machine. The present sequence represents an oligonucleotide which is used
CC in the exemplification of the present invention
XX
SQ Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3283
ABN87397
ID ABN87397 standard; DNA; 16 BP.
XX
AC ABN87397;
XX
DT 05-AUG-2002 (first entry)
XX
DE PTTG isolation related anchor primer SEQ ID NO:13.
XX
KW Pituitary tumour-specific gene; PTTG1; PTTG2; transformation;
KW pituitary tumour transforming gene; malignant tumour; cytostatic;
KW neoplastic cellular proliferation inhibition; primer; ss.
XX
OS Synthetic.
XX
PN WO200187039-A2.
XX
PD 22-NOV-2001.
XX
PF 12-MAY-2001; 2001WO-US015255.
XX
PR 12-MAY-2000; 2000US-00569956.
PR 13-OCT-2000; 2000US-00687911.
PR 04-DEC-2000; 2000US-00730469.
PR 05-FEB-2001; 2001US-00777422.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Prezant TR, Heaney AP, Melmed S;
XX
DR WPI; 2002-195496/25.
XX
PT Novel method of inhibiting neoplastic cellular proliferation and/or
PT transformation of a mammalian cell used for treating e.g. malignant
PT tumours.
XX
PS Example 1; Page 60; 175pp; English.
XX
CC The present invention describes a method for inhibiting neoplastic
CC cellular proliferation and/or transformation of a mammalian cell. The
CC method comprises delivering to a mammalian cell that endogenously over
CC expresses pituitary tumour transforming gene (PTTG1), a composition
CC comprising, an expression vector comprising a promoter and a
CC polynucleotide, where the polynucleotide comprises a first DNA segment
CC encoding a mammalian PTTG2 peptide the polynucleotide being operatively
CC linked to the promoter in a transcriptional unit, where PTTG2 is selected
CC from: (a) a peptide (I) consisting essentially of a 191 amino acid
CC sequence (see ABB79058) or a functional fragment comprising at least
CC amino acid residues 1-180; or (b) a mammalian PTTG2 peptide having at
CC least 95% sequence homology with (I). The expression vector is complexed
CC with a cellular uptake-enhancing agent such that the PTTG2 peptide is
CC expressed in the cell where neoplastic cellular proliferation and/or
CC transformation of the cell is inhibited. PTTG2 protein regulates
CC transactivating activity by PTTG1 and that PTTG2 peptide molecules have
CC the ability to down regulate PTTG1 gene expression and/or PTTG1 protein
CC function in a negative manner. The method is useful in inhibiting
CC neoplastic cellular proliferation and/or transformation of mammalian
CC cells both in vivo and in vitro. The method is also useful in treating
CC malignant tumours. The present sequence represents an anchor primer used
CC in the isolation of PTTG cDNA, which is used in an example from the
CC present invention
XX
SQ Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3284
ABA98031
ID ABA98031 standard; cDNA; 16 BP.
XX
AC ABA98031;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human PTTG4 encoding cDNA sequence SEQ ID NO 68.
XX
KW Human; mouse; rat; gene; cytostatic; immunosuppressive; antiasthmatic;
KW dermatalogical; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antipsoriatic; antiatherosclerotic; antiallergic;

KW T-lymphocyte cell; pituitary tumour transforming gene; PTTG; bFGF;
KW transcription; cell proliferation; lymphocyte; graft rejection; allergic;
KW asthmatic; autoimmune disease; rheumatoid arthritis; leukaemia; cancer;
KW tumour; Hodgkin's disease; ss.
XX
OS Homo sapiens.
XX
PN WO200188116-A2.
XX
PD 22-NOV-2001.
XX
PF 12-MAY-2001; 2001WO-US015438.
XX
PR 12-MAY-2000; 2000US-00569956.
PR 13-OCT-2000; 2000US-00687911.
PR 04-DEC-2000; 2000US-00730469.
PR 05-FEB-2001; 2001US-00777422.
PR 11-MAY-2001; 2001US-00854326.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Stoika R, Horwitz GA, Zhang X, Melmed S;
XX
DR WPI; 2002-188151/24.
XX
PT Inhibiting the activation of a mammalian T-lymphocyte cell useful for
PT treating immune-related disorders by inhibiting PTTG1 gene expression.
XX
PS Example 21; Page 112; 185pp; English.
XX
CC The invention relates to inhibiting the activation of a mammalian T-
CC lymphocyte cell comprising inhibiting pituitary tumour transforming gene
CC (PTTG1) expression and/or endogenous PTTG1 protein function in the T-
CC lymphocyte cell, whereby activation of the T-lymphocyte cell is
CC inhibited. PTTG upregulates bFGF secretion and transactivates DNA
CC transcription. Compositions and methods of the invention are useful for
CC inhibiting neoplastic and non-neoplastic proliferation of mammalian T-
CC lymphocyte cells, including activated normal lymphocytes and transformed
CC lymphocytes. The compositions and methods are useful in the prevention or
CC inhibition of xenograft or allograft rejection and in the treatment of
CC allergic, asthmatic and/or autoimmune conditions such as systemic lupus
CC erythematosus (SLE), autoimmune myasthenia gravis, rheumatoid arthritis,
CC autoimmune encephalomyelitis, psoriasis, atherosclerosis and other
CC autoimmune diseases. The inventive methods and compositions are also
CC useful in the treatment of T-cell neoplasias, such as leukaemia, or any
CC haematologic or lymphopoietic neoplasm e.g. Hodgkin's disease. The
CC present sequence is that of a PTTG encoding polynucleotide sequence
XX
SQ Sequence 16 BP; 2 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3285
ABZ96318
ID ABZ96318 standard; DNA; 16 BP.
XX
AC ABZ96318;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human C/EBP antisense fragment no.2178.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11560; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 16 BP; 0 A; 4 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3286
ACC69782
ID ACC69782 standard; DNA; 16 BP.
XX
AC ACC69782;
XX
DT 24-JUL-2003 (first entry)
XX
DE Human cervical cancer suppressor 5 related primer SEQ ID NO:4.
XX
KW Human; cervical cancer suppressor 5; HCCS-5; tumour suppressor;
KW cytostatic; gene therapy; apoptosis; proliferation suppression; cancer;
KW cervical cancer; primer; ss.
XX

```
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003025180-A1.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-KR001734.
XX
PR   18-SEP-2001; 2001KR-00057576.
XX
PA   (KIMJ/) KIM J.
XX
PI   Kim J;
XX
DR   WPI; 2003-363146/34.
XX
PT   New human cervical cancer suppressor gene (HCCS-5), useful for inducing
PT   apoptosis or suppressing proliferation of cancer cells, particularly for
PT   treating or preventing cancer (e.g. cervical cancer).
XX
PS   Example 1; Page 22; 23pp; English.
XX
CC   The present invention describes human cervical cancer suppressor 5 (HCCS-
CC   5), which is a tumour suppressor. Also described: (1) the HCCS-5 protein
CC   having 111 amino acids; (2) an expression vector comprising the HCCS-5
CC   gene or its fragment; (3) a microorganism cell or an animal cell
CC   transformed with the expression vector; (4) suppressing proliferation of
CC   cancer cells by introducing the expression vector into a cancer cell to
CC   induce its apoptosis; and (5) a composition for preventing or treating
CC   cancer comprising the HSSC-5 gene or its fragment, and a pharmaceutical
CC   carrier. HSSC-5 has cytostatic activity, and can be used for gene
CC   therapy. The HSSC-5 gene or the vector can be used for inducing apoptosis
CC   or suppressing proliferation of cancer cells, particularly for treating
CC   or preventing cancer (e.g. cervical cancer). The present sequence
CC   represents an H-T11A anchored oligo-dT primer, which was used in an
CC   example from the present invention
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3287
ABZ70966
ID   ABZ70966 standard; DNA; 16 BP.
XX
AC   ABZ70966;
XX
DT   24-APR-2003  (first entry)
XX
DE   Human cervical cancer proto-oncogene 7 related PCR primer SEQ ID NO:3.
XX
KW   Human; cervical cancer proto-oncogene 7; HCC-7 proto-oncogene; cancer;
KW   cytostatic; vaccine; gene therapy; chromosome 5; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003002743-A1.
XX
PD   09-JAN-2003.
XX
PF   27-JUN-2002; 2002WO-KR001226.
XX
PR   28-JUN-2001; 2001KR-00037588.
XX
PA   (KIMJ/) KIM J W.
XX
PI   Kim JW;
XX
DR   WPI; 2003-201506/19.
XX
PT   New human cervical cancer proto-oncogene, useful for preparing a
PT   composition for preventing or treating cancer.
XX
PS   Example 2; Page 27; 28pp; English.
XX
CC   The present invention describes a human cervical cancer proto-oncogene 7
CC   (HCC-7 proto-oncogene). HCC-7 proto-oncogene is located on human
CC   chromosome 5. HCC-7 proto-oncogene has cytostatic activity and can be
CC   used in vaccines and gene therapy. HCC-7 proto-oncogene can be used for
CC   preparing a composition for preventing or treating cancer. The HCC-7
CC   protein expressed from the proto-oncogene is useful for producing an
CC   antibody for diagnosing cancer. The present sequence represents a PCR
CC   primer which is used in an example from the present invention
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3288
ADB68508
ID   ADB68508 standard; DNA; 16 BP.
XX
AC   ADB68508;
XX
DT   04-DEC-2003  (first entry)
XX
DE   PNA-HypNA hybridisation oligomer.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
KW   phosphono-peptide nucleic acid; pPNA.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = P (Phosphono PNA monomer with phenyl
FT                   group attached to terminal phosphate"
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
```

```
PS   Example 17; Page 148; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the PNA-HypNA hybridisation oligomer of the invention. This
CC   sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
CC   (SerNA) components.
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3289
ADB68508/c
ID   ADB68508 standard; DNA; 16 BP.
XX
AC   ADB68508;
XX
DT   04-DEC-2003  (first entry)
XX
DE   PNA-HypNA hybridisation oligomer.
XX
KW   hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW   gene expression; respiration; secretion; signalling;
KW   ion-channel activity; cell motility; developmental phenotype;
KW   tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
KW   phosphono-peptide nucleic acid; pPNA.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   16
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = P (Phosphono PNA monomer with phenyl
FT                   group attached to terminal phosphate"
XX
PN   WO2003068798-A2.
XX
PD   21-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-US003904.
XX
PR   09-FEB-2002; 2002US-00072975.
XX
PA   (ACTI-) ACTIVE MOTIF.
XX
PI   Efimov V,  Fernandez J,  Archdeacon D,  Archdeachon J,  Choob M;
XX
DR   WPI; 2003-689653/65.
XX
PT   Method of inhibiting expression of genes or RNA transcripts, useful for
PT   therapy and determining effects of genes, by administering oligomers
PT   containing hydroxyproline nucleic acid.
XX
PS   Example 17; Page 148; 240pp; English.
XX
CC   The invention relates to a novel method of inhibiting the expression of
CC   one or more genes or RNA transcripts by administering at least one
CC   oligonucleotide analogue that includes at least one hydroxyproline
CC   nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC   oligonucleotides of the invention may be used to monitor properties
CC   including gene expression, respiration, secretion, signalling, ion-
CC   channel activity, cell motility, developmental phenotype and tumour
CC   regression. Furthermore, they may be utilised to determine the effects of
CC   particular genes, as antisense or homologous recombination constructs
CC   e.g. for creating animal models of disease and finally, for increasing
CC   the activity of some enzymes, such as polymerases. The current sequence
CC   is that of the PNA-HypNA hybridisation oligomer of the invention. This
CC   sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
CC   (SerNA) components.
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3290
ADD26193
ID   ADD26193 standard; DNA; 16 BP.
XX
AC   ADD26193;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Primer relating to the invention H-T11A SEQ ID NO:1.
XX
KW   ss; crosslinking; dermatological; cosmetic; skin; hair; primer; PCR.
XX
OS   Synthetic.
XX
PN   WO2003082923-A1.
XX
PD   09-OCT-2003.
XX
PF   09-AUG-2002; 2002WO-JP008179.
XX
PR   03-APR-2002; 2002JP-00101185.
XX
PA   (FUJI/) FUJIWARA H.
XX
PI   Fujiwara H;
XX
DR   WPI; 2003-853757/79.
XX
PT   Treatment of tyrosine-containing polypeptides with phenol oxidase to
PT   produce crosslinking for control of hardness of polymers for industrial,
PT   cosmetic, or pharmaceutical use.
XX
PS   Example 1; SEQ ID NO 1; 126pp; Japanese.
XX
CC   The invention relates to a novel process for crosslinking polypeptides
CC   containing one or more tyrosine residues surrounded by amino acid
CC   residues which are electrically neutral and contain side-chains of low
CC   molecular weight (not more than 132 Da) by treating the polypeptides with
CC   a phenol oxidase. The process of the invention has dermatological
CC   activity. The method is useful for raising or lowering the hardness of a
CC   polymer by controlling the degree of crosslinking, and for industrial,
CC   cosmetic or medical purposes, e.g. for treatment of skin or hair. The
CC   present sequence is used in the exemplification of the invention.
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3291
ADD26194
ID   ADD26194 standard; DNA; 16 BP.
XX
AC   ADD26194;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Primer relating to the invention H-T11C SEQ ID NO:2.
XX
KW   ss; crosslinking; dermatological; cosmetic; skin; hair; primer; PCR.
XX
OS   Synthetic.
XX
PN   WO2003082923-A1.
XX
PD   09-OCT-2003.
XX
PF   09-AUG-2002; 2002WO-JP008179.
XX
PR   03-APR-2002; 2002JP-00101185.
XX
PA   (FUJI/) FUJIWARA H.
XX
PI   Fujiwara H;
XX
DR   WPI; 2003-853757/79.
XX
PT   Treatment of tyrosine-containing polypeptides with phenol oxidase to
PT   produce crosslinking for control of hardness of polymers for industrial,
PT   cosmetic, or pharmaceutical use.
XX
PS   Example 1; SEQ ID NO 2; 126pp; Japanese.
XX
CC   The invention relates to a novel process for crosslinking polypeptides
CC   containing one or more tyrosine residues surrounded by amino acid
CC   residues which are electrically neutral and contain side-chains of low
CC   molecular weight (not more than 132 Da) by treating the polypeptides with
CC   a phenol oxidase. The process of the invention has dermatological
CC   activity. The method is useful for raising or lowering the hardness of a
CC   polymer by controlling the degree of crosslinking, and for industrial,
CC   cosmetic or medical purposes, e.g. for treatment of skin or hair. The
CC   present sequence is used in the exemplification of the invention.
XX
SQ   Sequence 16 BP; 2 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3292
ADE48126
ID   ADE48126 standard; DNA; 16 BP.
XX
AC   ADE48126;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Oligo-dT primer of the invention.
XX
KW   human tumour suppressor protein; cytostatic; apoptosis; ss; primer.
XX
OS   Synthetic.
XX
PN   WO2003089645-A1.
XX
PD   30-OCT-2003.
XX
PF   16-APR-2003; 2003WO-KR000769.
XX
PR   16-APR-2002; 2002KR-00020601.
XX
PA   (KIMJ/) KIM J W.
XX
PI   Kim JW;
XX
DR   WPI; 2003-854125/79.
XX
PT   New human tumor suppressor protein, useful for preventing or treating
PT   cancer, such as ovarian cancer by suppressing proliferation of cancer
PT   cells.
XX
PS   Example 1; SEQ ID NO 4; 26pp; English.
XX
CC   The present invention relates to a human tumour suppressor protein. The
CC   protein, gene and composition are useful for preventing or treating
CC   cancer by inducing apoptosis, such as ovarian cancer by suppressing
CC   proliferation of cancer cells. The present sequence represents an oligo-
CC   dT primer related to human tumour suppressor gene encoding sequence.
XX
SQ   Sequence 16 BP; 3 A; 1 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3293
ADE86353/c
ID   ADE86353 standard; DNA; 16 BP.
XX
AC   ADE86353;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human PTPN11 PCR primer SEQ ID NO:34.
XX
KW   Noonan syndrome; protein tyrosine phosphatase 11; PTPN11; mutant;
KW   variant; mutation; chromosome 12; enzyme; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003029422-A2.
XX
PD   10-APR-2003.
XX
PF   01-OCT-2002; 2002WO-US031290.
XX
PR   01-OCT-2001; 2001US-0326532P.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Gelb BD,  Tartaglia M;
XX
DR   WPI; 2003-381624/36.
XX
PT   Diagnosing and treating Noonan syndrome in a subject using a mutation in
PT   a protein tyrosine phosphatase 11 gene with increased expression or
```

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PT   activity.
XX
PS   Example 4; SEQ ID NO 34; 262pp; English.
XX
CC   The present invention describes a method for diagnosing Noonan syndrome
CC   in a subject. The method comprises detecting a mutation in the protein
CC   tyrosine phosphatase 11 (PTPN11) gene in a subject, where the mutation
CC   results in increased PTPN11 expression or activity as compared to
CC   control. The human PTPN11 gene is located on chromosome 12, more
CC   specifically to 12q24. Also described: (1) a kit for diagnosing Noonan
CC   syndrome, comprising an oligonucleotide that specifically hybridises to
CC   or adjacent to a site of mutation of a PTPN11 gene that results in
CC   increased activity of a PTPN11 protein encoded by the gene or an antibody
CC   that specifically recognises a mutation in a PTPN11 protein, and
CC   instructions for use; (2) diagnosing Noonan syndrome in a subject,
CC   comprising assessing the level of expression or activity of a PTPN11
CC   protein in the test subject, and comparing it to the level of expression
CC   or activity in a control subject, where an increased expression or basal
CC   activity of the PTPN11 protein in the test subject compared to the
CC   control is indicative of Noonan syndrome; (3) treating Noonan syndrome in
CC   a patient, comprising administering an agent that modulates the
CC   expression or activity of a PTPN11 protein in association with a carrier;
CC   (4) an isolated PTPN11 variant comprising a mutation resulting in
CC   increased level of PTPN11 activity; (5) an isolated cell comprising a
CC   vector comprising a nucleic acid encoding the PTPN11 variant of (4),
CC   operatively associated with an expression control sequence; (6) an
CC   isolated nucleic acid encoding the PTPN11 variant of (4); and (7) an
CC   isolated oligonucleotide which specifically hybridises to the nucleic
CC   acid of (6). The methods and compositions of the present invention are
CC   useful for diagnosing and treating a disorder associated with the
CC   aberrant expression and/or activity of the PTPN11 gene, specifically
CC   Noonan syndrome. The present sequence represents a PCR primer used in the
CC   amplification of human PTPN11, which is given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 16 BP; 0 A; 12 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGG 66
              |||||||||||||||
Db         16 CGGCGGGGGCGGCGG 2


RESULT 3294
AAX69799/c
ID   AAX69799 standard; RNA; 17 BP.
XX
AC   AAX69799;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         17 AAAAAAAAAAAAAAA 3


RESULT 3295
AAX69802
ID   AAX69802 standard; RNA; 17 BP.
XX
AC   AAX69802;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
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PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 2.1e+03;
  Matches    0;  Conservative   15;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ::::::::::::::::
Db          1 UUUUUUUUUUUUUUU 15


RESULT 3296
AAV37934
ID   AAV37934 standard; cDNA; 17 BP.
XX
AC   AAV37934;
XX
DT   05-OCT-1998  (first entry)
XX
DE   Primer of the specification.
XX
KW   Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9824815-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP004469.
XX
PR   05-DEC-1996;   96JP-00325752.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI   Ishiwata T,  Sakurada M,  Nishimura A,  Nakagawa S,  Kuga T,  Nishi T;
PI   Nomura N,  Nagase T,  Sawada S,  Takei M;
XX
DR   WPI; 1998-333259/29.
XX
PT   Protein from leukocytes and DNA encoding it - useful as reagents for
PT   diagnosing and treating IgA nephropathy.
XX
PS   Example 2; Page 33; 41pp; Japanese.
XX
CC   PCR primers AAV37933-39 are used in the course of the invention. The
CC   specification descibes a novel protein isolated from leukocytes of
CC   patients with IgA nephropathy. Oligonucleotides based on the DNA sequence
CC   encoding this protein are useful as reagents for diagnosing and treating
CC   IgA nephropathy
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3297
AAV49503/c
ID   AAV49503 standard; cDNA to mRNA; 17 BP.
XX
AC   AAV49503;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Human eosinophil cell activator HVC002 primer #1.
XX
KW   Eosinophil cell activator; treatment; diagnosis; malignant tumour;
KW   parasitic infection; allergic inflammation; eosinophilic pneumonia;
KW   rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9824817-A1.
XX
PD   11-JUN-1998.
XX
PF   05-DEC-1997;   97WO-JP004470.
XX
PR   05-DEC-1996;   96JP-00325762.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Yoshisue H,  Saito A,  Nakagawa S,  Kuga T,  Shinkai A,  Koike M;
PI   Nishi T;
XX
DR   WPI; 1998-333261/29.
XX
PT   DNA and encoded protein which activates eosinophil cells - for treatment
PT   of cancer, parasite infection, autoimmune disease and allergic
PT   inflammation.
XX
PS   Example 1; Page 64; 92pp; Japanese.
XX
CC   AAV49503-V49507 are primers used in the isolation of a human eosinophil
CC   cell activator. This protein and antibodies generated from the protein
CC   can be used for treatment and diagnosis of malignant tumours, parasitic
CC   infections, allergic inflammation, eosinophilic pneumonia, rapid onset
CC   eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
CC   the antisense DNA in gene therapy of these disorders. The protein can be
CC   used for screening of potential agonists or antagonists of its activity
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3298
AAA30179/c
ID   AAA30179 standard; DNA; 17 BP.
XX
AC   AAA30179;
XX
DT   16-AUG-2000  (first entry)
XX
DE   PCR primer GT15A used in pollenosis associated gene identification.
XX
KW   Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW   IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
```

OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3299
AAA30180
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15C used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3300
AAX82722
ID AAX82722 standard; DNA; 17 BP.
XX
AC AAX82722;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IgA nephropathy-associated cDNA primer #63.
XX
KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002855.
XX
PR 02-JUN-1998; 98JP-00152603.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
PT DNA sequences preferentially expressed in IgA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins.
XX
PS Claim 3; Page 170; 180pp; Japanese.
XX
CC This invention describes novel DNA sequences preferentially expressed in
CC IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC them. Independent claims cover diagnostic reagents for IgA nephropathy
CC incorporating the antisense sequences; the treatment of IgA nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transformed with DNA encoding them; diagnostic
CC reagents for IgA nephropathy containing the antibodies; and compositions
CC for the treatment of IgA nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC IgA nephropathy. This sequence represents a primer used in the isolation

```
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3301
AAX82720/c
ID   AAX82720 standard; DNA; 17 BP.
XX
AC   AAX82720;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Human IgA nephropathy-associated cDNA primer #61.
XX
KW   IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW   human; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963085-A1.
XX
PD   09-DEC-1999.
XX
PF   28-MAY-1999;   99WO-JP002855.
XX
PR   02-JUN-1998;   98JP-00152603.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Ishiwata T,  Sakurada M,  Kawabata A,  Nakagawa S,  Nishi T,  Kuga T;
PI   Sawada S,  Takei M,  Shibata K,  Furuya A;
XX
DR   WPI; 2000-097328/08.
XX
PT   DNA sequences preferentially expressed in IgA nephropathy patients,
PT   proteins encoded by them, and antibodies to those proteins.
XX
PS   Claim 3; Page 169; 180pp; Japanese.
XX
CC   This invention describes novel DNA sequences preferentially expressed in
CC   IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC   them. Independent claims cover diagnostic reagents for IgA nephropathy
CC   incorporating the antisense sequences; the treatment of IgA nephropathy
CC   using the antisense sequences for mRNA inhibition; proteins associated
CC   with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC   antibodies recognizing these proteins; the production of the proteins by
CC   culture of host cells transformed with DNA encoding them; diagnostic
CC   reagents for IgA nephropathy containing the antibodies; and compositions
CC   for the treatment of IgA nephropathy which contain the antibodies. The
CC   products of the invention can be used for the diagnosis and treatment of
CC   IgA nephropathy. This sequence represents a primer used in the isolation
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3302
AAZ36739/c
ID   AAZ36739 standard; DNA; 17 BP.
XX
AC   AAZ36739;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Anchored oligo(dT) primer AT15A used for modified differential display.
XX
KW   Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW   differentially expressed nucleic acid; disease state; cancer;
KW   autoimmune disease; infectious disease; aging; developmental disorder;
KW   proliferative disorder; neurological disorder; toxicity; primer;
KW   treatment resistance; differential expression; drug discovery;
KW   growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS   Synthetic.
XX
PN   WO9955913-A2.
XX
PD   04-NOV-1999.
XX
PF   27-APR-1999;   99WO-US009119.
XX
PR   27-APR-1998;   98US-0083331P.
PR   27-AUG-1998;   98US-0098070P.
PR   04-FEB-1999;   99US-0118624P.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   Mcclelland M,  Welsh J,  Trenkle T;
XX
DR   WPI; 2000-086388/07.
XX
PT   Measuring expression of low abundance reduced complexity target nucleic
PT   acid molecules.
XX
PS   Example 3; Page 91; 187pp; English.
XX
CC   AAZ36739-41 represent oligo(dT) primers used for modified differential
CC   display, in the method of the invention. The specification describes a
CC   method for measuring the level of two or more nucleic acid molecules in a
CC   target. The method comprises contacting a probe with an arbitrarily or
CC   statistically sampled target and detecting the amount of specific binding
CC   of the target to the probe. The methods can be used to identify
CC   differentially expressed nucleic acid molecules associated with disease
CC   states, such as cancer, autoimmune disease, infectious disease, aging,
CC   developmental disorder, proliferative disorder or neurological disorder.
CC   Alternatively the methods can be used to assess the efficacy or toxicity
CC   of or a resistance to a treatment. Also the methods can be used to
CC   determine differential expression of nucleic acid molecules in response
CC   to a stimulus, e.g. a chemical, drug or growth factor (especially
CC   epidermal growth factor), radiation, stress or a pathogen. The methods
CC   can also be used to determine co-regulated genes that can be potential
CC   targets for drug discovery
XX
SQ   Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3303
AAC64202/c
ID   AAC64202 standard; DNA; 17 BP.
```

```
XX
AC   AAC64202;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065046-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002730.
XX
PR   27-APR-1999;   99JP-00120489.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687339/67.
XX
PT   Pollinosis-associated gene 373 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT   in diagnosis of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 69; 80pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 373 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis gene 373; expression constructs and
CC   host cells comprising pollinosis-associated gene 373 nucleic acids;
CC   pollinosis-associated gene 373 primers and probes; antibodies against the
CC   protein encoded by the gene; methods of detection of pollinosis-
CC   associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC   diseases via the detection of pollinosis-associated gene 373 nucleic
CC   acids. The invention additionally encompasses methods of screening drug
CC   candidates for the treatment of allergic disease by measuring the
CC   expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC   T-cells in the presence of a test compound relative to a control.
CC   Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC   diseases and in the screening of drug candidates for the treatment of
CC   such diseases. The present sequence represents a PCR primer used in the
CC   isolation of human pollinosis-associated gene 373 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2

RESULT 3304
AAC64203
ID   AAC64203 standard; DNA; 17 BP.
XX
AC   AAC64203;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065046-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002730.
XX
PR   27-APR-1999;   99JP-00120489.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687339/67.
XX
PT   Pollinosis-associated gene 373 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT   in diagnosis of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 70; 80pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 373 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis gene 373; expression constructs and
CC   host cells comprising pollinosis-associated gene 373 nucleic acids;
CC   pollinosis-associated gene 373 primers and probes; antibodies against the
CC   protein encoded by the gene; methods of detection of pollinosis-
CC   associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC   diseases via the detection of pollinosis-associated gene 373 nucleic
CC   acids. The invention additionally encompasses methods of screening drug
CC   candidates for the treatment of allergic disease by measuring the
CC   expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC   T-cells in the presence of a test compound relative to a control.
CC   Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC   diseases and in the screening of drug candidates for the treatment of
CC   such diseases. The present sequence represents a PCR primer used in the
CC   isolation of human pollinosis-associated gene 373 cDNA
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16

RESULT 3305
AAC64181/c
ID   AAC64181 standard; DNA; 17 BP.
XX
AC   AAC64181;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
XX
KW   Human; pollinosis-associated gene 419; FAF-1 homologue;
KW   Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW   T-cell; reduced expression; detection; diagnosis; drug screening;
```

KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3306
AAC64182
ID AAC64182 standard; DNA; 17 BP.
XX
AC AAC64182;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
XX
KW Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065045-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002729.
XX
PR 27-APR-1999; 99JP-00120490.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 49; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control.Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3307
AAC64171/c
ID AAC64171 standard; DNA; 17 BP.
XX
AC AAC64171;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.

XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 38; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3308
AAC64172
ID AAC64172 standard; DNA; 17 BP.
XX
AC AAC64172;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 38; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3309
AAC64161/c
ID AAC64161 standard; DNA; 17 BP.
XX
AC AAC64161;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 39; 69pp; Japanese.
XX

CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
```

RESULT 3310
AAC64162
ID AAC64162 standard; DNA; 17 BP.
XX
AC AAC64162;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3311
AAC64213/c
ID AAC64213 standard; DNA; 17 BP.
XX
AC AAC64213;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 41; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence

```
CC   of a test compound relative to a control. Pollinosis-associated gene 627
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 627 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2

RESULT 3312
AAC64214
ID   AAC64214 standard; DNA; 17 BP.
XX
AC   AAC64214;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
XX
KW   Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065051-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002735.
XX
PR   27-APR-1999;   99JP-00120493.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687344/67.
XX
PT   Pollinosis-associated gene 627 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 42; 51pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 627 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates to methods of
CC   detection of pollinosis-associated gene 627 nucleic acids; a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 627 nucleic acids; and a method of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis-associated gene 627
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 627 cDNA
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16

RESULT 3313
AAC64231
ID   AAC64231 standard; DNA; 17 BP.
XX
AC   AAC64231;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.
XX
KW   Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW   immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW   detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065050-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002734.
XX
PR   27-APR-1999;   99JP-00120494.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2000-687343/67.
XX
PT   Pollinosis-associated gene 795 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Page 45; Example 6; 73pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 795 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. Pollinosis-associated gene 795 has
CC   homology with the human vimentin gene. The invention also relates also
CC   relates to the protein encoded by pollinosis gene 795; to expression
CC   constructs and host cells comprising pollinosis-associated gene 795
CC   nucleic acids; pollinosis-associated gene 795 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 795 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 795 nucleic acids. The invention additionally encompasses methods of
CC   screening drug candidates for the treatment of allergic disease by
CC   measuring the expression of pollinosis-associated gene 795 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3314
AAC64230/c
ID   AAC64230 standard; DNA; 17 BP.
XX
AC   AAC64230;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
XX
KW   Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW   immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW   detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065050-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002734.
XX
PR   27-APR-1999;   99JP-00120494.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2000-687343/67.
XX
PT   Pollinosis-associated gene 795 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Page 45; Example 6; 73pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 795 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. Pollinosis-associated gene 795 has
CC   homology with the human vimentin gene. The invention also relates also
CC   relates to the protein encoded by pollinosis gene 795; to expression
CC   constructs and host cells comprising pollinosis-associated gene 795
CC   nucleic acids; pollinosis-associated gene 795 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 795 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-associated
CC   gene 795 nucleic acids. The invention additionally encompasses methods of
CC   screening drug candidates for the treatment of allergic disease by
CC   measuring the expression of pollinosis-associated gene 795 in pollen
CC   antigen-stimulated T-cells in the presence of a test compound relative to
CC   a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC   allergic diseases and in the screening of drug candidates for the
CC   treatment of such diseases. The present sequence represents a PCR primer
CC   used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3315
AAC92292/c
ID   AAC92292 standard; DNA; 17 BP.
XX
AC   AAC92292;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 43; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3316
AAC92293
ID   AAC92293 standard; DNA; 17 BP.
XX
AC   AAC92293;
XX
DT   22-MAR-2001  (first entry)
XX
```

DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073439-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-061528/07.
XX
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 44; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3317
AAC91720
ID AAC91720 standard; DNA; 17 BP.
XX
AC AAC91720;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 40; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3318
AAC91719/c
ID AAC91719 standard; DNA; 17 BP.
XX
AC AAC91719;
XX
DT 27-MAR-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
XX
KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX

```
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-032159/04.
XX
PT   Pollinosis-associated gene 787 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 40; 54pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 787 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   after the pollen-scattering season, relative to expression levels in T-
CC   cells before the pollen-scattering season. The gene was isolated from T-
CC   cells from individuals allergic to pollen using the differential display
CC   method. The invention also relates to pollinosis-associated gene 787
CC   primers and probes; methods of detection of pollinosis-associated gene
CC   787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC   detection of pollinosis-associated gene 787 nucleic acids. The invention
CC   additionally encompasses a method of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis- associated gene 787
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 787 cDNA
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3319
AAC82875
ID   AAC82875 standard; DNA; 17 BP.
XX
AC   AAC82875;
XX
DT   20-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 441 primer #2.
XX
KW   Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW   pollen scattering; antigen; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073435-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003190.
XX
PR   27-MAY-1999;   99JP-00148783.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2001-061526/07.
XX
PT   Pollinosis-associated gene 441 which undergoes lower expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 35; 42pp; Japanese.
XX
CC   This invention describes a novel nucleic acid molecule comprising a
CC   sequence (I) which undergoes significantly low expression in subjects
CC   after pollen scattering, and is useful in diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3320
AAC82874/c
ID   AAC82874 standard; DNA; 17 BP.
XX
AC   AAC82874;
XX
DT   20-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 441 primer #1.
XX
KW   Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW   pollen scattering; antigen; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073435-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003190.
XX
PR   27-MAY-1999;   99JP-00148783.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2001-061526/07.
XX
PT   Pollinosis-associated gene 441 which undergoes lower expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 35; 42pp; Japanese.
XX
CC   This invention describes a novel nucleic acid molecule comprising a
CC   sequence (I) which undergoes significantly low expression in subjects
CC   after pollen scattering, and is useful in diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3321
AAH47127
ID   AAH47127 standard; DNA; 17 BP.
XX
AC   AAH47127;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15C.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 66; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3322
AAH47126/c
ID   AAH47126 standard; DNA; 17 BP.
XX
AC   AAH47126;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15A.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 65; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3323
ABK49634/c
ID   ABK49634 standard; DNA; 17 BP.
XX
AC   ABK49634;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW   Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW   differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
OS   Homo sapiens.
XX
PN   WO200224903-A1.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-JP008246.
XX
PR   25-SEP-2000; 2000JP-00291318.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Fujishima T,  Nagasu T,  Tsujimoto G;
PI   Takahashi E;
XX
DR   WPI; 2002-315738/35.
XX
PT   Examining allergic diseases by differential display of gene showing
PT   different expression particularly increased expression in remission stage
PT   in eosinophils of patients, also applicable in screening candidate
```

PT compounds for remedies.
XX
PS Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
```

RESULT 3324
ABK49635
ID ABK49635 standard; DNA; 17 BP.
XX
AC ABK49635;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 56; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3325
ABL59038/c
ID ABL59038 standard; DNA; 17 BP.
XX
AC ABL59038;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer GT15A.
XX
KW Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002095500-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-00291316.
XX
PR 25-SEP-2000; 2000JP-00291316.
XX
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR WPI; 2002-439993/47.
XX
PT Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.
XX
PS Example 1; Page 17; 20pp; Japanese.
XX
CC The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergosis. The present sequence represents a PCR primer, which is used
CC in the course of the invention

```
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3326
ABL59039
ID   ABL59039 standard; DNA; 17 BP.
XX
AC   ABL59039;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Nucleotide sequence of PCR primer GT15C.
XX
KW   Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002095500-A.
XX
PD   02-APR-2002.
XX
PF   25-SEP-2000; 2000JP-00291316.
XX
PR   25-SEP-2000; 2000JP-00291316.
XX
PA   (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA   (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR   WPI; 2002-439993/47.
XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3327
ABN99829/c
ID   ABN99829 standard; DNA; 17 BP.
XX
AC   ABN99829;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Human allergic disease related PCR primer SEQ ID NO: 18.
XX
KW   Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200233069-A1.
XX
PD   25-APR-2002.
XX
PF   28-SEP-2001; 2001WO-JP008574.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
XX
DR   WPI; 2002-372311/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   seventeen genes showing different expression particularly significant
PT   increase in eosinophils in patients with mild atopic dermatitis, also
PT   applicable in screening compounds.
XX
PS   Example 1; Page 109; 165pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   which involves determining the expression level of a gene, having one of
CC   the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC   eosinophils in a patient and comparing the expression level with that in
CC   the eosinophils of a healthy individual. The method can be used to
CC   examine allergic diseases, particularly atopic dermatitis, and its early
CC   diagnosis, which is also applicable in screening candidate compounds for
CC   remedies. The present sequence is a PCR primer described in the
CC   exemplification of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3328
ABN99830
ID   ABN99830 standard; DNA; 17 BP.
XX
AC   ABN99830;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Human allergic disease related PCR primer SEQ ID NO: 19.
XX
KW   Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200233069-A1.
XX
PD   25-APR-2002.
XX
PF   28-SEP-2001; 2001WO-JP008574.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
```

```
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
XX
DR   WPI; 2002-372311/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   seventeen genes showing different expression particularly significant
PT   increase in eosinophils in patients with mild atopic dermatitis, also
PT   applicable in screening compounds.
XX
PS   Example 1; Page 109; 165pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   which involves determining the expression level of a gene, having one of
CC   the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC   eosinophils in a patient and comparing the expression level with that in
CC   the eosinophils of a healthy individual. The method can be used to
CC   examine allergic diseases, particularly atopic dermatitis, and its early
CC   diagnosis, which is also applicable in screening candidate compounds for
CC   remedies. The present sequence is a PCR primer described in the
CC   exemplification of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3329
AAL49948/c
ID   AAL49948 standard; DNA; 17 BP.
XX
AC   AAL49948;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human B1153 expression in allergic disease related PCR primer GT15A.
XX
KW   Human; allergy; B1153; differential expression; antiallergic; asthma;
KW   antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200250269-A1.
XX
PD   27-JUN-2002.
XX
PF   21-DEC-2001; 2001WO-JP011286.
XX
PR   21-DEC-2000; 2000JP-00389476.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Matsumoto Y,  Imai Y,  Oshida T,  Sugita Y,  Nagasu T,  Tsujimoto G;
XX
DR   WPI; 2002-713252/77.
XX
PT   Examination of allergic diseases comprises detecting gene B1153 over-
PT   expressed in T cells of allergy patients for diagnosis treatment and
PT   investigation of atopic skin inflammation and asthma.
XX
PS   Example 6; Page 81; 102pp; Japanese.
XX
CC   The present invention relates to a method of examining allergic diseases
CC   which comprises comparing the expression level of gene B1153 in allergy
CC   patients with the expression level in healthy subjects. The method is
CC   useful for the treatment, prevention, diagnosis and study of allergic
CC   diseases including atopic skin inflammation and asthma. The present
CC   sequence is a PCR primer described in the exemplification of the
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3330
AAL49949
ID   AAL49949 standard; DNA; 17 BP.
XX
AC   AAL49949;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human B1153 expression in allergic disease related PCR primer GT15C.
XX
KW   Human; allergy; B1153; differential expression; antiallergic; asthma;
KW   antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200250269-A1.
XX
PD   27-JUN-2002.
XX
PF   21-DEC-2001; 2001WO-JP011286.
XX
PR   21-DEC-2000; 2000JP-00389476.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Matsumoto Y,  Imai Y,  Oshida T,  Sugita Y,  Nagasu T,  Tsujimoto G;
XX
DR   WPI; 2002-713252/77.
XX
PT   Examination of allergic diseases comprises detecting gene B1153 over-
PT   expressed in T cells of allergy patients for diagnosis treatment and
PT   investigation of atopic skin inflammation and asthma.
XX
PS   Example 6; Page 82; 102pp; Japanese.
XX
CC   The present invention relates to a method of examining allergic diseases
CC   which comprises comparing the expression level of gene B1153 in allergy
CC   patients with the expression level in healthy subjects. The method is
CC   useful for the treatment, prevention, diagnosis and study of allergic
CC   diseases including atopic skin inflammation and asthma. The present
CC   sequence is a PCR primer described in the exemplification of the
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3331
```

```
AAL47234/c
ID   AAL47234 standard; DNA; 17 BP.
XX
AC   AAL47234;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 2.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
XX
PF   11-OCT-2001; 2001WO-JP008937.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
PI   Takahashi E;
XX
DR   WPI; 2002-372313/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   intersectin 2 gene showing different expression particularly significant
PT   increase in eosinophils in patients.
XX
PS   Example 1; Page 52; 90pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   with intersectin 2 gene or a gene with equivalent function of intersectin
CC   2 as an indicator gene, which comprises determining the expression level
CC   of the gene in the eosinophils in a patient, and comparing the expression
CC   level with that in the eosinophils of a healthy individual. The method is
CC   for examining allergic diseases, particularly atopic dermatitis, which is
CC   also applicable in screening candidate compounds for remedies. The
CC   present sequence is an anchor primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
                ||||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2

RESULT 3332
AAL47235
ID   AAL47235 standard; DNA; 17 BP.
XX
AC   AAL47235;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 3.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
XX
PF   11-OCT-2001; 2001WO-JP008937.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
PI   Takahashi E;
XX
DR   WPI; 2002-372313/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   intersectin 2 gene showing different expression particularly significant
PT   increase in eosinophils in patients.
XX
PS   Example 1; Page 53; 90pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   with intersectin 2 gene or a gene with equivalent function of intersectin
CC   2 as an indicator gene, which comprises determining the expression level
CC   of the gene in the eosinophils in a patient, and comparing the expression
CC   level with that in the eosinophils of a healthy individual. The method is
CC   for examining allergic diseases, particularly atopic dermatitis, which is
CC   also applicable in screening candidate compounds for remedies. The
CC   present sequence is an anchor primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
                ||||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16

RESULT 3333
ABK49757
ID   ABK49757 standard; DNA; 17 BP.
XX
AC   ABK49757;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human atopic dermatitis cDNA related PCR primer GT15c.
XX
KW   Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW   allergic disease; antiallergic; dermatological; GT15c.
XX
OS   Synthetic.
XX
PN   WO200226962-A1.
XX
PD   04-APR-2002.
XX
PF   21-SEP-2001; 2001WO-JP008247.
XX
PR   26-SEP-2000; 2000JP-00293021.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Fujishima T,  Nagasu T,  Saito H;
XX
DR   WPI; 2002-330097/36.
```

```
XX
PT   Examining allergic diseases by differential display of genes showing
PT   different expression particularly increase in remission stage in
PT   eosinophils in patients.
XX
PS   Example 1; Page 55; 74pp; Japanese.
XX
CC   This invention relates to gene sequences that are differentially
CC   expressed in eosinophils from patients with atopic dermatitis in the
CC   increment stage as compared with those in the remission stage. These
CC   sequences are used in a novel method for examining allergic diseases
CC   comprising determining the expression levels of these genes and comparing
CC   the expression level with that in the eosinophils of a healthy
CC   individual. The method of the invention may have antiallergic or
CC   dermatological activities. The method can be used to diagnose allergic
CC   diseases particularly atopic dermatitis, and may also be used to screen
CC   candidate compounds for remedies. The method of the invention can be
CC   performed in high throughput, at low cost. The present sequence
CC   represents the GT15c PCR primer used to amplify the differentially
CC   amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3334
ABK49756/c
ID   ABK49756 standard; DNA; 17 BP.
XX
AC   ABK49756;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human atopic dermatitis cDNA related PCR primer GT15a.
XX
KW   Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW   allergic disease; antiallergic; dermatological; GT15a.
XX
OS   Synthetic.
XX
PN   WO200226962-A1.
XX
PD   04-APR-2002.
XX
PF   21-SEP-2001; 2001WO-JP008247.
XX
PR   26-SEP-2000; 2000JP-00293021.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Fujishima T,  Nagasu T,  Saito H;
XX
DR   WPI; 2002-330097/36.
XX
PT   Examining allergic diseases by differential display of genes showing
PT   different expression particularly increase in remission stage in
PT   eosinophils in patients.
XX
PS   Example 1; Page 54; 74pp; Japanese.
XX
CC   This invention relates to gene sequences that are differentially
CC   expressed in eosinophils from patients with atopic dermatitis in the
CC   increment stage as compared with those in the remission stage. These
CC   sequences are used in a novel method for examining allergic diseases
CC   comprising determining the expression levels of these genes and comparing
CC   the expression level with that in the eosinophils of a healthy
CC   individual. The method of the invention may have antiallergic or
CC   dermatological activities. The method can be used to diagnose allergic
CC   diseases particularly atopic dermatitis, and may also be used to screen
CC   candidate compounds for remedies. The method of the invention can be
CC   performed in high throughput, at low cost. The present sequence
CC   represents the GT15a PCR primer used to amplify the differentially
CC   amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3335
ABX79793
ID   ABX79793 standard; cDNA; 17 BP.
XX
AC   ABX79793;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #118.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 483; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
```

```
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3336
ADC84469
ID   ADC84469 standard; DNA; 17 BP.
XX
AC   ADC84469;
XX
DT   01-JAN-2004  (first entry)
XX
DE   PCR primer for amplifying  plant blastogenesis specific gene #SEQ ID 2.
XX
KW   Plant blastogenesis; transformation; gene expression; tissue specific;
KW   PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2003159071-A.
XX
PD   03-JUN-2003.
XX
PF   22-NOV-2001; 2001JP-00358366.
XX
PR   22-NOV-2001; 2001JP-00358366.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-818678/77.
XX
PT   New naturally derived DNA specifically expressed during blastogenesis of
PT   a plant, useful for producing a transformed plant and for compulsive
PT   expression of a protein.
XX
PS   Example 3; SEQ ID NO 2; 43pp; Japanese.
XX
CC   The invention relates to naturally derived DNA specifically expressed
CC   during plant blastogenesis. The DNA of the invention is useful for
CC   producing a transformed plant. Methods of the invention are also useful
CC   for compulsive expression of this DNA. Methods of the invention are
CC   useful for plant tissue specific expression of genes. Also, the growth
CC   stage of a plant can be controlled specifically. The current sequence
CC   represents a PCR primer for amplifying a plant blastogenesis specific
CC   gene of the invention.
XX
SQ   Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3337
ADC84468/c
ID   ADC84468 standard; DNA; 17 BP.
XX
AC   ADC84468;
XX
DT   01-JAN-2004  (first entry)
XX
DE   PCR primer for amplifying  plant blastogenesis specific gene #SEQ ID 1.
XX
KW   Plant blastogenesis; transformation; gene expression; tissue specific;
KW   PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2003159071-A.
XX
PD   03-JUN-2003.
XX
PF   22-NOV-2001; 2001JP-00358366.
XX
PR   22-NOV-2001; 2001JP-00358366.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-818678/77.
XX
PT   New naturally derived DNA specifically expressed during blastogenesis of
PT   a plant, useful for producing a transformed plant and for compulsive
PT   expression of a protein.
XX
PS   Example 3; SEQ ID NO 1; 43pp; Japanese.
XX
CC   The invention relates to naturally derived DNA specifically expressed
CC   during plant blastogenesis. The DNA of the invention is useful for
CC   producing a transformed plant. Methods of the invention are also useful
CC   for compulsive expression of this DNA. Methods of the invention are
CC   useful for plant tissue specific expression of genes. Also, the growth
CC   stage of a plant can be controlled specifically. The current sequence
CC   represents a PCR primer for amplifying a plant blastogenesis specific
CC   gene of the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3338
ADE77745
ID   ADE77745 standard; DNA; 17 BP.
XX
AC   ADE77745;
XX
DT   29-JAN-2004  (first entry)
XX
DE   DNA oligo (SeqID 5) related to the human B1799 gene.
XX
KW   ss; allergic disease; B1799; antiallergic; antiinflammatory;
KW   dermatological; gene therapy; atopic dermatitis.
XX
OS   Unidentified.
XX
PN   WO2003083139-A1.
XX
PD   09-OCT-2003.
XX
PF   25-FEB-2003; 2003WO-JP002047.
XX
PR   03-APR-2002; 2002JP-00100908.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN AGENCY NATION.
XX
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PI Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;
XX
DR WPI; 2003-804076/75.
XX
PT Examining allergic diseases, such as atopic dermatitis, comprises
PT comparing the expression levels of gene B1799 in T cells in a patient and
PT a healthy individual.
XX
PS Example 1; SEQ ID NO 5; 87pp; Japanese.
XX
CC This invention relates to a novel method for screening and examining
CC allergic diseases by the use of B1799 as the indicator gene.
CC Specifically, it comprises determining the expression level of this
CC indicator gene in a biological sample obtained from the patient, and
CC identifying differential expression (increased expression of B1799) in
CC comparison to that observed in a healthy individual. The present
CC invention describes the B1799 protein as antiallergic, antiinflammatory
CC and dermatological. As such, through the use of gene therapy, this method
CC can be used to treat allergic diseases particularly atopic dermatitis.
CC Furthermore, it is useful for determining a diagnosis that is convenient
CC and non-invasive, and is also applicable in high throughput screening to
CC identify candidate compounds for additional remedies. This
CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human
CC B1799 gene of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3339
AAV19118
ID AAV19118 standard; DNA; 17 BP.
XX
AC AAV19118;
XX
DT 28-AUG-1998 (first entry)
XX
DE Anchored oligo(T) primer.
XX
KW Secreted apoptosis-related protein; SARP; mSARP1; mouse; prostate cancer;
KW breast cancer; diagnosis; gene therapy; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9813493-A2.
XX
PD 02-APR-1998.
XX
PF 24-SEP-1997; 97WO-US017154.
XX
PR 24-SEP-1996; 96US-0026603P.
PR 11-OCT-1996; 96US-0028363P.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Umansky S, Melkonyan H;
XX
DR WPI; 1998-230704/20.
XX
PT New secreted apoptosis-related proteins - useful for modulating
PT apoptosis, particularly for treatment of prostatic or breast cancer, also
PT for diagnosis and monitoring of disease.
XX
PS Example 1; Page 30; 101pp; English.
XX
CC This oligo(T) synthetic oligonucleotide was used for first strand cDNA
CC synthesis from total RNA isolated from either logarithmically growing or
CC quiescent 10T1/2 mouse fibroblast cells. It was also used with an
CC arbitarary d(N10) primer in PCR. The PCR products were used in a
CC differential display to identify the mSARP1 gene (see AAV19112) that
CC codes for novel murine secreted apoposis-related protein mSARP1 (see
CC AAW37814). The invention relates to SARP polynucleotides (see also
CC AAV19113-15) and polypeptides (see also AAW37815-17), antibodies specific
CC for SARP, and use of such polynucleotides and antibodies in diagnostic
CC and therapeutic methods, and methods for treating diseases related to the
CC regulation of SARP expression in tissue and body fluid samples, including
CC cancers
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3340
AAX69437
ID AAX69437 standard; RNA; 17 BP.
XX
AC AAX69437;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #732.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 68; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention

```
XX
SQ   Sequence 17 BP; 1 A; 2 C; 2 G; 0 T; 12 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   26.7%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              ||:::::::::::||
Db          1 GCUUUUUUUUUUUGA 15


RESULT 3341
AAX69436
ID   AAX69436 standard; RNA; 17 BP.
XX
AC   AAX69436;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #731.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 68; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 2 G; 0 T; 12 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   26.7%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              ||:::::::::::||
Db          2 GCUUUUUUUUUUUGA 16


RESULT 3342
AAX69435
ID   AAX69435 standard; RNA; 17 BP.
XX
AC   AAX69435;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #730.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 68; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 3 G; 0 T; 12 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   26.7%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              ||:::::::::::||
Db          3 GCUUUUUUUUUUUGA 17


RESULT 3343
AAX55054
ID   AAX55054 standard; DNA; 17 BP.
XX
AC   AAX55054;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
```

```
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3344
AAA30181
ID   AAA30181 standard; DNA; 17 BP.
XX
AC   AAA30181;
XX
DT   16-AUG-2000  (first entry)
XX
DE   PCR primer GT15G used in pollenosis associated gene identification.
XX
KW   Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW   IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200020575-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-JP005506.
XX
PR   06-OCT-1998;   98JP-00284610.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Lu N,  Ogawa K;
XX
DR   WPI; 2000-317712/27.
XX
PT   Gene highly expressed in patients with high cedar pollen-specific IgE
PT   levels, useful for diagnosing pollenosis, and screening candidate
PT   compounds for pollenosis treatment.
XX
PS   Example 6; Page 38; 44pp; Japanese.
XX
CC   This sequence represents a PCR primer used in the identification of a
CC   human pollenosis associated gene. The gene is highly expressed in
CC   individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC   invention relates to the nucleotide sequence encoding the pollenosis
CC   associated protein, diagnosing pollenosis and screening candidate
CC   compounds for treating pollenosis. The gene can be used in diagnosing
CC   pollenosis, particularly cedar pollenosis, and screening candidate
CC   compounds for pollenosis treatment
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3345
AAA30181/c
ID   AAA30181 standard; DNA; 17 BP.
XX
AC   AAA30181;
XX
DT   16-AUG-2000  (first entry)
XX
DE   PCR primer GT15G used in pollenosis associated gene identification.
XX
KW   Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW   IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200020575-A1.
XX
PD   13-APR-2000.
XX
PF   06-OCT-1999;   99WO-JP005506.
XX
PR   06-OCT-1998;   98JP-00284610.
XX
PA   (GENO-) GENOX RES INC.
XX
```

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IgE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3346
AAA34501
ID AAA34501 standard; DNA; 17 BP.
XX
AC AAA34501;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2190.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 539; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
|||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3347
AAZ35714
ID AAZ35714 standard; DNA; 17 BP.
XX
AC AAZ35714;
XX
DT 31-JAN-2000 (first entry)
XX
DE Murine gene anchor PCR primer SEQ ID NO:3.
XX
KW Rare expressed gene; analysis; expression; nucleic acid sample;
KW PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN EP959141-A2.
XX
PD 24-NOV-1999.
XX
PF 18-MAY-1999; 99EP-00109795.
XX
PR 20-MAY-1998; 98JP-00153651.
XX
PA (HITA) HITACHI LTD.
XX
PI Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;
XX
DR WPI; 2000-001284/01.
XX
PT Preparation of nucleic acid sample, useful for analysis of rare expressed
PT genes.
XX
PS Disclosure; Page 11; 22pp; English.
XX
CC The present invention describes a process for the preparation of a

CC nucleic acid sample comprising: (a) providing a nucleic acid sample
CC having a plurality of species of sequences, and providing one or a
CC plurality of kinds of probes having a known sequence substantially
CC complementary to a portion of sequence of the nucleic acid sample; (b)
CC mixing and hybridizing the nucleic acid sample with probes; (c)
CC subsequently recovering nucleic acid molecules; or (i) providing a
CC nucleic acid sample having a plurality of species of sequences, and
CC providing one or a plurality of kinds of probes having a known sequence
CC substantially complementary to a portion of sequence of the nucleic acid
CC sample; (ii) mixing and hybridizing the nucleic acid sample with the
CC probes; (iii) treating the product of (ii) with nuclease activity of an
CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic
CC acid molecules not digested by the nuclease activity in (iii); or (I)
CC providing a nucleic acid sample having a plurality of species of
CC sequences and oligonucleotides primer having predetermined sequences for
CC synthesizing DNA strands; (II) providing one or a plurality of kinds of
CC probes having a known sequence substantially complementary to a portion
CC of a sequence of the nucleic acid sample having such a structure to
CC prevent a polymerase reaction from its 3' end and a nuclease reaction
CC from its 5' end; (III) mixing and hybridizing the nucleic acid sample
CC with the primers and probes; (IV) executing polymerase chain reaction for
CC the samples prepared in (III); and (V) subsequently recovering nucleic
CC acid molecules synthesized in (IV). The method is useful for the
CC preparation of a nucleic acid sample for the analysis of rare expressed
CC genes. The present sequence represents a PCR primer used in the
CC exemplification of the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3348
AAZ35714/c
ID AAZ35714 standard; DNA; 17 BP.
XX
AC AAZ35714;
XX
DT 31-JAN-2000 (first entry)
XX
DE Murine gene anchor PCR primer SEQ ID NO:3.
XX
KW Rare expressed gene; analysis; expression; nucleic acid sample;
KW PCR primer; ss.
XX
OS Synthetic.
OS Mus sp.
XX
PN EP959141-A2.
XX
PD 24-NOV-1999.
XX
PF 18-MAY-1999; 99EP-00109795.
XX
PR 20-MAY-1998; 98JP-00153651.
XX
PA (HITA) HITACHI LTD.
XX
PI Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;
XX
DR WPI; 2000-001284/01.
XX
PT Preparation of nucleic acid sample, useful for analysis of rare expressed
PT genes.
XX
PS Disclosure; Page 11; 22pp; English.
XX

CC The present invention describes a process for the preparation of a
CC nucleic acid sample comprising: (a) providing a nucleic acid sample
CC having a plurality of species of sequences, and providing one or a
CC plurality of kinds of probes having a known sequence substantially
CC complementary to a portion of sequence of the nucleic acid sample; (b)
CC mixing and hybridizing the nucleic acid sample with probes; (c)
CC subsequently recovering nucleic acid molecules; or (i) providing a
CC nucleic acid sample having a plurality of species of sequences, and
CC providing one or a plurality of kinds of probes having a known sequence
CC substantially complementary to a portion of sequence of the nucleic acid
CC sample; (ii) mixing and hybridizing the nucleic acid sample with the
CC probes; (iii) treating the product of (ii) with nuclease activity of an
CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic
CC acid molecules not digested by the nuclease activity in (iii); or (I)
CC providing a nucleic acid sample having a plurality of species of
CC sequences and oligonucleotides primer having predetermined sequences for
CC synthesizing DNA strands; (II) providing one or a plurality of kinds of
CC probes having a known sequence substantially complementary to a portion
CC of a sequence of the nucleic acid sample having such a structure to
CC prevent a polymerase reaction from its 3' end and a nuclease reaction
CC from its 5' end; (III) mixing and hybridizing the nucleic acid sample
CC with the primers and probes; (IV) executing polymerase chain reaction for
CC the samples prepared in (III); and (V) subsequently recovering nucleic
CC acid molecules synthesized in (IV). The method is useful for the
CC preparation of a nucleic acid sample for the analysis of rare expressed
CC genes. The present sequence represents a PCR primer used in the
CC exemplification of the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3349
AAX82721
ID AAX82721 standard; DNA; 17 BP.
XX
AC AAX82721;
XX
DT 10-NOV-2000 (first entry)
XX
DE Human IgA nephropathy-associated cDNA primer #62.
XX
KW IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW human; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9963085-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002855.
XX
PR 02-JUN-1998; 98JP-00152603.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI Sawada S, Takei M, Shibata K, Furuya A;
XX
DR WPI; 2000-097328/08.
XX
PT DNA sequences preferentially expressed in IgA nephropathy patients,
PT proteins encoded by them, and antibodies to those proteins.
XX
PS Claim 3; Page 170; 180pp; Japanese.

```
XX
CC   This invention describes novel DNA sequences preferentially expressed in
CC   IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC   them. Independent claims cover diagnostic reagents for IgA nephropathy
CC   incorporating the antisense sequences; the treatment of IgA nephropathy
CC   using the antisense sequences for mRNA inhibition; proteins associated
CC   with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC   antibodies recognizing these proteins; the production of the proteins by
CC   culture of host cells transformed with DNA encoding them; diagnostic
CC   reagents for IgA nephropathy containing the antibodies; and compositions
CC   for the treatment of IgA nephropathy which contain the antibodies. The
CC   products of the invention can be used for the diagnosis and treatment of
CC   IgA nephropathy. This sequence represents a primer used in the isolation
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3350
AAX82721/c
ID   AAX82721 standard; DNA; 17 BP.
XX
AC   AAX82721;
XX
DT   10-NOV-2000  (first entry)
XX
DE   Human IgA nephropathy-associated cDNA primer #62.
XX
KW   IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW   human; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9963085-A1.
XX
PD   09-DEC-1999.
XX
PF   28-MAY-1999;   99WO-JP002855.
XX
PR   02-JUN-1998;   98JP-00152603.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Ishiwata T,  Sakurada M,  Kawabata A,  Nakagawa S,  Nishi T,  Kuga T;
PI   Sawada S,  Takei M,  Shibata K,  Furuya A;
XX
DR   WPI; 2000-097328/08.
XX
PT   DNA sequences preferentially expressed in IgA nephropathy patients,
PT   proteins encoded by them, and antibodies to those proteins.
XX
PS   Claim 3; Page 170; 180pp; Japanese.
XX
CC   This invention describes novel DNA sequences preferentially expressed in
CC   IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC   them. Independent claims cover diagnostic reagents for IgA nephropathy
CC   incorporating the antisense sequences; the treatment of IgA nephropathy
CC   using the antisense sequences for mRNA inhibition; proteins associated
CC   with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC   antibodies recognizing these proteins; the production of the proteins by
CC   culture of host cells transformed with DNA encoding them; diagnostic
CC   reagents for IgA nephropathy containing the antibodies; and compositions
CC   for the treatment of IgA nephropathy which contain the antibodies. The
CC   products of the invention can be used for the diagnosis and treatment of
CC   IgA nephropathy. This sequence represents a primer used in the isolation
CC   and identification of the human IgA nephropathy-associated proteins
CC   described in the method of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3351
AAZ36740
ID   AAZ36740 standard; DNA; 17 BP.
XX
AC   AAZ36740;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Anchored oligo(dT) primer GT15G used for modified differential display.
XX
KW   Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW   differentially expressed nucleic acid; disease state; cancer;
KW   autoimmune disease; infectious disease; aging; developmental disorder;
KW   proliferative disorder; neurological disorder; toxicity; primer;
KW   treatment resistance; differential expression; drug discovery;
KW   growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS   Synthetic.
XX
PN   WO9955913-A2.
XX
PD   04-NOV-1999.
XX
PF   27-APR-1999;   99WO-US009119.
XX
PR   27-APR-1998;   98US-0083331P.
PR   27-AUG-1998;   98US-0098070P.
PR   04-FEB-1999;   99US-0118624P.
XX
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   Mcclelland M,  Welsh J,  Trenkle T;
XX
DR   WPI; 2000-086388/07.
XX
PT   Measuring expression of low abundance reduced complexity target nucleic
PT   acid molecules.
XX
PS   Example 3; Page 91; 187pp; English.
XX
CC   AAZ36739-41 represent oligo(dT) primers used for modified differential
CC   display, in the method of the invention. The specification describes a
CC   method for measuring the level of two or more nucleic acid molecules in a
CC   target. The method comprises contacting a probe with an arbitrarily or
CC   statistically sampled target and detecting the amount of specific binding
CC   of the target to the probe. The methods can be used to identify
CC   differentially expressed nucleic acid molecules associated with disease
CC   states, such as cancer, autoimmune disease, infectious disease, aging,
CC   developmental disorder, proliferative disorder or neurological disorder.
CC   Alternatively the methods can be used to assess the efficacy or toxicity
CC   of or a resistance to a treatment. Also the methods can be used to
CC   determine differential expression of nucleic acid molecules in response
CC   to a stimulus, e.g. a chemical, drug or growth factor (especially
CC   epidermal growth factor), radiation, stress or a pathogen. The methods
CC   can also be used to determine co-regulated genes that can be potential
CC   targets for drug discovery
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
```

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3352
AAZ36740/c
ID AAZ36740 standard; DNA; 17 BP.
XX
AC AAZ36740;
XX
DT 13-MAR-2000 (first entry)
XX
DE Anchored oligo(dT) primer GT15G used for modified differential display.
XX
KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS Synthetic.
XX
PN WO9955913-A2.
XX
PD 04-NOV-1999.
XX
PF 27-APR-1999; 99WO-US009119.
XX
PR 27-APR-1998; 98US-0083331P.
PR 27-AUG-1998; 98US-0098070P.
PR 04-FEB-1999; 99US-0118624P.
XX
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI Mcclelland M, Welsh J, Trenkle T;
XX
DR WPI; 2000-086388/07.
XX
PT Measuring expression of low abundance reduced complexity target nucleic
PT acid molecules.
XX
PS Example 3; Page 91; 187pp; English.
XX
CC AAZ36739-41 represent oligo(dT) primers used for modified differential
CC display, in the method of the invention. The specification describes a
CC method for measuring the level of two or more nucleic acid molecules in a
CC target. The method comprises contacting a probe with an arbitrarily or
CC statistically sampled target and detecting the amount of specific binding
CC of the target to the probe. The methods can be used to identify
CC differentially expressed nucleic acid molecules associated with disease
CC states, such as cancer, autoimmune disease, infectious disease, aging,
CC developmental disorder, proliferative disorder or neurological disorder.
CC Alternatively the methods can be used to assess the efficacy or toxicity
CC of or a resistance to a treatment. Also the methods can be used to
CC determine differential expression of nucleic acid molecules in response
CC to a stimulus, e.g. a chemical, drug or growth factor (especially
CC epidermal growth factor), radiation, stress or a pathogen. The methods
CC can also be used to determine co-regulated genes that can be potential
CC targets for drug discovery
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
```

RESULT 3353
AAF20623
ID AAF20623 standard; DNA; 17 BP.
XX
AC AAF20623;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2190.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary

```
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3354
AAA25448
ID   AAA25448 standard; DNA; 17 BP.
XX
AC   AAA25448;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          3 TTTTTTTTTTTTTTT 17


RESULT 3355
AAA25448/c
ID   AAA25448 standard; DNA; 17 BP.
XX
AC   AAA25448;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
```

```
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         17 AAAAAAAAAAAAAAA 3


RESULT 3356
AAC64204
ID   AAC64204 standard; DNA; 17 BP.
XX
AC   AAC64204;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065046-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002730.
XX
PR   27-APR-1999;   99JP-00120489.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687339/67.
XX
PT   Pollinosis-associated gene 373 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT   in diagnosis of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 70; 80pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 373 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis gene 373; expression constructs and
CC   host cells comprising pollinosis-associated gene 373 nucleic acids;
CC   pollinosis-associated gene 373 primers and probes; antibodies against the
CC   protein encoded by the gene; methods of detection of pollinosis-
CC   associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC   diseases via the detection of pollinosis-associated gene 373 nucleic
CC   acids. The invention additionally encompasses methods of screening drug
CC   candidates for the treatment of allergic disease by measuring the
CC   expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC   T-cells in the presence of a test compound relative to a control.
CC   Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC   diseases and in the screening of drug candidates for the treatment of
CC   such diseases. The present sequence represents a PCR primer used in the
CC   isolation of human pollinosis-associated gene 373 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3357
AAC64204/c
ID   AAC64204 standard; DNA; 17 BP.
XX
AC   AAC64204;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
XX
KW   Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
KW   cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW   drug screening; allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065046-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002730.
XX
PR   27-APR-1999;   99JP-00120489.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687339/67.
XX
PT   Pollinosis-associated gene 373 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT   in diagnosis of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 70; 80pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 373 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC   was isolated from T-cells from individuals allergic to cedar pollen using
CC   the differential display method. The invention also relates also relates
CC   to the protein encoded by pollinosis gene 373; expression constructs and
CC   host cells comprising pollinosis-associated gene 373 nucleic acids;
CC   pollinosis-associated gene 373 primers and probes; antibodies against the
CC   protein encoded by the gene; methods of detection of pollinosis-
CC   associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC   diseases via the detection of pollinosis-associated gene 373 nucleic
CC   acids. The invention additionally encompasses methods of screening drug
CC   candidates for the treatment of allergic disease by measuring the
CC   expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC   T-cells in the presence of a test compound relative to a control.
CC   Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC   diseases and in the screening of drug candidates for the treatment of
CC   such diseases. The present sequence represents a PCR primer used in the
CC   isolation of human pollinosis-associated gene 373 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
```

```
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3358
AAC64183
ID   AAC64183 standard; DNA; 17 BP.
XX
AC   AAC64183;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
KW   Human; pollinosis-associated gene 419; FAF-1 homologue;
KW   Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW   T-cell; reduced expression; detection; diagnosis; drug screening;
KW   allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065045-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002729.
XX
PR   27-APR-1999;   99JP-00120490.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687338/67.
XX
PT   Pollinosis-associated gene 419 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 50; 77pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 419 which
CC   exhibits reduced expression in the T-cells of individuals with high cedar
CC   pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC   T-cells from individuals allergic to cedar pollen using the differential
CC   display method. Pollinosis-associated gene 419 has homology with the gene
CC   encoding human Fas-associated factor-1 (FAF-1). The invention also
CC   relates to the protein encoded by pollinosis gene 419; expression
CC   constructs and host cells comprising pollinosis- associated gene 419
CC   nucleic acids; pollinosis-associated gene 419 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 419 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-
CC   associated gene 419 nucleic acids. The invention additionally encompasses
CC   methods of screening drug candidates for the treatment of allergic
CC   disease by measuring the expression of pollinosis-associated gene 419 in
CC   pollen antigen-stimulated T-cells in the presence of a test compound
CC   relative to a control.Pollinosis-associated gene 419 is useful in the
CC   diagnosis of allergic diseases and in the screening of drug candidates
CC   for the treatment of such diseases. The present sequence represents a PCR
CC   primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

```
RESULT 3359
AAC64183/c
ID   AAC64183 standard; DNA; 17 BP.
XX
AC   AAC64183;
XX
DT   21-FEB-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
KW   Human; pollinosis-associated gene 419; FAF-1 homologue;
KW   Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW   T-cell; reduced expression; detection; diagnosis; drug screening;
KW   allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200065045-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-JP002729.
XX
PR   27-APR-1999;   99JP-00120490.
XX
PA   (GENO-) GENOX RES INC.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K;
XX
DR   WPI; 2000-687338/67.
XX
PT   Pollinosis-associated gene 419 undergoing significantly low expression in
PT   subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT   of allergic diseases and screening drug candidates.
XX
PS   Example 6; Page 50; 77pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 419 which
CC   exhibits reduced expression in the T-cells of individuals with high cedar
CC   pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC   T-cells from individuals allergic to cedar pollen using the differential
CC   display method. Pollinosis-associated gene 419 has homology with the gene
CC   encoding human Fas-associated factor-1 (FAF-1). The invention also
CC   relates to the protein encoded by pollinosis gene 419; expression
CC   constructs and host cells comprising pollinosis- associated gene 419
CC   nucleic acids; pollinosis-associated gene 419 primers and probes;
CC   antibodies against the protein encoded by the gene; methods of detection
CC   of pollinosis-associated gene 419 nucleic acids; and a method of
CC   diagnosis of allergic diseases via the detection of pollinosis-
CC   associated gene 419 nucleic acids. The invention additionally encompasses
CC   methods of screening drug candidates for the treatment of allergic
CC   disease by measuring the expression of pollinosis-associated gene 419 in
CC   pollen antigen-stimulated T-cells in the presence of a test compound
CC   relative to a control.Pollinosis-associated gene 419 is useful in the
CC   diagnosis of allergic diseases and in the screening of drug candidates
CC   for the treatment of such diseases. The present sequence represents a PCR
CC   primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3360
AAC64173
ID   AAC64173 standard; DNA; 17 BP.
```

XX
AC AAC64173;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 39; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3361
AAC64173/c
ID AAC64173 standard; DNA; 17 BP.
XX
AC AAC64173;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.
XX
KW Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065049-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002733.
XX
PR 27-APR-1999; 99JP-00120491.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687342/67.
XX
PT Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 39; 46pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3362
AAC64163
ID AAC64163 standard; DNA; 17 BP.
XX
AC AAC64163;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.

XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids.. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3363
AAC64163/c
ID AAC64163 standard; DNA; 17 BP.
XX
AC AAC64163;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation.
XX
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065048-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002732.
XX
PR 27-APR-1999; 99JP-00120492.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687341/67.
XX
PT Pollenosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 40; 69pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control.Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3364
AAC64215
ID AAC64215 standard; DNA; 17 BP.
XX
AC AAC64215;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX

PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 42; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3365
AAC64215/c
ID AAC64215 standard; DNA; 17 BP.
XX
AC AAC64215;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation.
XX
KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065051-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002735.
XX
PR 27-APR-1999; 99JP-00120493.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2000-687344/67.
XX
PT Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 42; 51pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3366
AAC64232
ID AAC64232 standard; DNA; 17 BP.
XX
AC AAC64232;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 46; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection

CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3367
AAC64232/c
ID AAC64232 standard; DNA; 17 BP.
XX
AC AAC64232;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 46; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3368
AAC92294
ID AAC92294 standard; DNA; 17 BP.
XX
AC AAC92294;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073439-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-061528/07.
XX
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 44; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;

```
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3369
AAC92294/c
ID   AAC92294 standard; DNA; 17 BP.
XX
AC   AAC92294;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
XX
KW   Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW   allergic disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073439-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003191.
XX
PR   27-MAY-1999;   99JP-00148784.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-061528/07.
XX
PT   Pollinosis-associated gene 465 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 44; 61pp; Japanese.
XX
CC   The present invention describes the human pollinosis-associated gene 465
CC   which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC   (AAC92291), that undergoes significantly low expression in subjects after
CC   pollen scattering, and is useful in the diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen. The gene is useful in
CC   the diagnosis of allergic diseases and screening candidate compounds for
CC   remedies capable of regulating the response of T cells to the stimulus by
CC   an antigen. The present sequence represents a PCR primer which is used in
CC   an example from the present invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3370
AAS06653
ID   AAS06653 standard; DNA; 17 BP.
XX
AC   AAS06653;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human cDNA synthesis and differential display primer, HT11AG.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11AG.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Example 3; Page 27; 77pp; English.
XX
CC   The sequence represents a downstream PCR primer used in a DDRT-PCR
CC   experiment (and in cDNA synthesis), demonstrating the method of the
CC   invention. The method relates to evaluating a cellular response to an
CC   environmental compound, comprising determining or comparing the
CC   expression levels of at least one endogenous gene e.g by differential
CC   display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC   adapted to identify compounds that act on the level of endogenous gene
CC   expression through activating nuclear receptors. The method is useful in
CC   toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC   testicular, breast, prostate and endometrium), asthma, hypospadia,
CC   cryptorchism and/or allergy, and for evaluating the efficiency of a
CC   treatment for hormonal deficiency or hormonal replacement therapy, in a
CC   human such as a post-menopausal female. The method is also useful for
CC   identifying environmental chemicals or pharmaceutical compositions that
CC   interact with endocrine systems, and for detecting chemicals that pose a
CC   health threat. Expression levels of endogenous genes are determined
CC   rapidly using a sensitive technique, and the expression of any gene can
CC   be monitored. The assays are far more informative than the currently used
CC   assays, and significantly reduces the number of animals required for the
CC   testing, as it is expected that essentially all the animals in a test
CC   group will respond to the compound
XX
SQ   Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3371
AAS06656
ID   AAS06656 standard; DNA; 17 BP.
XX
AC   AAS06656;
```

```
XX
DT   12-SEP-2001  (first entry)
XX
DE   Human cDNA synthesis and differential display primer, HT11CC.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11CC.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Example 3; Page 27; 77pp; English.
XX
CC   The sequence represents a downstream PCR primer used in a DDRT-PCR
CC   experiment (and in cDNA synthesis), demonstrating the method of the
CC   invention. The method relates to evaluating a cellular response to an
CC   environmental compound, comprising determining or comparing the
CC   expression levels of at least one endogenous gene e.g by differential
CC   display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC   adapted to identify compounds that act on the level of endogenous gene
CC   expression through activating nuclear receptors. The method is useful in
CC   toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC   testicular, breast, prostate and endometrium), asthma, hypospadia,
CC   cryptorchism and/or allergy, and for evaluating the efficiency of a
CC   treatment for hormonal deficiency or hormonal replacement therapy, in a
CC   human such as a post-menopausal female. The method is also useful for
CC   identifying environmental chemicals or pharmaceutical compositions that
CC   interact with endocrine systems, and for detecting chemicals that pose a
CC   health threat. Expression levels of endogenous genes are determined
CC   rapidly using a sensitive technique, and the expression of any gene can
CC   be monitored. The assays are far more informative than the currently used
CC   assays, and significantly reduces the number of animals required for the
CC   testing, as it is expected that essentially all the animals in a test
CC   group will respond to the compound
XX
SQ   Sequence 17 BP; 2 A; 3 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3372
AAS06657
ID   AAS06657 standard; DNA; 17 BP.
XX
AC   AAS06657;
XX
```

```
DT   12-SEP-2001  (first entry)
XX
DE   Human cDNA synthesis and differential display primer, HT11CT.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11CT.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Example 3; Page 27; 77pp; English.
XX
CC   The sequence represents a downstream PCR primer used in a DDRT-PCR
CC   experiment (and in cDNA synthesis), demonstrating the method of the
CC   invention. The method relates to evaluating a cellular response to an
CC   environmental compound, comprising determining or comparing the
CC   expression levels of at least one endogenous gene e.g by differential
CC   display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC   adapted to identify compounds that act on the level of endogenous gene
CC   expression through activating nuclear receptors. The method is useful in
CC   toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC   testicular, breast, prostate and endometrium), asthma, hypospadia,
CC   cryptorchism and/or allergy, and for evaluating the efficiency of a
CC   treatment for hormonal deficiency or hormonal replacement therapy, in a
CC   human such as a post-menopausal female. The method is also useful for
CC   identifying environmental chemicals or pharmaceutical compositions that
CC   interact with endocrine systems, and for detecting chemicals that pose a
CC   health threat. Expression levels of endogenous genes are determined
CC   rapidly using a sensitive technique, and the expression of any gene can
CC   be monitored. The assays are far more informative than the currently used
CC   assays, and significantly reduces the number of animals required for the
CC   testing, as it is expected that essentially all the animals in a test
CC   group will respond to the compound
XX
SQ   Sequence 17 BP; 2 A; 2 C; 1 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3373
AAS06652
ID   AAS06652 standard; DNA; 17 BP.
XX
AC   AAS06652;
XX
DT   12-SEP-2001  (first entry)
```

```
XX
DE   Human cDNA synthesis and differential display primer, HT11AC.
XX
KW   Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;
KW   differential display of reverse transcribed mRNAs by PCR;
KW   testicular cancer; breast cancer; prostate cancer; endometrial cancer;
KW   asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;
KW   HRT; endocrine system; HT11AC.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200134834-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-DK000628.
XX
PR   11-NOV-1999;   99DK-00001626.
XX
PA   (RIGS-) RIGSHOSPITALET.
XX
PI   Leffers H,  Jorgensen M,  Skakkebaek NE;
XX
DR   WPI; 2001-335941/35.
XX
PT   Evaluating a cellular response to an environmental compound, for use in
PT   toxicological analysis, involves determining or comparing the expression
PT   levels of at least one endogenous gene.
XX
PS   Example 3; Page 27; 77pp; English.
XX
CC   The sequence represents a downstream PCR primer used in a DDRT-PCR
CC   experiment (and in cDNA synthesis), demonstrating the method of the
CC   invention. The method relates to evaluating a cellular response to an
CC   environmental compound, comprising determining or comparing the
CC   expression levels of at least one endogenous gene e.g by differential
CC   display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC   adapted to identify compounds that act on the level of endogenous gene
CC   expression through activating nuclear receptors. The method is useful in
CC   toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC   testicular, breast, prostate and endometrium), asthma, hypospadia,
CC   cryptorchism and/or allergy, and for evaluating the efficiency of a
CC   treatment for hormonal deficiency or hormonal replacement therapy, in a
CC   human such as a post-menopausal female. The method is also useful for
CC   identifying environmental chemicals or pharmaceutical compositions that
CC   interact with endocrine systems, and for detecting chemicals that pose a
CC   health threat. Expression levels of endogenous genes are determined
CC   rapidly using a sensitive technique, and the expression of any gene can
CC   be monitored. The assays are far more informative than the currently used
CC   assays, and significantly reduces the number of animals required for the
CC   testing, as it is expected that essentially all the animals in a test
CC   group will respond to the compound
XX
SQ   Sequence 17 BP; 3 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          1 AAGCTTTTTTTTTTT 15


RESULT 3374
AAC91721
ID   AAC91721 standard; DNA; 17 BP.
XX
AC   AAC91721;
XX
DT   27-MAR-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
KW   Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW   reduced expression; detection; diagnosis; drug screening;
KW   allergic disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200073440-A1.
XX
PD   07-DEC-2000.
XX
PF   18-MAY-2000; 2000WO-JP003192.
XX
PR   27-MAY-1999;   99JP-00148785.
XX
PA   (GENO-) GENOX RES INC.
PA   (EISA ) EISAI CO LTD.
XX
PI   Nagasu T,  Sugita Y,  Kashiwabara T,  Oshida T,  Obayashi M,  Gunji S;
PI   Obayashi I,  Imai Y,  Yoshida N,  Ogawa K,  Matsui K,  Takahashi E;
PI   Yokoi A;
XX
DR   WPI; 2001-032159/04.
XX
PT   Pollinosis-associated gene 787 undergoing significantly low expression in
PT   subjects after pollen scattering, useful in diagnosis of allergic
PT   diseases and screening candidate compounds to regulate response of T
PT   cells to antigen stimulus.
XX
PS   Example 6; Page 41; 54pp; Japanese.
XX
CC   The invention relates to the human pollinosis-associated gene 787 which
CC   exhibits significantly reduced expression in the T-cells of individuals
CC   after the pollen-scattering season, relative to expression levels in T-
CC   cells before the pollen-scattering season. The gene was isolated from T-
CC   cells from individuals allergic to pollen using the differential display
CC   method. The invention also relates to pollinosis-associated gene 787
CC   primers and probes; methods of detection of pollinosis-associated gene
CC   787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC   detection of pollinosis-associated gene 787 nucleic acids. The invention
CC   additionally encompasses a method of screening drug candidates for the
CC   treatment of allergic disease by measuring the expression of pollinosis-
CC   associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC   of a test compound relative to a control. Pollinosis- associated gene 787
CC   is useful in the diagnosis of allergic diseases and in the screening of
CC   drug candidates for the treatment of such diseases. The present sequence
CC   represents a PCR primer used in the isolation of human pollinosis-
CC   associated gene 787 cDNA
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3375
AAC91721/c
ID   AAC91721 standard; DNA; 17 BP.
XX
AC   AAC91721;
XX
DT   27-MAR-2001  (first entry)
XX
DE   PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
XX
KW   Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW   reduced expression; detection; diagnosis; drug screening;
```

KW allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200073440-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003192.
XX
PR 27-MAY-1999; 99JP-00148785.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2001-032159/04.
XX
PT Pollinosis-associated gene 787 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 41; 54pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 787 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC after the pollen-scattering season, relative to expression levels in T-
CC cells before the pollen-scattering season. The gene was isolated from T-
CC cells from individuals allergic to pollen using the differential display
CC method. The invention also relates to pollinosis-associated gene 787
CC primers and probes; methods of detection of pollinosis-associated gene
CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
CC detection of pollinosis-associated gene 787 nucleic acids. The invention
CC additionally encompasses a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis- associated gene 787
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 787 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3376
AAC82876
ID AAC82876 standard; DNA; 17 BP.
XX
AC AAC82876;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #3.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 36; 42pp; Japanese.
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3377
AAC82876/c
ID AAC82876 standard; DNA; 17 BP.
XX
AC AAC82876;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #3.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003190.
XX
PR 27-MAY-1999; 99JP-00148783.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX

```
PS   Example 6; Page 36; 42pp; Japanese.
XX
CC   This invention describes a novel nucleic acid molecule comprising a
CC   sequence (I) which undergoes significantly low expression in subjects
CC   after pollen scattering, and is useful in diagnosis of allergic diseases
CC   and screening candidate compounds for remedies capable of regulating the
CC   response of T cells to the stimulus by an antigen
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3378
AAH47128
ID   AAH47128 standard; DNA; 17 BP.
XX
AC   AAH47128;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15G.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 66; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3379
AAH47128/c
ID   AAH47128 standard; DNA; 17 BP.
XX
AC   AAH47128;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of primer GT15G.
XX
KW   B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200165259-A1.
XX
PD   07-SEP-2001.
XX
PF   23-FEB-2001; 2001WO-JP001372.
XX
PR   02-MAR-2000; 2000JP-00061832.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Nagasu T,  Oshida T,  Obayashi I,  Matsui K,  Saito H;
XX
DR   WPI; 2001-557789/62.
XX
PT   Diagnosis of allergies including atopic dermatitis.
XX
PS   Example 6; Page 66; 83pp; Japanese.
XX
CC   The invention provides a method of diagnosis of allergies that involves:
CC   assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC   in T-cells; and comparing them with the level of expression in healthy T-
CC   cells. The method is useful for diagnosing allergies, particularly atopic
CC   dermatitis. The present sequence represents a PCR primer used for
CC   analysis of the expression of the above genes
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3380
ABK49636
ID   ABK49636 standard; DNA; 17 BP.
XX
AC   ABK49636;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
XX
KW   Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW   differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
XX
OS   Homo sapiens.
XX
PN   WO200224903-A1.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-JP008246.
XX
PR   25-SEP-2000; 2000JP-00291318.
XX
```

PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 57; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3381
ABK49636/c
ID ABK49636 standard; DNA; 17 BP.
XX
AC ABK49636;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008246.
XX
PR 25-SEP-2000; 2000JP-00291318.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
PI Takahashi E;
XX
DR WPI; 2002-315738/35.
XX
PT Examining allergic diseases by differential display of gene showing
PT different expression particularly increased expression in remission stage
PT in eosinophils of patients, also applicable in screening candidate
PT compounds for remedies.
XX
PS Example 1; Page 57; 72pp; Japanese.
XX
CC The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
|||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3382
ABQ64253/c
ID ABQ64253 standard; DNA; 17 BP.
XX
AC ABQ64253;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 966.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
PS Example 2; Page 284; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1739 GGTGACAAGTACTGG 1753
||||||||||||||||
Db 17 GGTGACAAGTACTGG 3

RESULT 3383
ABQ64255/c
ID ABQ64255 standard; DNA; 17 BP.
XX
AC ABQ64255;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 968.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
PS Example 2; Page 284; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1739 GGTGACAAGTACTGG 1753
||||||||||||||||
Db 15 GGTGACAAGTACTGG 1

RESULT 3384
ABQ64254/c
ID ABQ64254 standard; DNA; 17 BP.
XX
AC ABQ64254;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 967.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.

```
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   23-MAY-2001; 2001US-00864761.
PR   28-AUG-2001; 2001US-0315676P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhang J;
XX
DR   WPI; 2002-479509/51.
XX
PT   New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT   acids encoding the protein, useful for treating subjects having defects
PT   in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT   e.g., liver or bone.
XX
PS   Example 2; Page 284; 418pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid encoding human
CC   KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC   invention has cytostatic activity. The nucleotide may have a use in gene
CC   therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC   monitor a disease caused by altered expression of human KTOM1.
CC   Compositions comprising the nucleic acids, proteins or antibodies may be
CC   used to treat subjects having defects in KTOM1 which can manifest as
CC   cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC   heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC   function. The sequence represents a probe used in the invention to scan
CC   the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ   Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1739 GGTGACAAGTACTGG 1753
              |||||||||||||||
Db         16 GGTGACAAGTACTGG 2


RESULT 3385
ABL59040
ID   ABL59040 standard; DNA; 17 BP.
XX
AC   ABL59040;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Nucleotide sequence of PCR primer GT15G.
XX
KW   Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002095500-A.
XX
PD   02-APR-2002.
XX
PF   25-SEP-2000; 2000JP-00291316.
XX
PR   25-SEP-2000; 2000JP-00291316.
XX
PA   (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA   (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR   WPI; 2002-439993/47.
XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3386
ABL59040/c
ID   ABL59040 standard; DNA; 17 BP.
XX
AC   ABL59040;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Nucleotide sequence of PCR primer GT15G.
XX
KW   Human; allergosis; eosinophil; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002095500-A.
XX
PD   02-APR-2002.
XX
PF   25-SEP-2000; 2000JP-00291316.
XX
PR   25-SEP-2000; 2000JP-00291316.
XX
PA   (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA   (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX
DR   WPI; 2002-439993/47.
XX
PT   Examining allergosis, involves measuring the expression levels of a
PT   specific gene, and comparing it to the levels in the eosinophils of a
PT   healthy control.
XX
PS   Example 1; Page 17; 20pp; Japanese.
XX
CC   The specification describes a method for examining allergosis. The method
CC   comprises measuring the expression level of the gene given in ABL59037,
CC   and comparing it with the expression level of the gene in the eosinophils
CC   of a healthy person. The method is used for the examination of
CC   allergosis. The present sequence represents a PCR primer, which is used
CC   in the course of the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
```

RESULT 3387
ABN99831
ID ABN99831 standard; DNA; 17 BP.
XX
AC ABN99831;
XX
DT 15-AUG-2002 (first entry)
XX
DE Human allergic disease related PCR primer SEQ ID NO: 20.
XX
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX
PD 25-APR-2002.
XX
PF 28-SEP-2001; 2001WO-JP008574.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX
DR WPI; 2002-372311/40.
XX
PT Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
PS Example 1; Page 110; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3388
ABN99831/c
ID ABN99831 standard; DNA; 17 BP.
XX
AC ABN99831;
XX
DT 15-AUG-2002 (first entry)
XX
DE Human allergic disease related PCR primer SEQ ID NO: 20.
XX
KW Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200233069-A1.
XX
PD 25-APR-2002.
XX
PF 28-SEP-2001; 2001WO-JP008574.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX
DR WPI; 2002-372311/40.
XX
PT Method for examining allergic diseases by differential display of
PT seventeen genes showing different expression particularly significant
PT increase in eosinophils in patients with mild atopic dermatitis, also
PT applicable in screening compounds.
XX
PS Example 1; Page 110; 165pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC which involves determining the expression level of a gene, having one of
CC the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC eosinophils in a patient and comparing the expression level with that in
CC the eosinophils of a healthy individual. The method can be used to
CC examine allergic diseases, particularly atopic dermatitis, and its early
CC diagnosis, which is also applicable in screening candidate compounds for
CC remedies. The present sequence is a PCR primer described in the
CC exemplification of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
```

RESULT 3389
AAL49950
ID AAL49950 standard; DNA; 17 BP.
XX
AC AAL49950;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human B1153 expression in allergic disease related PCR primer GT15G.
XX
KW Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN WO200250269-A1.
XX
PD 27-JUN-2002.
XX
PF 21-DEC-2001; 2001WO-JP011286.
XX
PR 21-DEC-2000; 2000JP-00389476.
XX
PA (GENO-) GENOX RES INC.

```
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Matsumoto Y,  Imai Y,  Oshida T,  Sugita Y,  Nagasu T,  Tsujimoto G;
XX
DR   WPI; 2002-713252/77.
XX
PT   Examination of allergic diseases comprises detecting gene B1153 over-
PT   expressed in T cells of allergy patients for diagnosis treatment and
PT   investigation of atopic skin inflammation and asthma.
XX
PS   Example 6; Page 82; 102pp; Japanese.
XX
CC   The present invention relates to a method of examining allergic diseases
CC   which comprises comparing the expression level of gene B1153 in allergy
CC   patients with the expression level in healthy subjects. The method is
CC   useful for the treatment, prevention, diagnosis and study of allergic
CC   diseases including atopic skin inflammation and asthma. The present
CC   sequence is a PCR primer described in the exemplification of the
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3390
AAL49950/c
ID   AAL49950 standard; DNA; 17 BP.
XX
AC   AAL49950;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human B1153 expression in allergic disease related PCR primer GT15G.
XX
KW   Human; allergy; B1153; differential expression; antiallergic; asthma;
KW   antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200250269-A1.
XX
PD   27-JUN-2002.
XX
PF   21-DEC-2001; 2001WO-JP011286.
XX
PR   21-DEC-2000; 2000JP-00389476.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI   Matsumoto Y,  Imai Y,  Oshida T,  Sugita Y,  Nagasu T,  Tsujimoto G;
XX
DR   WPI; 2002-713252/77.
XX
PT   Examination of allergic diseases comprises detecting gene B1153 over-
PT   expressed in T cells of allergy patients for diagnosis treatment and
PT   investigation of atopic skin inflammation and asthma.
XX
PS   Example 6; Page 82; 102pp; Japanese.
XX
CC   The present invention relates to a method of examining allergic diseases
CC   which comprises comparing the expression level of gene B1153 in allergy
CC   patients with the expression level in healthy subjects. The method is
CC   useful for the treatment, prevention, diagnosis and study of allergic
CC   diseases including atopic skin inflammation and asthma. The present
CC   sequence is a PCR primer described in the exemplification of the
CC   invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3391
AAL47236
ID   AAL47236 standard; DNA; 17 BP.
XX
AC   AAL47236;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX
KW   Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW   atopic dermatitis; human; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200233122-A1.
XX
PD   25-APR-2002.
XX
PF   11-OCT-2001; 2001WO-JP008937.
XX
PR   13-OCT-2000; 2000JP-00314093.
XX
PA   (GENO-) GENOX RES INC.
PA   (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA   (EISA ) EISAI CO LTD.
XX
PI   Sugita Y,  Hashida R,  Ogawa K,  Obayashi M,  Nagasu T,  Saito H;
PI   Takahashi E;
XX
DR   WPI; 2002-372313/40.
XX
PT   Method for examining allergic diseases by differential display of
PT   intersectin 2 gene showing different expression particularly significant
PT   increase in eosinophils in patients.
XX
PS   Example 1; Page 53; 90pp; Japanese.
XX
CC   The present invention relates to a method for examining allergic diseases
CC   with intersectin 2 gene or a gene with equivalent function of intersectin
CC   2 as an indicator gene, which comprises determining the expression level
CC   of the gene in the eosinophils in a patient, and comparing the expression
CC   level with that in the eosinophils of a healthy individual. The method is
CC   for examining allergic diseases, particularly atopic dermatitis, which is
CC   also applicable in screening candidate compounds for remedies. The
CC   present sequence is an anchor primer described in the exemplification of
CC   the invention
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3392
AAL47236/c
ID AAL47236 standard; DNA; 17 BP.
XX
AC AAL47236;
XX
DT 22-AUG-2002 (first entry)
XX
DE Allergic disease examination method related anchor primer SEQ ID NO: 4.
XX
KW Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW atopic dermatitis; human; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200233122-A1.
XX
PD 25-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008937.
XX
PR 13-OCT-2000; 2000JP-00314093.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.
XX
PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX
DR WPI; 2002-372313/40.
XX
PT Method for examining allergic diseases by differential display of
PT intersectin 2 gene showing different expression particularly significant
PT increase in eosinophils in patients.
XX
PS Example 1; Page 53; 90pp; Japanese.
XX
CC The present invention relates to a method for examining allergic diseases
CC with intersectin 2 gene or a gene with equivalent function of intersectin
CC 2 as an indicator gene, which comprises determining the expression level
CC of the gene in the eosinophils in a patient, and comparing the expression
CC level with that in the eosinophils of a healthy individual. The method is
CC for examining allergic diseases, particularly atopic dermatitis, which is
CC also applicable in screening candidate compounds for remedies. The
CC present sequence is an anchor primer described in the exemplification of
CC the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3393
ABK49758
ID ABK49758 standard; DNA; 17 BP.
XX
AC ABK49758;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15g.
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15g.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 55; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15g PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3394
ABK49758/c
ID ABK49758 standard; DNA; 17 BP.
XX
AC ABK49758;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human atopic dermatitis cDNA related PCR primer GT15g.
XX
KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; GT15g.
XX
OS Synthetic.
XX
PN WO200226962-A1.
XX
PD 04-APR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008247.
XX
PR 26-SEP-2000; 2000JP-00293021.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX

PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX
DR WPI; 2002-330097/36.
XX
PT Examining allergic diseases by differential display of genes showing
PT different expression particularly increase in remission stage in
PT eosinophils in patients.
XX
PS Example 1; Page 55; 74pp; Japanese.
XX
CC This invention relates to gene sequences that are differentially
CC expressed in eosinophils from patients with atopic dermatitis in the
CC increment stage as compared with those in the remission stage. These
CC sequences are used in a novel method for examining allergic diseases
CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the GT15g PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3395
ABZ96317
ID ABZ96317 standard; DNA; 17 BP.
XX
AC ABZ96317;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human C/EBP antisense fragment no.2177.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11559; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3396
ACC64290
ID ACC64290 standard; DNA; 17 BP.
XX
AC ACC64290;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour supression, SEQ ID 1537.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 210; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-

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CC   ACC68806), which are associated with tumour suppression, tumour
CC   reversion, apoptosis and virus resistance. The oligonucleotides are
CC   useful as (1) as probes and primers for detecting, identifying,
CC   quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC   gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC   recombinant polypeptides. The oligonucleotides are useful for preparation
CC   of pharmaceuticals for prevention and/or treatment of viral diseases that
CC   are characterised by development of tumours or cell degeneration,
CC   specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ   Sequence 17 BP; 1 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTT 2177
              |||||||||||||||
Db          3 TCCTTTTTTTTTTTT 17


RESULT 3397
ADC84470
ID   ADC84470 standard; DNA; 17 BP.
XX
AC   ADC84470;
XX
DT   01-JAN-2004  (first entry)
XX
DE   PCR primer for amplifying  plant blastogenesis specific gene #SEQ ID 3.
XX
KW   Plant blastogenesis; transformation; gene expression; tissue specific;
KW   PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2003159071-A.
XX
PD   03-JUN-2003.
XX
PF   22-NOV-2001; 2001JP-00358366.
XX
PR   22-NOV-2001; 2001JP-00358366.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-818678/77.
XX
PT   New naturally derived DNA specifically expressed during blastogenesis of
PT   a plant, useful for producing a transformed plant and for compulsive
PT   expression of a protein.
XX
PS   Example 3; SEQ ID NO 3; 43pp; Japanese.
XX
CC   The invention relates to naturally derived DNA specifically expressed
CC   during plant blastogenesis. The DNA of the invention is useful for
CC   producing a transformed plant. Methods of the invention are also useful
CC   for compulsive expression of this DNA. Methods of the invention are
CC   useful for plant tissue specific expression of genes. Also, the growth
CC   stage of a plant can be controlled specifically. The current sequence
CC   represents a PCR primer for amplifying a plant blastogenesis specific
CC   gene of the invention.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3398
ADC84470/c
ID   ADC84470 standard; DNA; 17 BP.
XX
AC   ADC84470;
XX
DT   01-JAN-2004  (first entry)
XX
DE   PCR primer for amplifying  plant blastogenesis specific gene #SEQ ID 3.
XX
KW   Plant blastogenesis; transformation; gene expression; tissue specific;
KW   PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2003159071-A.
XX
PD   03-JUN-2003.
XX
PF   22-NOV-2001; 2001JP-00358366.
XX
PR   22-NOV-2001; 2001JP-00358366.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
DR   WPI; 2003-818678/77.
XX
PT   New naturally derived DNA specifically expressed during blastogenesis of
PT   a plant, useful for producing a transformed plant and for compulsive
PT   expression of a protein.
XX
PS   Example 3; SEQ ID NO 3; 43pp; Japanese.
XX
CC   The invention relates to naturally derived DNA specifically expressed
CC   during plant blastogenesis. The DNA of the invention is useful for
CC   producing a transformed plant. Methods of the invention are also useful
CC   for compulsive expression of this DNA. Methods of the invention are
CC   useful for plant tissue specific expression of genes. Also, the growth
CC   stage of a plant can be controlled specifically. The current sequence
CC   represents a PCR primer for amplifying a plant blastogenesis specific
CC   gene of the invention.
XX
SQ   Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3399
AAV54170/c
ID   AAV54170 standard; cDNA; 18 BP.
XX
AC   AAV54170;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 7.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
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PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2


RESULT 3400
AAV54175
ID   AAV54175 standard; cDNA; 18 BP.
XX
AC   AAV54175;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 12.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 51; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3401
AAV54172
ID   AAV54172 standard; cDNA; 18 BP.
XX
AC   AAV54172;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 9.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3402
AAV35391/c
ID   AAV35391 standard; DNA; 18 BP.
XX
AC   AAV35391;
XX
DT   13-OCT-1998  (first entry)
XX
DE   HIV-1 gag protein DNA primer #4.
```

XX
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX
OS Synthetic.
XX
PN WO9822596-A1.
XX
PD 28-MAY-1998.
XX
PF 19-NOV-1997; 97WO-JP004216.
XX
PR 19-NOV-1996; 96JP-00323412.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (JAPG) NIPPON ZEON KK.
XX
PI Kojima A, Kurata T, Yasuda A;
XX
DR WPI; 1998-312481/27.
XX
PT Recombinant vaccinia virus containing fusion HIB gag gene - for
PT production in host cells of gag protein for use as vaccine.
XX
PS Example 1; Page 64; 84pp; Japanese.
XX
CC AAV35388-V35414 are primers used in a method which results in a
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
CC region (30-300 bases in length) of a retroviral gene other than the gag
CC gene. The gag gene may be altered so as to produce a gag protein modified
CC from the natural sequence by the addition, deletion or substitution of at
CC least 1 amino acid residue. The fusion gene is inserted into a region of
CC a vaccinia virus not essential to its propagation, to give a recombinant
CC vaccinia virus vector which is used to transform a host cell (such as
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
CC culturing the host cell produces particulate structures containing the
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
CC protein particles may be used in the production of vaccines for
CC protecting against infection with retroviruses such as HIV
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 18 AAAAAAAAAAAAAAA 4

RESULT 3403
AAZ90642
ID AAZ90642 standard; DNA; 18 BP.
XX
AC AAZ90642;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #3.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

RESULT 3404
AAZ90640/c
ID AAZ90640 standard; DNA; 18 BP.
XX
AC AAZ90640;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #1.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2
```

RESULT 3405
AAZ90651
ID AAZ90651 standard; DNA; 18 BP.
XX
AC AAZ90651;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #12.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

 Query Match 0.5%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16
```

RESULT 3406
AAA58385/c
ID AAA58385 standard; DNA; 18 BP.
XX
AC AAA58385;
XX
DT 01-NOV-2000 (first entry)
XX
DE Polynucleotide # 1 used in a biomolecule detection system.
XX
KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS Synthetic.
XX
PN WO200028088-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-US026612.
XX
PR 10-NOV-1998; 98US-0107828P.
PR 09-NOV-1999; 99US-00437076.
XX
PA (BIOC-) BIOCRYSTAL LTD.
XX
PI Barbera-Guillem E, Nelson MB, Castro S;
XX
DR WPI; 2000-376593/32.
XX
PT Functionalized nanocrystal carrying polynucleotide, used for detecting
PT target analyte, forms dendrimers with complementary nanocrystals to
PT amplify the fluorescent signal.
XX
PS Example 3; Page 68; 72pp; English.
XX
CC The present invention relates to functionalised nanocrystals for use in
CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC attached to their surfaces with one end of the polynucleotide extending
CC outwardly from the nanocrystal. The present sequence is one such
CC polynucleotide. These nanocrystals are used with a second series of
CC nanocrystals, which have polynucleotides complementary to the first
CC polynucleotides, so that the respective complementary strands hybridise
CC to each other and form a dendrimer. This dendrimer produces a signal
CC which can then be detected e.g. fluorescence. The present sequence is
CC composed mainly of Adenine bases. This sequence may therefore be used
CC with a polynucleotide composed mainly of Thymine bases (AAA58386)
XX
SQ Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

 Query Match 0.5%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         18 TTTTTTTTTTTTTTT 4
```

RESULT 3407
AAV54174
ID AAV54174 standard; cDNA; 18 BP.
XX
AC AAV54174;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 11.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.

```
XX
PS   Example 1; Page 50; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3408
AAZ90650
ID   AAZ90650 standard; DNA; 18 BP.
XX
AC   AAZ90650;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #11.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3409
AAV54171
ID   AAV54171 standard; cDNA; 18 BP.
XX
AC   AAV54171;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 8.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Sakaki Y;
XX
DR   WPI; 1998-495844/42.
XX
PT   Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT   treating diseases associated with apoptosis.
XX
PS   Example 1; Page 49; 70pp; Japanese.
XX
CC   This is the nucleotide sequence of a PCR primer used in the method of the
CC   invention, involving the use of novel apoptosis-related DNAs and
CC   proteins. The inventions can be used as diagnostic reagents for apoptosis
CC   e.g. (monoclonal) antibodies for the protein, as a reagent in
CC   immunohistological staining, as apoptosis inhibitors. It can also be used
CC   for treatment of apoptosis-related diseases
XX
SQ   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          2 TTTTTTTTTTTTTTT 16


RESULT 3410
AAV54171/c
ID   AAV54171 standard; cDNA; 18 BP.
XX
AC   AAV54171;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Nucleotide sequence PCR primer 8.
XX
KW   PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW   immunohistological staining.
XX
OS   Synthetic.
XX
PN   WO9839437-A1.
XX
PD   11-SEP-1998.
XX
PF   05-MAR-1998;   98WO-JP000905.
XX
PR   05-MAR-1997;   97JP-00050302.
XX
```

PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 49; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunchistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 16 AAAAAAAAAAAAAAA 2

RESULT 3411
AAX55053
ID AAX55053 standard; DNA; 18 BP.
XX
AC AAX55053;
XX
DT 05-JUL-1999 (first entry)
XX
DE C/EBP-beta antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 70; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3412
AAX87332
ID AAX87332 standard; DNA; 18 BP.
XX
AC AAX87332;
XX
DT 27-SEP-1999 (first entry)
XX
DE Reverse transcription primer P1.
XX
KW SAG gene; sensitive to apoptosis; mouse; cancer; tumour;
KW neurodegenerative disease; muscular dystrophy; wound healing; vulnerary;
KW therapy; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9932514-A2.
XX
PD 01-JUL-1999.
XX
PF 15-DEC-1998; 98WO-US026705.
XX
PR 19-DEC-1997; 97US-0068179P.
PR 11-SEP-1998; 98US-0099840P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Sun Y;
XX
DR WPI; 1999-430152/36.
XX
PT SAG: Sensitive to Apoptosis Gene and related proteins, useful for
PT promoting cell growth and protecting cells against apoptosis.
XX
PS Example 1; Page 14; 84pp; English.
XX
CC This primer was used for reverse transcription of RNA isolated from mouse
CC tumour lines L-RT101 (epidermal tumour cell line) and H-Tx (spontaneously
CC transformed liver line). It was also used as the reverse primer in PCR
CC amplification of the resulting cDNA. Primers P1 and P2 (see AAX87333)
CC reproducibly detected differential expression of a gene between 1,10-
CC phenanthroline (OP)-treated and OP-nontreated L-RT101 and H-Tx cells. An

CC OP-inducible clone was used as a probe to isolate a full-length clone
CC (see AAX87313) corresponding to the mouse sensitive to apoptosis gene
CC (SAG). SAG is a redox-sensitive, haem-binding protein domain that
CC promotes cell growth, protects cells from apoptosis, scavenges oxygen
CC radicals and can be used for the reversion of a tumour phenotype
XX
SQ Sequence 18 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 1 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3413
AAA34500
ID AAA34500 standard; DNA; 18 BP.
XX
AC AAA34500;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2189.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 539; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
|||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3414
AAZ90641
ID AAZ90641 standard; DNA; 18 BP.
XX
AC AAZ90641;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #2.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
XX
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 2 TTTTTTTTTTTTTTT 16

```
RESULT 3415
AAZ90641/c
ID   AAZ90641 standard; DNA; 18 BP.
XX
AC   AAZ90641;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human adipose tissue gene amplifying primer #2.
XX
KW   Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW   arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000037190-A.
XX
PD   08-FEB-2000.
XX
PF   23-JUL-1998;   98JP-00225228.
XX
PR   23-JUL-1998;   98JP-00225228.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-306578/27.
XX
PT   A physiologically active protein specifically derived from mammal tissue.
XX
PS   Example 2; Page 18; 50pp; Japanese.
XX
CC   The invention relates to identification of genes and proteins of adipose
CC   tissue relating to obesity, particularly complications of visceral
CC   obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC   hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC   proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC   and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC   represent PCR primers amplifying the human adipose tissue genes
XX
SQ   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         16 AAAAAAAAAAAAAAA 2

RESULT 3416
AAA58386
ID   AAA58386 standard; DNA; 18 BP.
XX
AC   AAA58386;
XX
DT   01-NOV-2000  (first entry)
XX
DE   Polynucleotide # 2 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999;   99WO-US026612.
XX
PR   10-NOV-1998;   98US-0107828P.
PR   09-NOV-1999;   99US-00437076.
XX
PA   (BIOC-) BIOCRYSTAL LTD.
XX
PI   Barbera-Guillem E,  Nelson MB,  Castro S;
XX
DR   WPI; 2000-376593/32.
XX
PT   Functionalized nanocrystal carrying polynucleotide, used for detecting
PT   target analyte, forms dendrimers with complementary nanocrystals to
PT   amplify the fluorescent signal.
XX
PS   Example 3; Page 69; 72pp; English.
XX
CC   The present invention relates to functionalised nanocrystals for use in
CC   nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC   proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC   attached to their surfaces with one end of the polynucleotide extending
CC   outwardly from the nanocrystal. The present sequence is one such
CC   polynucleotide. These nanocrystals are used with a second series of
CC   nanocrystals, which have polynucleotides complementary to the first
CC   polynucleotides, so that the respective complementary strands hybridise
CC   to each other and form a dendrimer. This dendrimer produces a signal
CC   which can then be detected e.g. fluorescence. The present sequence is
CC   composed mainly of Thymine bases. This sequence may therefore be used
CC   with a polynucleotide composed mainly of Adenine bases (AAA58385)
XX
SQ   Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          4 TTTTTTTTTTTTTTT 18

RESULT 3417
AAA58386/c
ID   AAA58386 standard; DNA; 18 BP.
XX
AC   AAA58386;
XX
DT   01-NOV-2000  (first entry)
XX
DE   Polynucleotide # 2 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999;   99WO-US026612.
XX
PR   10-NOV-1998;   98US-0107828P.
PR   09-NOV-1999;   99US-00437076.
XX
PA   (BIOC-) BIOCRYSTAL LTD.
XX
PI   Barbera-Guillem E,  Nelson MB,  Castro S;
XX
DR   WPI; 2000-376593/32.
XX
PT   Functionalized nanocrystal carrying polynucleotide, used for detecting
PT   target analyte, forms dendrimers with complementary nanocrystals to
PT   amplify the fluorescent signal.
XX
PS   Example 3; Page 69; 72pp; English.
XX
CC   The present invention relates to functionalised nanocrystals for use in
CC   nonisotopic detection systems for biomolecules e.g. nucleic acids,
```

CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC attached to their surfaces with one end of the polynucleotide extending
CC outwardly from the nanocrystal. The present sequence is one such
CC polynucleotide. These nanocrystals are used with a second series of
CC nanocrystals, which have polynucleotides complementary to the first
CC polynucleotides, so that the respective complementary strands hybridise
CC to each other and form a dendrimer. This dendrimer produces a signal
CC which can then be detected e.g. fluorescence. The present sequence is
CC composed mainly of Thymine bases. This sequence may therefore be used
CC with a polynucleotide composed mainly of Adenine bases (AAA58385)
XX
SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 18 AAAAAAAAAAAAAAA 4

RESULT 3418
AAZ71127
ID AAZ71127 standard; DNA; 18 BP.
XX
AC AAZ71127;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5483.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1400; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 4 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2410 ATGGGGTCTGTAAAT 2424
|||||||||||||||
Db 3 ATGGGGTCTGTAAAT 17

RESULT 3419
AAF20622
ID AAF20622 standard; DNA; 18 BP.
XX
AC AAF20622;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2189.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide

CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3420
AAH74930
ID AAH74930 standard; DNA; 18 BP.
XX
AC AAH74930;
XX
DT 29-OCT-2001 (first entry)
XX
DE DNA sequence of cap adaptor.
XX
KW Nucleotide sequence signature; nucleotide sequencing; ss.
XX
OS Synthetic.
XX
PN WO200161044-A1.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-US005032.
XX
PR 15-FEB-2000; 2000US-0182454P.
PR 01-SEP-2000; 2000US-0654187P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Corcoran KC, Eletr S;
XX
DR WPI; 2001-522608/57.
XX
PT Determining nucleotide sequence signature, by obtaining optical values
PT for each nucleotide position in a group, adjusting them to get ratio of
PT final highest values near predetermined factor, generating base call.
XX
PS Disclosure; Page 19; 73pp; English.
XX
CC The specification describes a method for determining a nucleotide
CC sequence signature. The method comprises obtaining optical measurements
CC with values indicating each nucleotide in a group of nucleotide
CC positions, adjusting the values until the ratio of highest value in the
CC set to next highest values in the set is at least a predetermined factor,
CC and generating a base call for a position in the group based on results
CC after the adjustment of values. The method is used for determining a
CC signature of a nucleotide sequence, and for determining a nucleotide
CC sequence of a polynucleotide from a series of optical measurements. The
CC present sequence represents an adaptor, which is used in the course of
CC the invention
XX
SQ Sequence 18 BP; 14 A; 0 C; 3 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAA 2799
|||||||||||||||
Db 4 GAAAAAAAAAAAAAA 18

RESULT 3421
ABA91525/c
ID ABA91525 standard; DNA; 18 BP.
XX
AC ABA91525;
XX
DT 23-APR-2002 (first entry)
XX
DE Rifampicin resistant Mycobacterium tuberculosis probe segment.
XX
KW Rifampicin resistance; drug resistance; nucleic acid detection; probe;
KW ss.
XX
OS Mycobacterium tuberculosis.
OS Synthetic.
XX
PN WO200206531-A2.
XX
PD 24-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US022166.
XX
PR 14-JUL-2000; 2000US-00616761.
PR 30-MAR-2001; 2001US-00823647.
XX
PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI Dattagupta N;
XX
DR WPI; 2002-171819/22.
XX
PT Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.
XX
PS Example 2; Page 46; 72pp; English.
XX
CC The present sequence comprises a segment of a hairpin probe (see
CC ABA91524) used in an assay of Mycobacterium tuberculosis rifampicin
CC resistance. The present oligonucleotide was immobilised on a solid
CC support and hybridised with the oligonucleotide given in ABA91526 to
CC produce an immobilised hairpin probe. The hairpin probe is an example of
CC probes of the invention that form a hairpin structure with a double-
CC stranded stem segment and a single-stranded loop and which are capable of
CC both intramolecular and intermolecular hybridisation. The hairpin probes,
CC preferably immobilised, are used in nucleic acid hybridisations,
CC providing reduced background and improved specificity
XX
SQ Sequence 18 BP; 3 A; 2 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAA 2794
|||||||||||||||
Db 15 GAATTGAAAAAAAAA 1

RESULT 3422
ABZ96316

```
ID   ABZ96316 standard; DNA; 18 BP.
XX
AC   ABZ96316;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human C/EBP antisense fragment no.2176.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 11558; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3423
AAL53956/c
ID   AAL53956 standard; DNA; 18 BP.
XX
AC   AAL53956;
XX
DT   18-FEB-2003  (first entry)
XX
DE   DNA mutation detection related oligo, SEQ ID No 6.
XX
KW   Detecting; point mutation; hybridising; target DNA; duplex; RNase H;
KW   single nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   US2002142308-A1.
XX
PD   03-OCT-2002.
XX
PF   30-MAR-2001; 2001US-00823634.
XX
PR   30-MAR-2001; 2001US-00823634.
XX
PA   (DATT/) DATTAGUPTA N.
PA   (TSEN/) TSENG T.
XX
PI   Dattagupta N,  Tseng T;
XX
DR   WPI; 2003-102506/09.
XX
PT   Detecting point mutation in DNA strand, by hybridizing target DNA strand
PT   having mutation with test DNA strand to form duplex, contacting the
PT   duplex with RNase H and determining the cleavage of test strand by RNase
PT   H.
XX
PS   Example 2; Page 13; 26pp; English.
XX
CC   The invention relates to a novel method for detecting a point mutation in
CC   a DNA strand. The novel method comprises hybridising a target DNA strand
CC   containing or suspected of containing a point mutation with a test
CC   nucleic acid strand complementary to the DNA strand to form a target DNA
CC   strand/test nucleic acid strand duplex, contacting the duplex with an
CC   RNase H, and determining whether the ribonucleotide residues within the
CC   nucleotide sequence are cleaved by RNase H. The method is useful for
CC   detecting a point mutation in a DNA strand, where the point mutation to
CC   be detected is a single nucleotide polymorphism, preferably a
CC   polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian
CC   or human genome. The method is useful to detect any nucleic acids from
CC   any species of organisms such as Acintobacter, Bacillus, Candida,
CC   Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
CC   This polynucleotide sequence represents an oligo relating to the mutation
CC   detecting method of the invention
XX
SQ   Sequence 18 BP; 3 A; 2 C; 1 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAA 2794
              |||||||||||||||
Db         15 GAATTGAAAAAAAAA 1


RESULT 3424
ADC64943
ID   ADC64943 standard; DNA; 18 BP.
XX
AC   ADC64943;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Camellia sinensis L. (O.) Kuntze related PCR primer T11G.
XX
KW   Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
```

XX
OS Synthetic.
OS Camellia sinensis.
XX
PN CN1377966-A.
XX
PD 06-NOV-2002.
XX
PF 30-MAR-2001; 2001CN-00112459.
XX
PR 30-MAR-2001; 2001CN-00112459.
XX
PA (SCIN-) SCI & IND RES COMMISSION.
XX
DR WPI; 2003-230959/23.
XX
PT Cloning of a new gene sequence expressed and inhibited during winter
PT dormancy of a tea tree top plumelet, comprises identification, cloning
PT and analysis of a new primer in the gene sequence.
XX
PS Example 3; Page 32; 66pp; Chinese.
XX
CC The present invention describes the cloning of a new gene sequence
CC expressed and inhibited during hibernation of the top plumelet of a
CC Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC identification, cloning and analysis of a primer terminal in the gene
CC sequence expressed and inhibited during hibernation of the top plumelet
CC of the tea tree. The present sequence represents a PCR primer which is
CC used in an example from the present invention.
XX
SQ Sequence 18 BP; 2 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3425
ADC64942
ID ADC64942 standard; DNA; 18 BP.
XX
AC ADC64942;
XX
DT 18-DEC-2003 (first entry)
XX
DE Camellia sinensis L. (O.) Kuntze related PCR primer T11C.
XX
KW Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
OS Synthetic.
OS Camellia sinensis.
XX
PN CN1377966-A.
XX
PD 06-NOV-2002.
XX
PF 30-MAR-2001; 2001CN-00112459.
XX
PR 30-MAR-2001; 2001CN-00112459.
XX
PA (SCIN-) SCI & IND RES COMMISSION.
XX
DR WPI; 2003-230959/23.
XX
PT Cloning of a new gene sequence expressed and inhibited during winter
PT dormancy of a tea tree top plumelet, comprises identification, cloning
PT and analysis of a new primer in the gene sequence.
XX
PS Example 3; Page 32; 66pp; Chinese.
XX
CC The present invention describes the cloning of a new gene sequence
CC expressed and inhibited during hibernation of the top plumelet of a
CC Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC identification, cloning and analysis of a primer terminal in the gene
CC sequence expressed and inhibited during hibernation of the top plumelet
CC of the tea tree. The present sequence represents a PCR primer which is
CC used in an example from the present invention.
XX
SQ Sequence 18 BP; 2 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3426
ADC64941
ID ADC64941 standard; DNA; 18 BP.
XX
AC ADC64941;
XX
DT 18-DEC-2003 (first entry)
XX
DE Camellia sinensis L. (O.) Kuntze related PCR primer T11A.
XX
KW Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
OS Synthetic.
OS Camellia sinensis.
XX
PN CN1377966-A.
XX
PD 06-NOV-2002.
XX
PF 30-MAR-2001; 2001CN-00112459.
XX
PR 30-MAR-2001; 2001CN-00112459.
XX
PA (SCIN-) SCI & IND RES COMMISSION.
XX
DR WPI; 2003-230959/23.
XX
PT Cloning of a new gene sequence expressed and inhibited during winter
PT dormancy of a tea tree top plumelet, comprises identification, cloning
PT and analysis of a new primer in the gene sequence.
XX
PS Example 3; Page 32; 66pp; Chinese.
XX
CC The present invention describes the cloning of a new gene sequence
CC expressed and inhibited during hibernation of the top plumelet of a
CC Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC identification, cloning and analysis of a primer terminal in the gene
CC sequence expressed and inhibited during hibernation of the top plumelet
CC of the tea tree. The present sequence represents a PCR primer which is
CC used in an example from the present invention.
XX
SQ Sequence 18 BP; 3 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 1 AAGCTTTTTTTTTTT 15

RESULT 3427

```
AAX55052
ID   AAX55052 standard; DNA; 19 BP.
XX
AC   AAX55052;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 19 BP; 0 A; 6 C; 12 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15
```

```
RESULT 3428
AAA34499
ID   AAA34499 standard; DNA; 19 BP.
XX
AC   AAA34499;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2188.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 539; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 19 BP; 0 A; 6 C; 12 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          53 GGCGGGGGCGGCGGC 67
               |||||||||||||||
Db           1 GGCGGGGGCGGCGGC 15


RESULT 3429
AAF20621
ID   AAF20621 standard; DNA; 19 BP.
XX
AC   AAF20621;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2188.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 264; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 19 BP; 0 A; 6 C; 12 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          53 GGCGGGGGCGGCGGC 67
               |||||||||||||||
Db           1 GGCGGGGGCGGCGGC 15


RESULT 3430
ABK94423
ID   ABK94423 standard; DNA; 19 BP.
XX
AC   ABK94423;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human MLH1 DNA mismatch repair gene, exon 12, PCR primer 12.1F.
XX
KW   hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
KW   breast and ovarian cancer susceptibility gene; TGDS; human;
KW   two-dimensional DNA electrophoresis; tumour suppressor gene;
KW   breast cancer; ovarian cancer; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200236819-A1.
XX
PD   10-MAY-2002.
XX
PF   06-NOV-2000; 2000WO-IB001607.
XX
PR   06-NOV-2000; 2000WO-IB001607.
XX
PA   (SCSC-) ACAD APPLIED SCI.
XX
PI   Vijg J;
XX
DR   WPI; 2002-471507/50.
XX
PT   Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT   amplification products to 2-dimensional gel electrophoresis to produce a
PT   characteristic spot pattern for a specific mutation in either the BRCA1
PT   or the hMLH1 gene.
XX
PS   Claim 6; Page 21; 57pp; English.
XX
CC   The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC   comprising subjecting a set of amplification products to two-dimensional
CC   DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC   specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC   are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC   PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC   KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC   detecting mutations in the BRCA1 (breast and ovarian cancer
CC   susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
CC   mismatch repair gene). The present sequence is a PCR primer specific to
CC   hMLH1 used in the method of the invention
XX
SQ   Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3431
ABZ96315
ID   ABZ96315 standard; DNA; 19 BP.
XX
AC   ABZ96315;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human C/EBP antisense fragment no.2175.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 11557; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 19 BP; 0 A; 6 C; 12 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3432
AAT73293
ID   AAT73293 standard; DNA; 20 BP.
XX
AC   AAT73293;
XX
DT   12-DEC-1997  (first entry)
XX
DE   Primer for pUC19 DNA amplification.
XX
KW   primer; PCR; polymerase chain reaction; sequencing; walking;
KW   complementary extension reaction; low redundancy; universal primer; ss.
XX
OS   Synthetic.
XX
PN   EP767240-A2.
XX
PD   09-APR-1997.
XX
PF   17-SEP-1996;   96EP-00114907.
XX
PR   18-SEP-1995;   95JP-00238141.
PR   30-JAN-1996;   96JP-00013634.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K;
XX
DR   WPI; 1997-205424/19.
XX
PT   Efficient sequencing of long DNA by fragment walking - with simultaneous
PT   sequencing of restriction enzyme fragment and adjacent region of intact
PT   DNA, avoids the need for cloning and requires fewer primers.
XX
PS   Example 1; Page 23; 50pp; English.
XX
CC   A method for DNA analysis based on a complementary extension reaction
CC   using a DNA polymerase, comprises a combination of fragment walking and
CC   DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC   restriction enzyme and the targeted DNA sequence can be determined
CC   directly from the digested DNA fragments. By exploring the overlapping
CC   sequence of the determined base sequence, the overall base sequence of a
CC   lengthy DNA can be determined with low redundancy without cloning or
CC   subcloning. In addition, the method can be done with commercially
CC   available universal primers or with fewer primers than required in
CC   existing methods. AAT73291-92 are primers used in determination of the
CC   pUC19 sequence. Primer extension was carried out using 16 primers
CC   AAT73293
XX
SQ   Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3433
ABZ89014
ID   ABZ89014 standard; DNA; 20 BP.
XX
AC   ABZ89014;
XX
```

DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4256; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 6 AAAAAAAAAAAAAAA 20

RESULT 3434
ABA05915
ID ABA05915 standard; DNA; 20 BP.
XX
AC ABA05915;
XX
DT 05-MAR-2002 (first entry)
XX
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 5.
XX
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW PCR primer; ss.
XX
OS Hepatitis B virus.
XX
PN EP1152063-A1.
XX
PD 07-NOV-2001.
XX
PF 03-MAY-2000; 2000EP-00109436.
XX
PR 03-MAY-2000; 2000EP-00109436.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Schroeder KH, Koike K;
XX
DR WPI; 2002-068256/10.
XX
PT Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT risk for hepatocellular carcinoma, comprises identifying full length HBV
PT transcripts and truncated HBV transcripts in a serum sample.
XX
PS Example 1; Page 6; 25pp; English.
XX
CC The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC stages comprising identification of full length HBV transcripts (I) and
CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC is indicative of a particular infection stage. The method is useful for
CC diagnosing HBV infection stages and determining the risk for developing
CC hepatocellular carcinoma. The present sequence is that of a HBV
CC diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 1 TTTTTTTTTTTTTTT 15

RESULT 3435
ABZ89119/c
ID ABZ89119 standard; DNA; 20 BP.
XX
AC ABZ89119;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX

PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4361; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTA 2187
||||||||||||||||
Db 20 TTTTTTTTTTTTTTA 6

RESULT 3436
AAC82910
ID AAC82910 standard; DNA; 20 BP.
XX
AC AAC82910;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human beta-actin derived oligonucleotide #3.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
PS Example; Fig 1; 8pp; German.
XX
CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
SQ Sequence 20 BP; 3 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAA 2188
|||||||||||||||
Db 1 TTTTTTTTTTTTTAA 15

RESULT 3437
AAZ09195
ID AAZ09195 standard; DNA; 20 BP.
XX
AC AAZ09195;
XX
DT 19-OCT-1999 (first entry)
XX
DE Oligonucleotide 7 for DNA analysis.
XX
KW Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS Synthetic.
XX
PN JP11196874-A.
XX
PD 27-JUL-1999.
XX
PF 14-JAN-1998; 98JP-00005399.
XX
PR 14-JAN-1998; 98JP-00005399.
XX
PA (HITA) HITACHI LTD.
XX
DR WPI; 1999-496652/42.
XX
PT Analysis of DNA fragment - comprises addition of known common
PT oligonucleotide, amplification of resultant DNA fragment and analysis and
PT labelling of amplified DNA.
XX
PS Example 1; Page 12; 17pp; Japanese.
XX
CC This invention descibes a novel method for the analysis of a DNA fragment
CC which comprises: (i) addition of a known common oligonucleotide sequence
CC to at least one terminal of each DNA fragment, (ii) amplification of the
CC resultant DNA fragment as a primer using a first common primer containing
CC a complementary nucleotide sequence to the above mentioned known common
CC oligonucleotide sequence, a second common primer containing a
CC complementary nucleotide sequence to the prepared known common
CC oligonucleotide sequence optionally having been introduced with

CC complementary nucleotide sequence at a terminal, and a specific primer
CC capable of hybridisation with a DNA fragment containing whole or part of
CC the gene having known sequence, to give amplified DNA, (iii) analysis of
CC the amplified DNA to find the information of the DNA fragment, in which
CC the specific primer is designed to prepare fragments of the common first
CC and second primers and to give short fragment of amplified DNA and (iv)
CC labelling them to make their differentiation. Differentiation of
CC informations of known and unknown genes readily provides information of
CC unknown gene and simultaneous monitoring of signals derived from minor
CC genes. Furthermore, labelling of DNAs according to functions of known
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC used to illustrate the method of the invention
XX
SQ Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||||||||||||
Db 6 AAAAAAAAAAAAAAA 20

RESULT 3438
AAZ09195/c
ID AAZ09195 standard; DNA; 20 BP.
XX
AC AAZ09195;
XX
DT 19-OCT-1999 (first entry)
XX
DE Oligonucleotide 7 for DNA analysis.
XX
KW Primer; DNA analysis; amplification; hybridisation; ss.
XX
OS Synthetic.
XX
PN JP11196874-A.
XX
PD 27-JUL-1999.
XX
PF 14-JAN-1998; 98JP-00005399.
XX
PR 14-JAN-1998; 98JP-00005399.
XX
PA (HITA) HITACHI LTD.
XX
DR WPI; 1999-496652/42.
XX
PT Analysis of DNA fragment - comprises addition of known common
PT oligonucleotide, amplification of resultant DNA fragment and analysis and
PT labelling of amplified DNA.
XX
PS Example 1; Page 12; 17pp; Japanese.
XX
CC This invention descibes a novel method for the analysis of a DNA fragment
CC which comprises: (i) addition of a known common oligonucleotide sequence
CC to at least one terminal of each DNA fragment, (ii) amplification of the
CC resultant DNA fragment as a primer using a first common primer containing
CC a complementary nucleotide sequence to the above mentioned known common
CC oligonucleotide sequence, a second common primer containing a
CC complementary nucleotide sequence to the prepared known common
CC oligonucleotide sequence optionally having been introduced with
CC complementary nucleotide sequence at a terminal, and a specific primer
CC capable of hybridisation with a DNA fragment containing whole or part of
CC the gene having known sequence, to give amplified DNA, (iii) analysis of
CC the amplified DNA to find the information of the DNA fragment, in which
CC the specific primer is designed to prepare fragments of the common first
CC and second primers and to give short fragment of amplified DNA and (iv)
CC labelling them to make their differentiation. Differentiation of
CC informations of known and unknown genes readily provides information of
CC unknown gene and simultaneous monitoring of signals derived from minor
CC genes. Furthermore, labelling of DNAs according to functions of known
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
CC used to illustrate the method of the invention
XX
SQ Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
|||||||||||||||
Db 20 TTTTTTTTTTTTTTT 6

RESULT 3439
AAX55051
ID AAX55051 standard; DNA; 20 BP.
XX
AC AAX55051;
XX
DT 05-JUL-1999 (first entry)
XX
DE C/EBP-beta antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 70; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary

```
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 20 BP; 0 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3440
AAX32003
ID   AAX32003 standard; DNA; 20 BP.
XX
AC   AAX32003;
XX
DT   14-JUN-1999  (first entry)
XX
DE   MSH2 gene specific primer.
XX
KW   Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW   CFTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW   Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW   colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW   BAP1 gene; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9906598-A2.
XX
PD   11-FEB-1999.
XX
PF   04-AUG-1998;   98WO-US016574.
XX
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 1999-153820/13.
XX
PT   Determining common functional alleles in a population - useful in the
PT   diagnosis of disease associated with allelic heterogeneity.
XX
PS   Example 1; Page 24; 78pp; English.
XX
CC   The invention relates to methods of determining a functional allele
CC   profile of a gene in a population. Functional allele profiles comprise
CC   the commonly occurring alleles in a population, and the relative
CC   frequencies at which such alleles of a given gene occur. The methods are
CC   used to identify and determine the frequency of the functional alleles of
CC   genes which display extensive allelic heterogeneity, particularly those
CC   implicated in disease or conditions, such as the BRCA1 gene associated
CC   with breast cancer, CFTR associated with cystic fibrosis, dystrophin
CC   associated with Duchenne muscular dystrophy and Becker muscular
CC   dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
CC   also be employed for diseases where allelic and genetic heterogeneity
CC   exist, such as breast cancer, neurofibromatosis, and hereditary non-
CC   polyposis colorectal cancer. Identification of functional alleles is
CC   necessary for identification of mutations which may be implicated in the
CC   disease. Sequences AAX32001-172 represent primers for determining the
CC   functional allele profiles of various genes. The primers are specific for
CC   genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
XX
SQ   Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3441
AAA34498
ID   AAA34498 standard; DNA; 20 BP.
XX
AC   AAA34498;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2187.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 539; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
```

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 20 BP; 0 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||| |
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3442
AAF20620
ID AAF20620 standard; DNA; 20 BP.
XX
AC AAF20620;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2187.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 20 BP; 0 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||| |
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3443
AAC80380/c
ID AAC80380 standard; DNA; 20 BP.
XX
AC AAC80380;
XX
DT 03-MAY-2001 (first entry)
XX
DE Forward primer #149 used for amplification of HLA-C exon 4.
XX
KW HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200061795-A2.
XX
PD 19-OCT-2000.
XX
PF 05-APR-2000; 2000WO-EP002998.
XX
PR 09-APR-1999; 99EP-00870068.
PR 11-JUN-1999; 99US-0138614P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Canck I, Rombout A, Rossau R;
XX
DR WPI; 2000-647426/62.
XX
PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
PT primer sets, useful for subtyping or typing of HLA Class I alleles.
XX
PS Claim 4; Page 47; 128pp; English.
XX
CC The present invention relates to a method for the locus-specific,
CC separate amplification of exon 2, exon 3, and/or exon 4 of human
CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
CC for subtyping or typing of HLA class 1 alleles. The present sequence is
CC an amplification primer used in the method
XX
SQ Sequence 20 BP; 4 A; 5 C; 5 G; 4 T; 0 U; 2 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1055 GCTCATGTGACTCTCCTGA 1073
              |: ||||||||: ||||||
Db         20 GSCCATGTGACYATCCTGA 2


RESULT 3444
AAC82923
ID   AAC82923 standard; DNA; 20 BP.
XX
AC   AAC82923;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #7.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 2 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3445
AAC82917
ID   AAC82917 standard; DNA; 20 BP.
XX
AC   AAC82917;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #1.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3446
AAC82918
ID   AAC82918 standard; DNA; 20 BP.
XX
AC   AAC82918;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #2.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
```

```
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 3 A; 1 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3447
AAC82911
ID   AAC82911 standard; DNA; 20 BP.
XX
AC   AAC82911;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #4.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3448
AAC82912
ID   AAC82912 standard; DNA; 20 BP.
XX
AC   AAC82912;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #5.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 3 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3449
AAC82919
ID   AAC82919 standard; DNA; 20 BP.
XX
AC   AAC82919;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #3.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 4 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3450
AAC82908
ID   AAC82908 standard; DNA; 20 BP.
XX
AC   AAC82908;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #1.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3451
AAC82920
ID   AAC82920 standard; DNA; 20 BP.
XX
AC   AAC82920;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #4.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
```

XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
PS Example; Fig 1; 8pp; German.
XX
CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAA 2188
||||||||||||||| |
Db 1 TTTTTTTTTTTTTAA 15

RESULT 3452
AAC82921
ID AAC82921 standard; DNA; 20 BP.
XX
AC AAC82921;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human S-9 derived oligonucleotide #5.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
PS Example; Fig 1; 8pp; German.
XX
CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
SQ Sequence 20 BP; 2 A; 2 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAA 2188
||||||||||||||| |
Db 1 TTTTTTTTTTTTTAA 15

RESULT 3453
AAF87713
ID AAF87713 standard; DNA; 20 BP.
XX
AC AAF87713;
XX
DT 06-JUL-2001 (first entry)
XX
DE Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.
XX
KW Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;
KW hepatic cell proliferative disorder; liver cancer; anticancer;
KW tumourigenesis; detection; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200126536-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-US028427.
XX
PR 13-OCT-1999; 99US-0159168P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Nelson WG, Lin X, Tchou JC, Bakker J;
XX
DR WPI; 2001-290647/30.
XX
PT Detecting hepatic cell proliferative disorder useful for detecting
PT hepatocellular carcinoma comprises detecting a methylated CpG-containing
PT glutathione-S-transferase nucleic acid.
XX
PS Claim 83; Page 42; 64pp; English.
XX
CC The present invention describes a method for detecting hepatic cell
CC proliferative disorders. The method comprises detecting a methylated CpG-
CC containing glutathione-S-transferase (GST) nucleic acid (I) in a hepatic
CC specimen or a biological fluid, where a methylated GST nucleic acid is
CC indicative of a hepatic cell proliferative disorder. The method can be
CC used to diagnose hepatocellular carcinoma, and to monitor progress of its
CC treatment. Increasing the level of GST is useful in the treatment of
CC liver cancer, in humans or animals. The method can detect the early
CC stages of tumourigenesis in liver cells simply. The present sequence
CC represents a PCR primer which is used in the amplification of the human
CC glutathione S-transferase pi gene (GSTP1) promoter in an example from the
CC present invention for mapping somatic GSTP1 CpG island DNA
CC hyperethylation changes by genomic sequencing after bisulfite treatment
XX
SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;

```
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          5 TTTTTTTTTTTTTAA 19


RESULT 3454
ABL57070
ID   ABL57070 standard; DNA; 20 BP.
XX
AC   ABL57070;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .20
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 1-20 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 2; Page 26; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3455
ABL57070/c
ID   ABL57070 standard; DNA; 20 BP.
XX
AC   ABL57070;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .20
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 1-20 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 2; Page 26; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3456
ABZ87682/c
```

```
ID   ABZ87682 standard; DNA; 20 BP.
XX
AC   ABZ87682;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 2924; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAA 2798
              |||||||||||||||
Db         15 TGAAAAAAAAAAAAA 1


RESULT 3457
ABZ96314
```

```
ID   ABZ96314 standard; DNA; 20 BP.
XX
AC   ABZ96314;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human C/EBP antisense fragment no.2174.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 11556; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3458
ABZ85313/c
```

ID ABZ85313 standard; DNA; 20 BP.
XX
AC ABZ85313;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 555; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 3 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAA 2797
||||||||||||||
Db 15 TTGAAAAAAAAAAAA 1

RESULT 3459
ABZ89178/c

ID ABZ89178 standard; DNA; 20 BP.
XX
AC ABZ89178;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4420; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAA 2188
||||||||||||||
Db 20 TTTTTTTTTTTTTAA 6

RESULT 3460
ADA45244

```
ID   ADA45244 standard; DNA; 20 BP.
XX
AC   ADA45244;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MSH2 gene PCR primer #3.
XX
KW   Functional allele profile; genetic inheritance; haplotype; population;
KW   disease; pharmacogenetic application; selective pressure; human; MSH2;
KW   MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2003096236-A1.
XX
PD   22-MAY-2003.
XX
PF   08-AUG-2001; 2001US-00923327.
XX
PR   12-FEB-1996;   96US-00598591.
PR   12-FEB-1997;   97US-00798691.
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
PR   04-AUG-1998;   98US-00129134.
PR   14-MAR-2000; 2000US-00524794.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 2003-576875/54.
XX
PT   Determining a functional allele profile of a gene in a population by
PT   identifying the nucleotide sequence of a gene of genomic DNA from each of
PT   the individuals with a family history of functional alleles of the gene
PT   of interest.
XX
PS   Example 1; Page 9; 28pp; English.
XX
CC   The present invention relates to a method for determining a functional
CC   allele profile of a gene in a population. The method comprises
CC   identifying the nucleotide sequence of a gene of interest out of genomic
CC   DNA from each of a population of individuals identified as having a
CC   family history which indicates inheritance of functional alleles of the
CC   gene of interest, and rank ordering the frequency of occurrence of each
CC   haplotype, where the identity of the alleles containing each haplotype
CC   and the determination of their relative frequencies constitutes the
CC   functional allele profile of the gene of interest in the population. The
CC   method is useful for determining functional allele profiles which are
CC   useful in the treatment and diagnosis of diseases, for genetic and
CC   pharmacogenetic applications, and for evaluating the degree to which the
CC   gene(s) are under selective pressure. The present sequence represents a
CC   PCR primer used in the method of the invention.
XX
SQ   Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          1 TTTTTTTTTTTTTAA 15


RESULT 3461
AAD57844
ID   AAD57844 standard; DNA; 20 BP.
XX
AC   AAD57844;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #1 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3462
AAD57844/c
ID   AAD57844 standard; DNA; 20 BP.
XX
AC   AAD57844;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #1 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
```

```
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         15 TTTTTTTTTTTTTTT 1


RESULT 3463
ABL57071/c
ID   ABL57071 standard; DNA; 21 BP.
XX
AC   ABL57071;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence.
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .21
FT                   /*tag=  a
FT                   /bound_moiety= "Molecular beacon"
FT                   /note= "forms double-stranded region with bases 1-21 of
FT                   sequence in ABL57069"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 62; 62pp; English.
XX
CC   The present sequence is that of a perfectly matched target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Single mismatches can be detected.
CC   The invention relates generally to the use of metal surface quenchers
CC   such as particles or films for high sensitivity applications in, for
CC   example, detection and diagnostic systems
XX
SQ   Sequence 21 BP; 15 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db         16 TTTTTTTTTTTTTTT 2


RESULT 3464
ABS97681
ID   ABS97681 standard; DNA; 21 BP.
XX
AC   ABS97681;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Histamine N-methyl transferase (HNMT) sequencing Primer #4.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological; sequencing.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
```

```
PS   Example 13; Page 124; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   sequencing primer used to sequence the polymorphic genes of the invention
XX
SQ   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          3 AAAAAAAAAAAAAAA 17


RESULT 3465
ABS97669
ID   ABS97669 standard; DNA; 21 BP.
XX
AC   ABS97669;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Histamine N-methyl transferase (HNMT) PCR Primer #4.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 13; Page 123; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a PCR
CC   primer used to amplify the sequences of the invention
XX
SQ   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
```

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                |||||||||||||||
Db          3 AAAAAAAAAAAAAAA 17


RESULT 3466
AAZ26619
ID   AAZ26619 standard; DNA; 21 BP.
XX
AC   AAZ26619;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 808.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 12 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAA 2797
                |||||||||||||||
Db          7 TTGAAAAAAAAAAAA 21
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RESULT 3467
AAZ26366
ID   AAZ26366 standard; DNA; 21 BP.
XX
AC   AAZ26366;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 555.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 3 A; 5 C; 11 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        112 GGGCTGGGGGGATCC 126
                |||||||||||||||
Db          1 GGGCTGGGGGGATCC 15


RESULT 3468
AAX55050
ID   AAX55050 standard; DNA; 21 BP.
XX
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```
AC   AAX55050;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 21 BP; 0 A; 6 C; 14 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3469
AAA34497
```

```
ID   AAA34497 standard; DNA; 21 BP.
XX
AC   AAA34497;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2186.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 539; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 21 BP; 0 A; 6 C; 14 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
```

```
                  ||||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3470
AAF20619
ID   AAF20619 standard; DNA; 21 BP.
XX
AC   AAF20619;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2186.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 264; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 21 BP; 0 A; 6 C; 14 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              ||||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3471
AAH62016/c
ID   AAH62016 standard; DNA; 21 BP.
XX
AC   AAH62016;
XX
DT   10-SEP-2001  (first entry)
XX
DE   IL8 hairpin/hammerhead ribozyme recognition site SEQ ID NO:4440.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 22; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
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CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 1 A; 1 C; 10 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1852 CAACAGACCCACACA 1866
||||||||||||||||
Db 16 CAACAGACCCACACA 2

RESULT 3472
ABZ96313
ID ABZ96313 standard; DNA; 21 BP.
XX
AC ABZ96313;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human C/EBP antisense fragment no.2173.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11555; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 0 A; 6 C; 14 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
|||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3473
ADB88602/c
ID ADB88602 standard; DNA; 21 BP.
XX
AC ADB88602;
XX
DT 04-DEC-2003 (first entry)
XX
DE Frizzled-4 (FZD4) modulating agent related oligo, SEQ ID No 49.
XX
KW Frizzled-4; FZD4; immunodulatory compound; ophthalmological; vasotropic;
KW antiinflammatory; vulnerary; osteopathic; antimicrobial; antipsoriatic;
KW antidiabetic; modulator; neovascularisation; myocardial ischaemia;
KW coronary artery disease; wound healing; fracture; tendon repair;
KW cancer tumour growth; metastatis; ocular neovascularisation; bone;
KW cartilage destruction; inflammatory; infectious disease; psoriasis;
KW pre-eclampsia; respiratory distress; peritoneal sclerosis; diabetes;
KW FzD4; ss.
XX
OS Homo sapiens.
XX
PN WO2003005034-A2.
XX
PD 16-JAN-2003.
XX
PF 04-JUL-2002; 2002WO-CA001004.
XX
PR 05-JUL-2001; 2001US-0303285P.
PR 29-OCT-2001; 2001US-0340409P.
XX
PA (XENO-) XENON GENETICS INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Macdonald ML, Zeisler JM, Samuels M, Goldberg YP, Robataille JM;
PI Hayden MR;
XX
DR WPI; 2003-221619/21.
XX
PT Identifying Frizzled-4 (FZD4) gene modulators for treating e.g. familial
PT exudative vitreoretinopathy or Coat's disease, comprises contacting a
PT compound with an FZD4 polypeptide or with a cell expressing FZD4
PT polypeptide.
XX
PS Disclosure; Page 103; 116pp; English.
XX
CC The invention relates to a novel method for identifying a Frizzled-4
CC (FZD4) modulating agent. The method comprises contacting a compound with
CC an FZD4 polypeptide or with a cell expressing an FZD4 polypeptide, and
CC determining the difference in the biological activity or expression of
CC the FZD4 polypeptide compared with when the compound is not present. The
CC immunodulatory compounds of the invention can have the follwing
CC activities of ophthalmological, vasotropic, antiinflammatory, vulnerary,
CC osteopathic, antimicrobial, antipsoriatic, and antidiabetic. The method
CC is useful for identifying modulators of FZD4, and such modulators are
CC useful in treating diseases related to Fzd-4 expression or activity. The

CC modulators are particularly useful in treating e.g. familial exudative
CC vitreoretinopathy, retinopathy of prematurity, Coat's disease, Norrie
CC disease, retinal angiomatosis, ocular toxocariasis, retinoblastoma,
CC retinal dysplasia, neovascular inflammatory vitreoretinopathy or
CC retinitis pigmentosa. The modulators are also useful for treating other
CC diseases involving the physiological and pathological processes of
CC neovascularisation, such as indications that may require stimulation of
CC neovascularisation (e.g. myocardial ischaemia, coronary artery disease,
CC wound healing, or fracture and tendon repair), indications that may
CC require inhibition of neovascularisation (e.g. cancer tumour growth and
CC metastatis, ocular neovascularisation, bone and cartilage destruction,
CC inflammatory and infectious diseases), indications that require vascular
CC remodeling (e.g. psoriasis or pre-eclampsia), and indications that
CC require inhibition of neovascularisation (e.g. respiratory distress,
CC peritoneal sclerosis, or diabetes). This polynucleotide sequence
CC represents an oligo relating to the FzD4 gene of the invention.
XX
SQ Sequence 21 BP; 4 A; 4 C; 0 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAA 2796
||||||||||||||| |
Db 15 ATTGAAAAAAAAAAA 1

RESULT 3474
AAT28045
ID AAT28045 standard; DNA; 22 BP.
XX
AC AAT28045;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer B for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent
CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 2 A; 5 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||| |
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3475
AAT28046
ID AAT28046 standard; DNA; 22 BP.
XX
AC AAT28046;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer C for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 5' AAGCTTTTTTTTTTT 19

RESULT 3476
AAT28048
ID AAT28048 standard; DNA; 22 BP.
XX
AC AAT28048;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer E for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 2 A; 3 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3477
AAT28049
ID AAT28049 standard; DNA; 22 BP.
XX
AC AAT28049;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer F for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||| |
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3478
AAT28054
ID AAT28054 standard; DNA; 22 BP.
XX
AC AAT28054;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer L for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
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CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||| |
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3479
AAT28055
ID AAT28055 standard; DNA; 22 BP.
XX
AC AAT28055;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer M for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
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PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3480
AAT28047
ID AAT28047 standard; DNA; 22 BP.
XX
AC AAT28047;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer D for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 2 A; 3 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3481
AAT28044
ID AAT28044 standard; DNA; 22 BP.
XX
AC AAT28044;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer A for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent

CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 2 A; 4 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19
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RESULT 3482
AAT58488
ID AAT58488 standard; DNA; 22 BP.
XX
AC AAT58488;
XX
DT 24-MAR-1997 (first entry)
XX
DE First primer #5 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX
PF 29-APR-1994; 94US-00235180.
XX
PR 29-APR-1994; 94US-00235180.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Feng J, Villeponteau B, Funk W;
XX
DR WPI; 1997-033564/03.
XX
PT Detection of differentially expressed mRNA mols. - using two-step
PT polymerase chain reaction amplification method.
XX
PS Claim 9; Col 15; 15pp; English.
XX
CC An improved method of Differential Display, named Enhanced Differential
CC Display (EDD) has been designed as a technique for screening differences
CC in gene expression between various cell types or between different stages
CC of cell development. The technique is highly reproducible, leading to
CC precise typing of the expressed genes in any given cell. EDD analysis
CC permits the identification of novel genes involved in differentiation,
CC aging and disease, and enables direct comparisons of different cell types
CC and disease states. By using longer primers, and/or an alteration in the
CC annealing temperatures, the number of false positives can be reduced.
CC First, cDNA is prepared from total cellular RNA using 12 different 22-
CC base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC of pol II mRNA transcripts. The last two bases of each primer varies so
CC as to anchor the primer to the 3' end of different sets of mRNAs. A
CC second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC amplification of a subset of cDNAs is carried out in a two step process
CC using particular 5' and 3' primers. The amplified gene products can then
CC be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ Sequence 22 BP; 2 A; 3 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19
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RESULT 3483
AAT58494
ID AAT58494 standard; DNA; 22 BP.
XX
AC AAT58494;
XX
DT 24-MAR-1997 (first entry)
XX
DE First primer #11 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX
PF 29-APR-1994; 94US-00235180.
XX
PR 29-APR-1994; 94US-00235180.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Feng J, Villeponteau B, Funk W;
XX
DR WPI; 1997-033564/03.
XX
PT Detection of differentially expressed mRNA mols. - using two-step
PT polymerase chain reaction amplification method.
XX
PS Claim 9; Col 17; 15pp; English.
XX
CC An improved method of Differential Display, named Enhanced Differential
CC Display (EDD) has been designed as a technique for screening differences
CC in gene expression between various cell types or between different stages
CC of cell development. The technique is highly reproducible, leading to
CC precise typing of the expressed genes in any given cell. EDD analysis
CC permits the identification of novel genes involved in differentiation,
CC aging and disease, and enables direct comparisons of different cell types
CC and disease states. By using longer primers, and/or an alteration in the
CC annealing temperatures, the number of false positives can be reduced.
CC First, cDNA is prepared from total cellular RNA using 12 different 22-
CC base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC of pol II mRNA transcripts. The last two bases of each primer varies so
CC as to anchor the primer to the 3' end of different sets of mRNAs. A
CC second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC amplification of a subset of cDNAs is carried out in a two step process
CC using particular 5' and 3' primers. The amplified gene products can then
CC be directly sequenced or rapidly subcloned for DNA sequencing

```
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3484
AAT58489
ID   AAT58489 standard; DNA; 22 BP.
XX
AC   AAT58489;
XX
DT   24-MAR-1997  (first entry)
XX
DE   First primer #6 for use in enhanced differential display method.
XX
KW   Differential Display; Enhanced Differential Display; EDD; screening;
KW   gene expression; cell type; different; cell development; gene typing;
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 15; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3485
AAT58487
ID   AAT58487 standard; DNA; 22 BP.
XX
AC   AAT58487;
XX
DT   21-MAR-1997  (first entry)
XX
DE   First primer #4 for use in enhanced differential display method.
XX
KW   Differential Display; Enhanced Differential Display; EDD; screening;
KW   gene expression; cell type; different; cell development; gene typing;
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 15; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 2 A; 3 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3486
AAT58495
ID   AAT58495 standard; DNA; 22 BP.
XX
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AC AAT58495;
XX
DT 24-MAR-1997 (first entry)
XX
DE First primer #12 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX
PF 29-APR-1994; 94US-00235180.
XX
PR 29-APR-1994; 94US-00235180.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Feng J, Villeponteau B, Funk W;
XX
DR WPI; 1997-033564/03.
XX
PT Detection of differentially expressed mRNA mols. - using two-step
PT polymerase chain reaction amplification method.
XX
PS Claim 9; Col 17; 15pp; English.
XX
CC An improved method of Differential Display, named Enhanced Differential
CC Display (EDD) has been designed as a technique for screening differences
CC in gene expression between various cell types or between different stages
CC of cell development. The technique is highly reproducible, leading to
CC precise typing of the expressed genes in any given cell. EDD analysis
CC permits the identification of novel genes involved in differentiation,
CC aging and disease, and enables direct comparisons of different cell types
CC and disease states. By using longer primers, and/or an alteration in the
CC annealing temperatures, the number of false positives can be reduced.
CC First, cDNA is prepared from total cellular RNA using 12 different 22-
CC base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC of pol II mRNA transcripts. The last two bases of each primer varies so
CC as to anchor the primer to the 3' end of different sets of mRNAs. A
CC second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC amplification of a subset of cDNAs is carried out in a two step process
CC using particular 5' and 3' primers. The amplified gene products can then
CC be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ Sequence 22 BP; 4 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19
```

RESULT 3487
AAT58484
ID AAT58484 standard; DNA; 22 BP.
XX
AC AAT58484;
XX
DT 21-MAR-1997 (first entry)
XX
DE First primer #1 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX
PF 29-APR-1994; 94US-00235180.
XX
PR 29-APR-1994; 94US-00235180.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Feng J, Villeponteau B, Funk W;
XX
DR WPI; 1997-033564/03.
XX
PT Detection of differentially expressed mRNA mols. - using two-step
PT polymerase chain reaction amplification method.
XX
PS Claim 9; Col 13; 15pp; English.
XX
CC An improved method of Differential Display, named Enhanced Differential
CC Display (EDD) has been designed as a technique for screening differences
CC in gene expression between various cell types or between different stages
CC of cell development. The technique is highly reproducible, leading to
CC precise typing of the expressed genes in any given cell. EDD analysis
CC permits the identification of novel genes involved in differentiation,
CC aging and disease, and enables direct comparisons of different cell types
CC and disease states. By using longer primers, and/or an alteration in the
CC annealing temperatures, the number of false positives can be reduced.
CC First, cDNA is prepared from total cellular RNA using 12 different 22-
CC base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC of pol II mRNA transcripts. The last two bases of each primer varies so
CC as to anchor the primer to the 3' end of different sets of mRNAs. A
CC second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC amplification of a subset of cDNAs is carried out in a two step process
CC using particular 5' and 3' primers. The amplified gene products can then
CC be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ Sequence 22 BP; 2 A; 4 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19
```

RESULT 3488
AAT58485
ID AAT58485 standard; DNA; 22 BP.
XX
AC AAT58485;
XX
DT 21-MAR-1997 (first entry)
XX
DE First primer #2 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX

```
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 13; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 2 A; 5 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3489
AAT58486
ID   AAT58486 standard; DNA; 22 BP.
XX
AC   AAT58486;
XX
DT   21-MAR-1997  (first entry)
XX
DE   First primer #3 for use in enhanced differential display method.
XX
KW   Differential Display; Enhanced Differential Display; EDD; screening;
KW   gene expression; cell type; different; cell development; gene typing;
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 13; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3490
AAV58375
ID   AAV58375 standard; DNA; 22 BP.
XX
AC   AAV58375;
XX
DT   26-NOV-1998  (first entry)
XX
DE   Biotinylated primer for mouse thymus and spleen mRNA.
XX
KW   PCR primer; differential mRNA expression; gene expression analysis;
KW   thymus; spleen; mouse; mRNA expression detection; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "biotinylated"
XX
PN   US5814445-A.
XX
PD   29-SEP-1998.
XX
PF   11-JUL-1995;   95US-00499899.
XX
PR   11-JUL-1994;   94RU-00024056.
XX
PA   (NYBL-) NEW YORK BLOOD CENTER INC.
XX
PI   Ivanova NB,  Belyavsky AV;
XX
DR   WPI; 1998-541742/46.
XX
PT   Identification of differential mRNA expression - based on signal
```

PT intensities from separated cDNA restriction fragments.
XX
PS Example; Col 7; 15pp; English.
XX
CC This sequence represents a PCR primer used in the method of the
CC invention. The method is for the identification of differential mRNA
CC expression among two or more different sources, comprises: (a) obtaining
CC mRNA samples from two or more sources; (b) synthesising a set of double
CC stranded cDNA from each of the mRNA samples; (c) generating a set of cDNA
CC fragments for each sample by cleaving the sets of cDNA with at least one
CC restriction endonuclease; (d) separating cDNA fragments obtained through
CC step (c) by gel electrophoresis; (e) obtaining pictures of the separated
CC cDNA fragments; (f) comparing pictures of separated cDNA fragments, and
CC (g) identifying specific cDNA fragments exhibiting different signal
CC intensities in the pictures of separated cDNA fragments, where
CC differential signal intensity of the cDNA fragments is indicative of
CC differential expression of mRNA species among the sources. This primer
CC was specifically used to differentiate between mRNA differentially
CC expressed in mouse thymus and spleen. The method is useful in medicine
CC and molecular biology for analysis of gene expression and diagnosis and
CC identification of mechanisms of pathology at the genetic level
XX
SQ Sequence 22 BP; 1 A; 3 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTT 2178
|||||||||||||||
Db 8 CCTTTTTTTTTTTTT 22

RESULT 3491
AAV03675
ID AAV03675 standard; DNA; 22 BP.
XX
AC AAV03675;
XX
DT 21-MAY-1998 (first entry)
XX
DE Oligo dT primer.
XX
KW Jagged; Notch; angiogenesis; endothelial cell; migration; human;
KW wound repair; vulnerary; injury repair; signal transduction;
KW motor neurone disease; amyotrophic lateral sclerosis; polymyelitis;
KW diagnosis; gene therapy; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9745143-A1.
XX
PD 04-DEC-1997.
XX
PF 30-MAY-1997; 97WO-US009407.
XX
PR 31-MAY-1996; 96US-0018841P.
XX
PA (NAAM-) NAT AMERICAN RED CROSS.
PA (UYGE-) UNIV GENEVE.
XX
PI Zimrin AB, Maciag T, Pepper M, Montesano R, Wong MK;
XX
DR WPI; 1998-032340/03.
XX
PT New human Jagged protein - used to inhibit or promote angiogenesis and to
PT control migration of endothelial cells in injured blood vessels.
XX
PS Example 3; Page 38; 81pp; English.
XX
CC This oligo-dT primer was used in the synthesis of cDNA from total RNA
CC isolated from human umbilical vein endothelial cells (HUVEC) stimulated
CC with fibrin. It was also used as a 3' primer with a 5' primer (see
CC AAV03676) in the PCR amplification of the cDNA. The PCR product was
CC cloned into a TA vector and used to screen a HUVEC cDNA library. RT-PCR
CC analysis (see AAV03677-84) was performed to analyse expression of Jagged,
CC Notch 1, Notch 2 and glyceraldehyde 3-phosphate dehydrogenase in human
CC endothelial cell populations. The novel human Jagged gene (see AAV03684)
CC and protein (see AAW40827) can be used to control migration of
CC endothelial cells and in methods of modulating angiogenesis
XX
SQ Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
|||||||||||||||
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3492
AAX55049
ID AAX55049 standard; DNA; 22 BP.
XX
AC AAX55049;
XX
DT 05-JUL-1999 (first entry)
XX
DE C/EBP-beta antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 70; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung

```
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 22 BP; 0 A; 7 C; 14 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3493
AAX77101
ID   AAX77101 standard; DNA; 22 BP.
XX
AC   AAX77101;
XX
DT   03-AUG-1999  (first entry)
XX
DE   GC6 gene 3' primer E.
XX
KW   Cellular senescence; modulator; GC6 gene; senescent gene expression;
KW   pGC6; human; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9925878-A2.
XX
PD   27-MAY-1999.
XX
PF   19-NOV-1998;   98WO-US024996.
XX
PR   19-NOV-1997;   97US-00974180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Funk W;
XX
DR   WPI; 1999-347496/29.
XX
PT   New human GC6 gene, useful for identifying agents for treating diseases
PT   and/or conditions associated with cell senescence.
XX
PS   Disclosure; Page 12; 79pp; English.
XX
CC   The invention relates to methods for modulating and identifying cellular
CC   senescence. Recombinant expression vectors comprising a recombinant
CC   polynucleotide corresponding to a polynucleotide in a human GC6 gene, are
CC   useful for altering senescent gene expression. The vectors and host cells
CC   comprising the vectors are useful for identifying agents that prevent or
CC   modulate senescent gene expression. The polynucleotides are useful for
CC   producing the protein, pGC6 and nucleic acid derivatives. The proteins
CC   encoded are useful for raising antibodies specific for pGC6, which are
CC   useful for isolating pGC6, and for detecting cells comprising pGC6 in
CC   complex cell mixtures. The characterization of the polynucleotides enable
CC   the identification of therapeutic agents that identify and distinguish
CC   between young and senescent cells. This enables treatment of aging
CC   diseases induced or exacerbated by cellular senescence
XX
SQ   Sequence 22 BP; 2 A; 3 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3494
AAA34496
ID   AAA34496 standard; DNA; 22 BP.
XX
AC   AAA34496;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2185.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 539; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
```

```
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 22 BP; 0 A; 7 C; 14 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3495
AAZ47353
ID   AAZ47353 standard; DNA; 22 BP.
XX
AC   AAZ47353;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer M used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3496
AAZ47347
ID   AAZ47347 standard; DNA; 22 BP.
XX
AC   AAZ47347;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer F used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
```

```
                  ||||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3497
AAZ47346
ID   AAZ47346 standard; DNA; 22 BP.
XX
AC   AAZ47346;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer E used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 2 A; 3 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
                ||||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3498
AAZ47352
ID   AAZ47352 standard; DNA; 22 BP.
XX
AC   AAZ47352;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer L used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
                ||||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3499
AAZ47342
ID   AAZ47342 standard; DNA; 22 BP.
XX
AC   AAZ47342;
XX
```

DT 06-MAR-2000 (first entry)
XX
DE PCR primer A used in differential display analysis of Aspergillus oryzae.
XX
KW Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS Synthetic.
OS Aspergillus oryzae.
XX
PN WO9960136-A1.
XX
PD 25-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010689.
XX
PR 15-MAY-1998; 98US-00079344.
PR 15-MAY-1998; 98US-00079601.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO-NORDISK AS.
XX
PI Wahleithner J, Christensen T;
XX
DR WPI; 2000-062459/05.
XX
PT New isolated Aspergillus oryzae signaling sequences, used to increase the
PT production of polypeptides by recombinant host filamentous fungal cells.
XX
PS Example 2; Page 35; 78pp; English.
XX
CC Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC differential display analysis of the Aspergillus oryzae strains HC4.01
CC and 27. The strains were analysed to find the genetic basis for phenotype
CC differences in the strains which are used in a method for producing a
CC polypeptide in an enhanced amount. The method involves cultivating a
CC mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC The mutant cell contains the nucleotide sequence encoding the polypeptide
CC to be synthesised and one or more second nucleotide sequences encoding a
CC DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC the polypeptide than the parent cell and the polypeptide can be recovered
CC from the nutrient medium of the mutant cell. The method can be used for
CC the production of polypeptides such as hormones, receptors, antibodies,
CC reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC ribonuclease, transglutaminase or xylanase
XX
SQ Sequence 22 BP; 2 A; 4 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3500
AAZ47344
ID AAZ47344 standard; DNA; 22 BP.
XX
AC AAZ47344;
XX
DT 06-MAR-2000 (first entry)
XX
DE PCR primer C used in differential display analysis of Aspergillus oryzae.
XX
KW Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS Synthetic.
OS Aspergillus oryzae.
XX
PN WO9960136-A1.
XX
PD 25-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010689.
XX
PR 15-MAY-1998; 98US-00079344.
PR 15-MAY-1998; 98US-00079601.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO-NORDISK AS.
XX
PI Wahleithner J, Christensen T;
XX
DR WPI; 2000-062459/05.
XX
PT New isolated Aspergillus oryzae signaling sequences, used to increase the
PT production of polypeptides by recombinant host filamentous fungal cells.
XX
PS Example 2; Page 35; 78pp; English.
XX
CC Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC differential display analysis of the Aspergillus oryzae strains HC4.01
CC and 27. The strains were analysed to find the genetic basis for phenotype
CC differences in the strains which are used in a method for producing a
CC polypeptide in an enhanced amount. The method involves cultivating a
CC mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC The mutant cell contains the nucleotide sequence encoding the polypeptide
CC to be synthesised and one or more second nucleotide sequences encoding a
CC DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC the polypeptide than the parent cell and the polypeptide can be recovered
CC from the nutrient medium of the mutant cell. The method can be used for
CC the production of polypeptides such as hormones, receptors, antibodies,
CC reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC ribonuclease, transglutaminase or xylanase
XX
SQ Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1767 AAGCTTTTTTTTTTT 1781
||||||||||||||||
Db 5 AAGCTTTTTTTTTTT 19

RESULT 3501
AAZ47343
ID AAZ47343 standard; DNA; 22 BP.
XX
AC AAZ47343;
XX
DT 06-MAR-2000 (first entry)
XX
DE PCR primer B used in differential display analysis of Aspergillus oryzae.
XX
KW Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS Synthetic.
OS Aspergillus oryzae
XX

```
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 2 A; 5 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3502
AAZ47345
ID   AAZ47345 standard; DNA; 22 BP.
XX
AC   AAZ47345;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer D used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 2 A; 3 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
             |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3503
AAA99617
ID   AAA99617 standard; DNA; 22 BP.
XX
AC   AAA99617;
XX
DT   22-JAN-2001  (first entry)
XX
DE   (T)-primer for first strand cDNA synthesis.
XX
KW   cDNA synthesis; gene expression analysis; genetic diagnosis; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /note= "labelled with biotin"
XX
PN   US6120996-A.
XX
PD   19-SEP-2000.
XX
PF   06-NOV-1997;   97US-00964143.
XX
PR   11-JUL-1994;   94RU-00024056.
PR   11-JUL-1995;   95US-00499899.
```

XX
PA (NYBL-) NEW YORK BLOOD CENT INC.
XX
PI Ivanova NB, Belyavsky AV;
XX
DR WPI; 2000-627874/60.
XX
PT Identifying differentially expressed messenger RNAs, useful for analyzing
PT gene expression or identifying mechanisms of pathology, comprises
PT assessing amounts of separated complementary DNA fragments corresponding
PT to the mRNA.
XX
PS Example; Col 7; 15pp; English.
XX
CC The present sequence is a primer used for first strand synthesis of cDNA
CC molecules from RNA extracted from mouse thymus and spleen. This was
CC performed as part of novel method for identifying differentially
CC expressed mRNA. The method comprises synthesising sets of fragments of
CC cDNA from a set of mRNA sequences, assessing the amounts of cDNA
CC fragments corresponding to the mRNA species, and comparing the signal
CC intensity from the separated cDNA fragments. The method is useful for the
CC analysis of gene expression and the diagnosis and identification of
CC genetic mechanisms of pathology. Unlike RT-PCR using arbitrary primers,
CC many sequences are amplified in a single reaction. The method is more
CC reproducible than prior art, allowing for a reliable comparison to be
CC made with independently conducted experiments. The method also makes it
CC possible to eliminate the excess of information that is characteristic
CC for the method with arbitrary primers
XX
SQ Sequence 22 BP; 1 A; 3 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2164 CCTTTTTTTTTTTTT 2178
              |||||||||||||||
Db          8 CCTTTTTTTTTTTTT 22
```

RESULT 3504
AAF20618
ID AAF20618 standard; DNA; 22 BP.
XX
AC AAF20618;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human C/EBP polynucleotide fragment #2185.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 22 BP; 0 A; 7 C; 14 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15
```

RESULT 3505
AAH22185
ID AAH22185 standard; DNA; 22 BP.
XX
AC AAH22185;
XX
DT 20-AUG-2001 (first entry)
XX
DE Human hepatocyte auxin related 3'-(T-rich) primer A.
XX
KW Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1280985-A.
XX
PD 24-JAN-2001.
XX
PF 20-JUL-1999; 99CN-00110801.
XX

```
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 2 A; 4 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3506
AAH22189
ID   AAH22189 standard; DNA; 22 BP.
XX
AC   AAH22189;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer E.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 2 A; 3 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3507
AAH22188
ID   AAH22188 standard; DNA; 22 BP.
XX
AC   AAH22188;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer D.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
```

```
CC   of the present invention
XX
SQ   Sequence 22 BP; 2 A; 3 C; 4 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3508
AAH22187
ID   AAH22187 standard; DNA; 22 BP.
XX
AC   AAH22187;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer C.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 2 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3509
AAH22190
ID   AAH22190 standard; DNA; 22 BP.
XX
AC   AAH22190;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer F.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 3 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3510
AAH22195
ID   AAH22195 standard; DNA; 22 BP.
XX
AC   AAH22195;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer K.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3511
AAH22186
ID   AAH22186 standard; DNA; 22 BP.
XX
AC   AAH22186;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer B.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
PF   20-JUL-1999;   99CN-00110801.
XX
PR   20-JUL-1999;   99CN-00110801.
XX
PA   (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI   Kong X,  Yi X,  Zeng P;
XX
DR   WPI; 2001-291394/31.
XX
PT   Novel recombinant human hepatocyte auxin, its preparation and clinical
PT   application.
XX
PS   Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC   The present invention describes a differential indication PCR (polymerase
CC   chain reaction) technique which is used to obtain a new complete gene
CC   able to promote the repair of damaged liver cells and with substance
CC   total length of 0.7 kb by screening the cDNA library of human foetal
CC   liver. The induction expression of engineering bacteria, the separation
CC   and cracking of inclusion body and the process for restoring and
CC   decontaminating proteins are built up to obtain high purity recombinant
CC   human hepatocyte auxin. It can externally promote the reproduction of
CC   primary culture liver cells and liver cancer cells BEL-7402 and
CC   internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC   damaged and the repair of liver cells. The method may be used to treat
CC   serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC   present sequence represents a primer which is used in the exemplification
CC   of the present invention
XX
SQ   Sequence 22 BP; 2 A; 5 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTT 1781
              |||||||||||||||
Db          5 AAGCTTTTTTTTTTT 19


RESULT 3512
ABZ96312
ID   ABZ96312 standard; DNA; 22 BP.
XX
AC   ABZ96312;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human C/EBP antisense fragment no.2172.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
```

PS Disclosure; SEQ ID NO 11554; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 22 BP; 0 A; 7 C; 14 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3513
AAL56810
ID AAL56810 standard; DNA; 22 BP.
XX
AC AAL56810;
XX
DT 06-NOV-2003 (first entry)
XX
DE T(13) bio-primer oligonucleotide to synthesise the first cDNA strand.
XX
KW PCR; primer; ss; differential expression; gene expression analysis;
KW signal intensity; T(13) bio-primer; mouse; murine.
XX
OS Mus sp.
XX
PN US2003017490-A1.
XX
PD 23-JAN-2003.
XX
PF 18-JUN-2002; 2002US-00173509.
XX
PR 11-JUL-1994; 94RU-00024056.
PR 11-JUL-1995; 95US-00499899.
PR 06-NOV-1997; 97US-00964143.
PR 11-FEB-1999; 99US-00247871.
PR 18-SEP-2000; 2000US-00664534.
XX
PA (NYBL-) NEW YORK BLOOD CENT INC.
XX
PI Belyavsky AV, Ivanova NB;
XX
DR WPI; 2003-584989/55.
XX
PT Identifying differentially expressed mRNA, by separating cDNAs
PT synthesized from mRNA of various cells by electrophoresis, comparing the
PT separation pictures, identifying fragments with differential signal
PT intensities.
XX
PS Example; Fig 1; 13pp; English.
XX
CC This invention relates to a novel method for identifying differentially
CC expressed mRNA molecules. It comprises synthesising cDNA molecules from
CC sets of mRNA fragments derived from different cell types and separating
CC the resultant cDNAs by gel electrophoresis. By comparison of these
CC separation pictures it is possible to identify those cDNA fragments that
CC exhibit differential signal intensities between various cell types.
CC Furthermore, those cDNA molecules identified as being differentially
CC expressed can be amplified and cloned as required. For the formation of a
CC set of fragments, the cDNA is cleaved by restriction endonucleases, such
CC that the fragments specifically correspond to the 3' or 5' end regions of
CC the mRNA molecules. The method of this invention can be useful in
CC medicine for diagnostic purposes, molecular biology for the analysis of
CC gene expression, as well as in the identification of pathology mechanisms
CC at a genetic level. This oligonucleotide sequence is the T(13) bio-primer
CC used to synthesise the first cDNA chain from the total RNA preparation,
CC extracted from the cell type of interest, a method of the invention
XX
SQ Sequence 22 BP; 1 A; 3 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTT 2178
|||||||||||||||
Db 8 CCTTTTTTTTTTTTT 22

RESULT 3514
AAZ99839/c
ID AAZ99839 standard; DNA; 23 BP.
XX
AC AAZ99839;
XX
DT 12-JUL-2000 (first entry)
XX
DE Nucleotide sequence of reverse transcription primer.
XX
KW Mono-length cDNA library; differential display; gene expression;
KW gene identification; drug response; primer; ss.
XX
OS Synthetic.
XX
PN WO200014273-A2.
XX
PD 16-MAR-2000.
XX
PF 26-AUG-1999; 99WO-CA000789.
XX
PR 03-SEP-1998; 98US-00145936.
XX
PA (SIGN-) SIGNALGENE INC.
XX
PI Belouchi AM, Fournier H, Gee M, Gauvreau D;
XX
DR WPI; 2000-257012/22.
XX
PT Determining differential display of gene expression, useful for
PT monitoring drug responses at the gene expression level and locating genes
PT involved in a particular response, by comparisons between mono-length
PT cRNA libraries.
XX
PS Example 3; Page 48; 73pp; English.
XX
CC The present sequence represents a primer used for reverse transcription
CC of mRNA to produce cDNA. The cDNA is used for cDNA library production, in
CC the course of the invention. The specification describes a method of
CC determining differential display of gene expression, by comparison of
CC mono-length cRNA libraries. These libraries are probe hybridised to
CC accessible ordered arrays to determine differential hybridisation display
CC sites between mono-length segment libraries and to locate genes of
CC expression differential. The methods are useful for determining

```
CC   differential hybridisation display sites between mono-length segment
CC   libraries and to locate genes of expression differential. The methods are
CC   also useful in gene identification related to complex traits. The methods
CC   also permit monitoring drug responses at the gene expression level and
CC   locating genes involved in a particular response. The methods are also
CC   useful for pharmacogenomic research in evaluating how variability in
CC   genetic background influences positive or negative response to a drug
XX
SQ   Sequence 23 BP; 0 A; 4 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         23 AAAAAAAAAAAAAAA 9


RESULT 3515
AAQ36059/c
ID   AAQ36059 standard; DNA; 23 BP.
XX
AC   AAQ36059;
XX
DT   25-MAR-2003  (revised)
DT   20-MAY-1993  (first entry)
XX
DE   HIV-2 detection sequence, map position 4661.3.
XX
KW   Ligase chain reaction; LCR; detect; HIV-2; gag; gap filling; gaps; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   23
FT                   /*tag=  a
FT                   /note= "Labelled with biotin hapten"
XX
PN   WO9300447-A1.
XX
PD   07-JAN-1993.
XX
PF   26-JUN-1992;   92WO-US005477.
XX
PR   28-JUN-1991;   91US-00722798.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Birkenmeyer LG,  Carrino JJ,  Dille BL,  Kratochvil JD,  Laffler TG;
PI   Marshall RL,  Rinehardt LA,  Solomon NA;
XX
DR   WPI; 1993-036392/04.
XX
PT   Ligase chain reaction - includes using gap filling method, used for
PT   detecting target nucleic acid sequences in e.g. bacteria and viruses.
XX
PS   Claim 10; Page 30; 52pp; English.
XX
CC   The sequences given in AAQ35499-500 and AAQ36055-64 are ligase chain
CC   reaction (LCR) nucleic acids which were used to detect HIV-2. These
CC   primers are specific to positions within the gag region of the HIV-2
CC   genome. These primers are used in an improved "gap filling" LCR, in that
CC   only a single type or two types of dNTPs are required to fill double
CC   gaps, each being pref. 1-3 bases. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 23 BP; 12 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         92 ATTTTGGATTTACCGCTTGGGGG 114
              |||||| ||||   |||||| ||
Db         23 ATTTTGAATTTTTTGCTTGGAGG 1


RESULT 3516
AAV30513/c
ID   AAV30513 standard; DNA; 23 BP.
XX
AC   AAV30513;
XX
DT   14-OCT-1998  (first entry)
XX
DE   Sunflower ORF522 primer #1.
XX
KW   Cytoplasmic male sterile; chicory; Cichorium intybus; open reading frame;
KW   orf522; sunflower; transgenic plant; protoplast fusion; primer; PCR; ss;
KW   amplification; hybrid; breeding program; self-pollination; ss.
XX
OS   Synthetic.
OS   Helianthus annuus.
XX
PN   WO9745548-A1.
XX
PD   04-DEC-1997.
XX
PF   30-MAY-1997;   97WO-FR000944.
XX
PR   31-MAY-1996;   96FR-00006725.
XX
PA   (FLOR-) FLORIMOND DESPREZ VEUVE & FILS.
XX
PI   Delesalle L,  Dhellemmes C,  Desprez M;
XX
DR   WPI; 1998-032654/03.
XX
PT   Recombinant chicory genome containing sunflower male sterility gene - and
PT   related mitochondria, cytoplasm and plant cells, useful in production of
PT   chicory hybrids.
XX
PS   Example 2; Page 8; 20pp; French.
XX
CC   The invention relates to the manufacture of cytoplasmic male sterile
CC   chicory plants (Cichorium intybus) by the introduction of the open
CC   reading frame (ORF) 522 from sunflower (Helianthus annuus) plant genome
CC   by protoplast fusion. The primers AAV30513-V30514 are used to amplify a
CC   347 bp fragment of the orf522 sequence for identifying positive
CC   recombinant plant cell lines. Male sterile chicory plants are used in
CC   hybrid breeding programs to avoid problems of self-pollination
XX
SQ   Sequence 23 BP; 1 A; 11 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        482 CGCCAGAGCCAGGAGGGAGCGGG 504
              |||| || |||  |||||| |||
Db         23 CGCCGGATCCACCAGGGAGGGGG 1


RESULT 3517
AAX55048
ID   AAX55048 standard; DNA; 23 BP.
XX
AC   AAX55048;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
```

KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US019419.
XX
PR 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
PS Disclosure; Page 70; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (AAX52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC -end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AAX55272-74. These multiple target oligonucleotides
CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
SQ Sequence 23 BP; 0 A; 7 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3518
AAA34495
ID AAA34495 standard; DNA; 23 BP.
XX
AC AAA34495;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2184.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 539; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 23 BP; 0 A; 7 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3519
AAZ47417/c
ID AAZ47417 standard; DNA; 23 BP.
XX

```
AC   AAZ47417;
XX
DT   06-MAR-2000  (first entry)
XX
DE   Probe 1 used to confirm the correct amplification of GST-Pi.
XX
KW   Glutathione-S-transferase-Pi; GST-Pi; methylated; diagnose; bisulphite;
KW   cytosine deamination; prostate cancer; breast cancer; cervical cancer;
KW   liver cancer; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9955905-A1.
XX
PD   04-NOV-1999.
XX
PF   23-APR-1999;   99WO-AU000306.
XX
PR   23-APR-1998;   98AU-00003129.
XX
PA   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI   Clark SJ,  Millar DS,  Molloy PL;
XX
DR   WPI; 2000-062041/05.
XX
PT   Diagnosis and prognosis of diseases involving cytosine methylation of the
PT   glutathione-S-transferase gene, especially prostatic cancer.
XX
PS   Claim 46; Page 71; 111pp; English.
XX
CC   Sequences AAZ47417-Z47422 are used as probes to determine that any
CC   amplified PCR products of the invention are due to DNA in which all
CC   unmethylated cytosines are converted to uracils. The invention relates to
CC   a diagnostic or prognostic assay. The assay includes amplification of a
CC   target region of the glutathione-S-transferase (GST) Pi gene under
CC   conditions which result in amplification occurring only if at least one
CC   cytosine is methylated. The amplified sequence can then be subjected to
CC   analysis and abnormal cytosine methylation can then be detected. The
CC   target region of DNA is treated with a high concentration of bisulphite
CC   resulting in selective deamination of cytosine, converting it to uracil.
CC   Methylated cytosines are resistant to the chemical deamination, and
CC   therefore when PCR amplification is carried out on the target DNA,
CC   cytosines that were methylated in the original sample prior to bisulphite
CC   treatment will still be read as cytosine, while unmethylated cytosines
CC   will be read as thymine. PCR primers are designed to anneal to the target
CC   sequence after bisulphite treatment. The primers can be either selective
CC   or non-selective for methylated sites, non-selective primers avoid sites
CC   that may or may not be methylated. There is a strong correlation between
CC   the methylation of regulatory regions of genes and their lack of
CC   expression. Expression of the GST-Pi gene is lost in nearly all cases of
CC   prostate cancer. The method is used for the diagnosis of cancer,
CC   particularly of prostate, breast, cervix, or liver cancer
XX
SQ   Sequence 23 BP; 17 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
                || ||| ||| |||||||  |||
Db         23 TTGTTTGTTTATTTTTTAGGTTT 1


RESULT 3520
AAZ49423
ID   AAZ49423 standard; DNA; 23 BP.
XX
AC   AAZ49423;
XX
DT   04-APR-2000  (first entry)
XX
DE   Human Galectin 11 cDNA 5'end specific PCR primer-4.
XX
KW   Galectin 11; PCR primer; cell differentiation; proliferation; metastasis;
KW   tumour; apoptosis; anti-galectin 11 antibody; treatment;
KW   autoimmune disease; cancer; inflammatory disease; asthma; allergy;
KW   neuropathy; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200001728-A1.
XX
PD   13-JAN-2000.
XX
PF   02-JUL-1999;   99WO-US015169.
XX
PR   06-JUL-1998;   98US-00109864.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ni J,  Gentz RL;
XX
DR   WPI; 2000-126931/11.
XX
PT   New human galectin polypeptide, useful for treating cell growth disorders
PT   in mammals e.g. cancer, autoimmune diseases, inflammatory diseases,
PT   asthma and allergic diseases.
XX
PS   Example 5; Page 82; 99pp; English.
XX
CC   The present sequence is a PCR primer specific to the 5' end of human
CC   galectin 11 cDNA (nucleotides 49-61) and to vector sequences 3' to the
CC   gene. It is used to amplify galectin 11 polynucleotide sequence
XX
SQ   Sequence 23 BP; 4 A; 12 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        415 CGCCGCCGCCATCAACCCCCTGC 437
              ||||||| |||| | ||||  ||
Db          1 CGCCGCCACCATGAGCCCCAGGC 23


RESULT 3521
AAZ55321
ID   AAZ55321 standard; DNA; 23 BP.
XX
AC   AAZ55321;
XX
DT   21-MAR-2000  (first entry)
XX
DE   Neisseria species ORF cloning PCR primer #706.
XX
KW   Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
KW   antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW   antibacterial; gene therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Neisseria sp.
XX
PN   WO9957280-A2.
XX
PD   11-NOV-1999.
XX
PF   30-APR-1999;   99WO-US009346.
XX
PR   01-MAY-1998;   98US-0083758P.
PR   31-JUL-1998;   98US-0094869P.
PR   02-SEP-1998;   98US-0098994P.
PR   02-SEP-1998;   98US-0099062P.
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PR   09-OCT-1998;   98US-0103749P.
PR   09-OCT-1998;   98US-0103794P.
PR   09-OCT-1998;   98US-0103796P.
PR   25-FEB-1999;   99US-0121528P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (GENO-) INST GENOMIC RES.
XX
PI   Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI   Petersen J, Pizza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI   Tettelin H, Venter JC;
XX
DR   WPI; 2000-062150/05.
XX
PT   Novel Neisserial polypeptides predicted to be useful antigens for
PT   vaccines and diagnostics.
XX
PS   Example 16; Page 160; 1453pp; English.
XX
CC   AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC   represent novel Neisseria meningitis and N. gonorrheae polynucleotides
CC   and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC   PCR primers used in the exemplification of the present invention. The
CC   polypeptides, the polynucleotides, antibodies and compositions of the
CC   invention can be used as vaccines, as diagnostic reagents, and as
CC   immunogenic compositions. The polypeptides can be used in the manufacture
CC   of medicaments for treating or preventing infection due to Neisserial
CC   bacteria (e.g. meningitis and septicaemia), to detect the presence of
CC   Neisseria bacteria, or to raise antibodies. They may also be used to
CC   screen for agonists or antagonists, which may themselves have use as
CC   antibacterial agents. The polynucleotides of the invention may also be
CC   used in gene therapy protocols
XX
SQ   Sequence 23 BP; 3 A; 9 C; 10 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         44 CCCGCGCGCGGCGGGGGCGGCGG 66
              ||||| || | |||| ||||| |
Db          1 CCCGCTCGAGACGGGCGCGGCAG 23


RESULT 3522
AAA10628
ID   AAA10628 standard; cDNA; 23 BP.
XX
AC   AAA10628;
XX
DT   29-JUN-2000  (first entry)
XX
DE   PCR primer #2 used in YAC analysis of barley Rar1.
XX
KW   Rar1; resistance response; pathogen defence; antifungal; barley;
KW   transgenic plant; powdery mildew; increase resistance; gene modification;
KW   PCR primer; yeast artificial chromosome; YAC; ss.
XX
OS   Synthetic.
XX
PN   WO200008160-A2.
XX
PD   17-FEB-2000.
XX
PF   06-AUG-1999;   99WO-GB002590.
XX
PR   06-AUG-1998;   98GB-00017169.
XX
PA   (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI   Schulze-Lefert PMJ, Shirasu K, Lahaye T;
XX
DR   WPI; 2000-317041/27.
XX
PT   Novel polynucleotide encoding a Rar1 polypeptide from barley, useful for
PT   producing transgenic plants with increased pathogen resistance e.g. to
PT   powdery mildew, and for identifying homologous sequences in other
PT   species.
XX
PS   Example 1; Page 99; 131pp; English.
XX
CC   This sequence represents a PCR primer used in yeast artificial chromosome
CC   (YAC) analysis of barley Rar1 nucleotide sequences. Rar1 is a protein
CC   involved in the Barley resistance signalling pathways, and plant pathogen
CC   defence response signalling pathway. Rar1 is required for the action of
CC   the R (resistance) gene Mla-12. The invention relates to barley Rar1
CC   sequences and to putative homologues of Rar1, OsRar1-h1 (from rice) and
CC   AtRar1-h1 (from arabidopsis thaliana). Rar1 has antipathogenic and
CC   antifungal properties, and functions via gene modification. The Rar1
CC   polynucleotides are useful in the production of transgenic plants in
CC   which a defence response is modulated, especially barley with improved
CC   resistance to pathogens e.g. powdery mildew. They can be used to produce
CC   probes and primers useful to identify or isolate the polynucleotides
CC   (e.g. in a plant or plant cell) by standard methods and to isolate Rar1
CC   homologues from other species, which in turn are useful to manipulate
CC   resistance to agronomically important diseases. The polypeptides and
CC   antibodies raised against them are useful to identify and isolate the
CC   polypeptides or homologous polypeptides e.g. in other species
XX
SQ   Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        310 CACTGGAGTCGCCGAATATCAGC 332
              | ||||||  ||||| | |||||
Db          1 CTCTGGAGGAGCCGAGTGTCAGC 23


RESULT 3523
AAF20617
ID   AAF20617 standard; DNA; 23 BP.
XX
AC   AAF20617;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2184.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
```

DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Claim 14; Page 264; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 23 BP; 0 A; 7 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 GGCGGGGGCGGCGGC 67
||||||||||||||||
Db 1 GGCGGGGGCGGCGGC 15

RESULT 3524
AAA53817/c
ID AAA53817 standard; DNA; 23 BP.
XX
AC AAA53817;
XX
DT 04-DEC-2000 (first entry)
XX
DE Primer BTU1-75 hybridizing to BTU1 gene 5' flanking region.
XX
KW BTU1; beta-tubulin; protein expression system; negative selection;
KW paclitaxel sensitivity; cell surface; antigen; protozoa; ciliate;
KW live vaccine; Ichthyophthiius multifiliis; immobilization-antigen;
KW i-antigen; freshwater; fish; protozoacide; primer; ss.
XX
OS Tetrahymena thermophila.
XX
PN WO200046381-A1.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US002966.
XX
PR 04-FEB-1999; 99US-0118634P.
PR 02-MAR-1999; 99US-0122372P.
PR 17-MAR-1999; 99US-0124905P.
PR 27-APR-1999; 99US-0131121P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (GAER/) GAERTIG J.
PA (DICK/) DICKERSON H W.
PA (CLAR/) CLARK T G.
XX
PI Gaertig J, Dickerson HW, Clark TG;
XX
DR WPI; 2000-514962/46.
XX
PT Recombinant expression systems for expressing heterologous nucleic acids
PT and producing recombinant protein, comprises nonpathogenic protozoa such
PT as Tetrahymena resistant to paclitaxel.
XX
PS Example 2; Page 36; 83pp; English.
XX
CC Primers AAA53817-18 were used to amplify genomic DNA from T. thermophila
CC transformants to identify sequences integrated into the BTU1 locus.
CC Tetrahymena thermophila expresses two major beta-tubulin genes (BTU1 and
CC BTU2), which encode identical beta-tubulin proteins. Either of these two
CC genes (but not both at once) can be disrupted without a detectable change
CC in the cell phenotype. A K350L substitution in the BTU1 beta-tubulin
CC protein confers increased resistance to microtubule-depolymerizing drugs
CC and increased sensitivity to paclitaxel, a microtubule-stabilizing drug.
CC Cells carrying the Btu1-1K350M allele can be transformed to paclitaxel
CC resistance by gene replacement of Btu1-1K350M with a wild-type BTU1 gene
CC fragment, eliminating the need to incorporate a means for positive
CC selection. Where the host organism is not a T. thermophila mutant
CC containing the Btu1-1K350M allele, BTU1::neo1 construct, which
CC substitutes the coding region of the neo1 gene (conferring resistance to
CC parmomycin) for that of BTU1, can be used to generate BTU1 gene knockouts
CC and for positive selection. Heterologous nucleic acids (especially
CC encoding antigenic polypeptides) can be inserted into a BTU gene for
CC successful cell-surface expression that is maintained by way of negative
CC selection. Preferred expression vectors disrupt the Btu1-1K350M gene by
CC homologous recombination-mediated insertion of a heterologous nucleic
CC acid, thereby restoring resistance to paclitaxel in the resulting
CC transgenic host. Transgenic ciliated protozoa are useful as live vaccines
CC for stimulating an immune response in a vertebrate. The transgenic
CC protozoan host cells are also useful for producing polyclonal antibodies
CC (claimed). In particular, Tetrahymena expressing Ichthyophthiius
CC multifiliis immobilization-antigen (i-antigen) protein on their surface
CC are effective vehicles for vaccination of freshwater fish against
CC infection by I. multifiliis
XX
SQ Sequence 23 BP; 17 A; 0 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTT 2177
|||||||| |||| ||||||
Db 23 TTTTTTTCAAACTTTTATTTTTT 1

RESULT 3525
AAC66214
ID AAC66214 standard; DNA; 23 BP.
XX
AC AAC66214;
XX
DT 15-FEB-2001 (first entry)
XX
DE Galectin 11 PCR primer SEQ ID 10.
XX
KW Human; galectin 11; immunosuppressive; thyromimetic; hepatotropic;
KW antiinflammatory; vasotropic; dermatological; nephrotropic; cytostatic;
KW antirheumatic; antiarthritic; antiviral; anti-HIV; nootropic; cardiant;
KW neuroprotective; antiParkinsonian; ophthalmological; antianaemic;

```
KW   cerebroprotective; antibacterial; immunomodulatory; cancer; allergy;
KW   autoimmune disease; inflammatory disease; arthritis; Parkinson's disease;
KW   Alzheimer's disease; ischaemia; stroke; anorexia; shock; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063221-A2.
XX
PD   26-OCT-2000.
XX
PF   21-APR-2000; 2000WO-US010714.
XX
PR   21-APR-1999;   99US-0130390P.
PR   10-DEC-1999;   99US-0169932P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (LJOL-) LAJOLLA INST ALLERGY & IMMUNOLOGY.
XX
PI   Ni J,  Rosen CA,  Gentz RL,  Lui F;
XX
DR   WPI; 2000-665238/64.
XX
PT   Novel galectin polynucleotides and polypeptides, used in the diagnosis
PT   and treatment of cancers, autoimmune disorders, and inflammatory
PT   disorders, and to screen for antagonists and agonists.
XX
PS   Example 5; Page 198; 314pp; English.
XX
CC   Polynucleotides AAC66206 - AAC66208 encode human galectin 11, 11alpha and
CC   11beta AAB35705 - AAB35707 respectively. Galectin 11 polynucleotide and
CC   protein sequences have immunosuppressive; thyromimetic; hepatotropic;
CC   antiinflammatory; vasotropic; dermatological; nephrotropic; antirheumatic
CC   ; antiarthritic; antiviral; anti-HIV; nootropic; neuroprotective;
CC   antiParkinsonian; ophthalmological; cytostatic; antianaemic; cardiant;
CC   cerebroprotective; antibacterial; and immunomodulatory activity. Galectin
CC   11 polypeptides can be used to treat cell growth disorders, particularly
CC   cancer, autoimmune diseases, inflammatory diseases, asthma, or allergic
CC   diseases, in a mammal. The proteins and polynucleotides can be
CC   administered to regulate cell growth or differentiation in mammals.
CC   Antibodies specific for galectin 11 can be used to detect galectin 11
CC   polypeptides in a samples, used in diagnosis techniques. Proteins,
CC   polynucleotides and antibodies, can be used to treat, e.g. Hashimoto's
CC   thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease,
CC   polymyositis, systemic lupus erythematosus, glomerulonephritis,
CC   rheumatoid arthritis, viral infections, inflammation, graft versus host
CC   disease, graft rejection, acquired immunodeficiency syndrome, Alzheimer's
CC   disease, Parkinson's disease, amyotrophic lateral sclerosis, Retinitis
CC   pigmentosa, cerebellar degeneration, brain tumour, multiple sclerosis,
CC   Sjogren's syndrome, aplastic anaemia, ischaemia, myocardial infarction,
CC   stroke, reperfusion injury, liver injury, septic shock, cachexia, and
CC   anorexia. PCR primers AAC66211 - AAC66215 are used to amplify galectin 11
CC   encoding DNA. Oligonucleotides AAC66216 - AAC66224 are used in the
CC   identification and characterisation of the galectin 11 polynucleotides
XX
SQ   Sequence 23 BP; 4 A; 12 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        415 CGCCGCCGCCATCAACCCCCTGC 437
              ||||||| |||| | ||||  ||
Db          1 CGCCGCCACCATGAGCCCCAGGC 23


RESULT 3526
AAC83568/c
ID   AAC83568 standard; DNA; 23 BP.
XX
AC   AAC83568;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Human FMR1 gene 5' untranslated region partial sequence SEQ ID NO: 3.
XX
KW   Human; FMR1; FMRP; Fragile X syndrome; methylation; diagnosis;
KW   chromosome Xq27.3; ds.
XX
OS   Homo sapiens.
XX
PN   US6143504-A.
XX
PD   07-NOV-2000.
XX
PF   27-OCT-1999;   99US-00429499.
XX
PR   27-OCT-1999;   99US-00429499.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Das S,  Ledbetter DH;
XX
DR   WPI; 2001-006432/01.
XX
PT   Determining methylation state of FMR1 gene promoter for diagnosing
PT   fragile X syndrome in males involves denaturing DNA sample, subjecting
PT   DNA to bisulfite modification, amplifying DNA and detecting products.
XX
PS   Example 2; Fig 1; 20pp; English.
XX
CC   The present invention describes a novel method of diagnosing Fragile X
CC   syndrome using a PCR-based method of methylation analysis. The FMR1 gene
CC   promoter, located at chromosome Xq27.3, is composed of a CGG
CC   trinucleotide repeat. The expansion of this repeat leads to a premutation
CC   and then a full mutation, the latter of which is likely to cause the
CC   methylation of a nearby CpG island, causing the Fragile X syndrome
CC   phenotype. This method is useful in the design of appropriate therapies
CC   and counselling for affected individuals and carriers
XX
SQ   Sequence 23 BP; 1 A; 14 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              | ||| | ||||||||| | |||
Db         23 GAGGCAGTGGCGGCGGCGGGCGC 1


RESULT 3527
AAC92334/c
ID   AAC92334 standard; DNA; 23 BP.
XX
AC   AAC92334;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human hTMPT27 PCR primer SEQ ID NO:5.
XX
KW   Human; hTMPT27; TPAr1; tissue plasminogen activator regulating protein;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1268567-A.
XX
PD   04-OCT-2000.
XX
PF   02-MAR-2000; 2000CN-00111773.
XX
PR   02-MAR-2000; 2000CN-00111773.
XX
PA   (SCHR-) SOUTH CHINA RES CENT NAT HUMAN GENE GROU.
XX
PI   Zhang X,  Gao X,  Liu F;
```

XX
DR WPI; 2001-050471/07.
XX
PT New human plasminogen activating factor regulating protein and its coding
PT sequence.
XX
PS Example 1; Page 11; 23pp; Chinese.
XX
CC The present invention describes the human tissue plasminogen activating
CC factor regulating protein designated hTMPT27, which is expressed in the
CC hypothalamus. Also described is a method for the preparation of the
CC hTMPT27 protein and nucleic acid sequences, and a method of detecting
CC human hTMPT27 nucleic acid and the polypeptide sequences in a sample. The
CC present sequence represents a PCR primer which is used in the isolation
CC of hTMPT27 in an example from the present invention
XX
SQ Sequence 23 BP; 6 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1382 TGTGCCGCGGTGTCTGCCCTGCA 1404
||||| | || |||| || ||||
Db 23 TGTGCAGTGGGGTCTACCATGCA 1

RESULT 3528
AAH28300
ID AAH28300 standard; RNA; 23 BP.
XX
AC AAH28300;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from neuronal cadherin gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 23 BP; 4 A; 0 C; 0 G; 0 T; 19 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 23;
Best Local Similarity 0.0%; Pred. No. 3.7e+03;
Matches 0; Conservative 18; Mismatches 5; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTTTTTT 2181
::: : :::::: ::::::::
Db 1 UUUUUAAUUUUUUAAUUUUUUUU 23

RESULT 3529
AAS13613
ID AAS13613 standard; DNA; 23 BP.
XX
AC AAS13613;
XX
DT 17-DEC-2001 (first entry)
XX
DE Forward PCR primer used to amplify exon 14 of the human VMGLOM gene.
XX
KW Human; VMGLOM; glomulin; venous malformation glomangioma; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200160856-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-EP001760.
XX
PR 16-FEB-2000; 2000EP-00870022.
PR 10-APR-2000; 2000US-0195777P.
PR 22-DEC-2000; 2000EP-00870320.
XX
PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.
XX
PI Vikkula M;
XX
DR WPI; 2001-557643/62.
XX
PT New VMGLOM genes and polypeptides, useful in gene therapy or for
PT preventing, treating or alleviating disorders with vascular component,
PT e.g. varicosities, cardiopathies, cerebral disorders or cancer.
XX
PS Disclosure; Page 72; 157pp; English.
XX
CC The present invention relates to the isolation of novel human and mouse
CC VMGLOM polypeptides (long form and short form), and the nucleic acid
CC molecules encoding them. VMGLOMs (also referred to as glomulins) are a
CC subtype of venous malformations (VMs) called glomangiomas. In humans,
CC VMGLOM has been mapped to chromosome 1p21-22. VMGLOMs and the nucleic
CC acids encoding for them are useful as a medicament or for incorporation
CC into a diagnostic kit. Such medicaments are useful for preventing,
CC treating or alleviating disorders with a vascular component, particularly
CC where alteration of vascular smooth muscle cell phenotype is needed, e.g.
CC varicosities, cardiopathies or cardiomyopathies, cerebral disorders and
CC cancer. The nucleic acids are also useful in gene therapy. The present
CC sequence for forward PCR primer is used to amplify exon 14 of the human
CC VMGLOM gene in the methods of the present invention
XX
SQ Sequence 23 BP; 5 A; 1 C; 6 G; 11 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1924 TTTTTTCAGTGTTAAGGTAATGG 1946
              ||||| ||||| |||||| | |
Db          1 TTTTTGTAGTGTCAAGGTATTAG 23


RESULT 3530
ABT05505/c
ID   ABT05505 standard; DNA; 23 BP.
XX
AC   ABT05505;
XX
DT   11-OCT-2002  (first entry)
XX
DE   NOVX related probe SEQ ID No 179.
XX
KW   Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic;
KW   neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
KW   tranquiliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory;
KW   anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
KW   metabolic disorder; obesity; infectious disease; Alzheimer's disease;
KW   anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
KW   immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
KW   metabolic syndrome X; wasting disorder; cancer; neurological disorder;
KW   epilepsy; stroke; mental disorder; schizophrenic disorders; goiter;
KW   vesicular transport; cystic fibrosis; gastrointestinal disorder;
KW   diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
KW   multiple sclerosis; rheumatoid arthritis; transgenic animal;
KW   gene therapy; probe; ss.
XX
OS   Unidentified.
XX
PN   WO200246409-A2.
XX
PD   13-JUN-2002.
XX
PF   06-DEC-2001; 2001WO-US046586.
XX
PR   06-DEC-2000; 2000US-0251660P.
PR   12-DEC-2000; 2000US-0255029P.
PR   08-JAN-2001; 2001US-0260326P.
PR   24-JAN-2001; 2001US-0263800P.
PR   20-FEB-2001; 2001US-0269942P.
PR   24-APR-2001; 2001US-0286183P.
PR   20-AUG-2001; 2001US-0313627P.
PR   12-SEP-2001; 2001US-0318712P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Guo X,  Li L,  Patturajan M,  Shimkets RA,  Casman SJ,  Malyankar UM;
PI   Tchernev VT,  Vernet CAM,  Spytek KA,  Shenoy SG,  Alsobrook JP;
PI   Edinger S,  Peyman JA,  Stone DJ,  Ellerman K,  Gangolli EA,  Boldog FL;
PI   Colman SD,  Eisen AJ,  Liu X,  Padigaru M,  Spaderna SK,  Zerhusen BD;
XX
DR   WPI; 2002-547774/58.
XX
PT   Novel isolated polypeptide, designated NOVX, useful for treating or
PT   preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and
PT   metabolic, neurodegenerative, immune and hematopoietic disorders.
XX
PS   Example 2; Page 274; 421pp; English.
XX
CC   The invention relates to an isolated polypeptide, designated NOVX,
CC   comprising a sequence fully defined in the specification. The isolated
CC   protein, its encoding polynucleotide or an antibody created from the
CC   protein is useful in the manufacture of a medicament for treating a
CC   syndrome associated with a human disease, preferably a NOVX-associated
CC   disorder, or for treating or preventing a NOVX-associated disorder in a
CC   subject, preferably human. The isolated protein, its encoding
CC   polynucleotide or an antibody created from the protein are also useful
CC   for treating or preventing metabolic disorders, diabetes, obesity,
CC   infectious disease, anorexia, neurodegenerative disorder, Alzheimer's
CC   disease, Parkinson's disorder, immune disorders, haematopoietic
CC   disorders, and various dyslipidaemias, metabolic disturbances associated
CC   with obesity, the metabolic syndrome X, wasting disorders associated with
CC   chronic diseases, and cancer. The isolated protein, its encoding
CC   polynucleotide or an antibody created from the protein are useful for
CC   treating or preventing neurological disorders such as epilepsy, stroke,
CC   mental disorders including mood, anxiety, schizophrenic disorders,
CC   disorders of vesicular transport such as cystic fibrosis, diabetes
CC   mellitus, goiter, gastrointestinal disorders including ulcerative
CC   colitis, other conditions associated with abnormal vesicle trafficking
CC   including AIDS, allergic reactions, multiple sclerosis and rheumatoid
CC   arthritis. A cell comprising the vector of the invention is useful for
CC   producing non-human transgenic animals. The polynucleotide of the
CC   invention can be used to treat disorders by gene therapy. This
CC   polynucleotide sequence represents a probe of a sequence relating to the
CC   NOVX proteins of the invention
XX
SQ   Sequence 23 BP; 5 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   78.3%;  Pred. No. 3.7e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        714 AGCACCTGTTGCTGCACGATCAG 736
              |||| || ||||||| | ||||
Db         23 AGCATGTGGTGCTGCAGGGTCAG 1


RESULT 3531
ABZ96311
ID   ABZ96311 standard; DNA; 23 BP.
XX
AC   ABZ96311;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human C/EBP antisense fragment no.2171.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 11553; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
```

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CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 23 BP; 0 A; 7 C; 14 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGGC 67
              |||||||||||||||
Db          1 GGCGGGGGCGGCGGC 15


RESULT 3532
ABV74137
ID   ABV74137 standard; DNA; 23 BP.
XX
AC   ABV74137;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "5' polylinker"
FT   misc_feature     16. .21
FT                    /*tag=  b
FT                    /note= "each N represents A, C, G or T"
FT   misc_feature     22. .23
FT                    /*tag=  c
FT                    /note= "NN represents every possible dinucleotide
FT                    combination"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of an oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 8 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||||
Db          1 TTTTTTTTTTTTTTT 15


RESULT 3533
ABV74137/c
ID   ABV74137 standard; DNA; 23 BP.
XX
AC   ABV74137;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Oligonucleotide used in cDNA library array.
XX
KW   G-protein coupled receptor; odourant; receptor; olfaction; array;
KW   microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "5' polylinker"
FT   misc_feature     16. .21
FT                    /*tag=  b
FT                    /note= "each N represents A, C, G or T"
FT   misc_feature     22. .23
FT                    /*tag=  c
FT                    /note= "NN represents every possible dinucleotide
```

```
FT                      combination"
XX
PN   WO200277200-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009559.
XX
PR   27-MAR-2001; 2001US-0279168P.
PR   31-JAN-2002; 2002US-0353392P.
XX
PA   (INSC-) INSCENT INC.
XX
PI   Woods D,  Dimitratos S;
XX
DR   WPI; 2003-029930/02.
XX
PT   Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT   receptors, useful for isolating odorant binding proteins or pesticide
PT   alternatives, by analyzing sequences from a male- and female-specific
PT   nucleic acid library.
XX
PS   Disclosure; Fig 5; 83pp; English.
XX
CC   The present sequence is that of an oligonucleotide used in a method
CC   designed to rapidly array and normalize a complex cDNA library obtained
CC   from a target species. Clones are arrayed into multi-well plates. Each
CC   well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC   capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC   which allows an anchored oligonucleotide in each well to selectively
CC   hybridise only to those cDNA clones with a complementary 5' end. The
CC   unique 3' key sequences are designed to give a comprehensive level of
CC   degeneracy since they are diverse and numerous enough to ensure that
CC   every possible cDNA sequence can be bound by an individual, specific
CC   oligonucleotide in a single well. The cDNA library is heated to denature
CC   the clones into single stranded DNA, and an aliquot is added to every
CC   well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC   the common 5' region present in every cDNA clone serves as the 5' priming
CC   site. Denaturing and washing leave anchored cDNA in each well. The
CC   library is now arrayed and normalised. The method was used to identify
CC   and isolate clones encoding G-protein coupled receptors, especially
CC   odourant receptors, and active effectors involved in the olfactory
CC   pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC   or other olfactory or neuronal proteins. The identified receptors and
CC   proteins are useful for identifying compounds that reduce a target
CC   animal's sensitivity to odours, for manufacturing compounds or devices
CC   that mask odours, or trapping invertebrates with odourants.
CC   Semiochemicals (e.g. arometics or pheromone mimetics) can be developed
CC   with desirable effects on specific species, for the development of pest
CC   monitoring systems or non-toxic, species-specific pesticide alternatives,
CC   for controlling insect feeding and breeding behaviour, detecting the
CC   presence of small air-borne molecules, etc
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 8 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         15 AAAAAAAAAAAAAAA 1


RESULT 3534
AAH75424/c
ID   AAH75424 standard; DNA; 24 BP.
XX
AC   AAH75424;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human homo laminin protein 24 PCR primer 1.
XX
KW   Human; homo laminin protein 24; cytostatic; virucidal; immunomodulatory;
KW   antiinflammatory; haemostatic; cancer; haemopathy; HIV; phlogosis;
KW   Human Immunodeficiency Virus; immunological diseases; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155183-A1.
XX
PD   02-AUG-2001.
XX
PF   21-JAN-2001; 2001WO-CN000093.
XX
PR   28-JAN-2000; 2000CN-00111622.
XX
PA   (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-483216/52.
XX
PT   Human laminin protein 24 and encoded polynucleotide, applicable in
PT   diagnosis and treatment of cancer, hemopathy, immunological diseases and
PT   phlogosis.
XX
PS   Example 3; Page 12; 38pp; Chinese.
XX
CC   The invention relates to the human homo laminin protein 24 with
CC   cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
CC   activity. The polypeptide and encoding polynucleotide are applicable in
CC   diagnosis and treatment of cancer, haemopathy, Human Immunodeficiency
CC   Virus (HIV) infection, immunological diseases and phlogosis. The present
CC   sequence is that of a homo laminin protein 24 PCR primer
XX
SQ   Sequence 24 BP; 1 A; 4 C; 3 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              |||||||||||||||
Db         22 GAAAAAAAAAAAAAA 8


RESULT 3535
ABL60935
ID   ABL60935 standard; DNA; 24 BP.
XX
AC   ABL60935;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human nucleotide reducing enzyme 59.62 cDNA isolating primer 2.
XX
KW   Nucleotide reducing enzyme 59.62; embryo development; teratogenesis;
KW   blood system disease; human; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1333352-A.
XX
PD   30-JAN-2002.
XX
PF   07-JUL-2000; 2000CN-00117037.
XX
PR   07-JUL-2000; 2000CN-00117037.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305607/35.
```

```
XX
PT   Human nucleotide reducing enzyme 59.62 polypeptide and its encoding
PT   polynucleotide, for treating e.g. embryo development teratogenesis.
XX
PS   Example 2; Page 17 (disclosure); 34pp; Chinese.
XX
CC   The invention relates to a novel human nucleotide reducing enzyme 59.62
CC   polypeptide and encoding polynucleotide. The polynucleotide, polypeptide
CC   and its antagonist are useful for treating e.g. embryo development
CC   teratogenesis, blood system disease, and growth development disturbance
CC   disease. The present sequence represents the human nucleotide reducing
CC   enzyme 59.62 cDNA isolating RT-PCR primer
XX
SQ   Sequence 24 BP; 6 A; 2 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAA 2188
              |||||||||||||||
Db          3 TTTTTTTTTTTTTAA 17


RESULT 3536
ABV93494/c
ID   ABV93494 standard; DNA; 24 BP.
XX
AC   ABV93494;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Bacillus thuringiensis toxin Cry mutant oligonucleotide #18.
XX
KW   Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW   pepsin; PCS; ss.
XX
OS   Bacillus thuringiensis.
OS   Synthetic.
XX
PN   FR2822157-A1.
XX
PD   20-SEP-2002.
XX
PF   19-MAR-2001; 2001FR-00003691.
XX
PR   19-MAR-2001; 2001FR-00003691.
XX
PA   (AVET ) AVENTIS CROPSCIENCE SA.
XX
PI   Freyssinet G,  Rang C,  Frutos R;
XX
DR   WPI; 2003-002439/01.
XX
PT   New modified Cry protein, useful as insecticide, comprises at least one
PT   additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS   Example 3; Page 26; 134pp; French.
XX
CC   The present invention describes a modified Cry protein (I) that is
CC   sensitive to pepsin and comprises at least one additional pepsin cleavage
CC   site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC   proteins by incorporating at least one extra PCS; (b) polynucleotides
CC   (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC   (II) and terminator; (d) expression or transformation vector (III) that
CC   contains CG; (e) host organism (IV) transformed with (III), also, where
CC   the organism is a plant, its parts and seeds; (f) production of (I) by
CC   growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC   against (I). (I) has insecticide activity. (I) can be used as
CC   insecticides, particularly where expressed in transgenic plants. (I) are
CC   sensitive to enzymes in the digestive tract of mammals, so do not persist
CC   in the tract (lack of persistence is required by regulatory authorities
CC   for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC   increase degradation in the digestive tract of insects, so have no effect
CC   on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   78.3%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2802
              ||||  ||| || || |||||||
Db         24 GAATAAAAATAATAATAAAAAAA 2

RESULT 3537
ABV93779/c
ID   ABV93779 standard; DNA; 24 BP.
XX
AC   ABV93779;
XX
DT   08-JAN-2003  (first entry)
XX
DE   B. thuringiensis toxin Cry oligonucleotide mutant #18 SEQ ID NO:30.
XX
KW   Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW   pepsin; PCS; ss.
XX
OS   Bacillus thuringiensis.
OS   Synthetic.
XX
PN   FR2822157-A1.
XX
PD   20-SEP-2002.
XX
PF   19-MAR-2001; 2001FR-00003691.
XX
PR   19-MAR-2001; 2001FR-00003691.
XX
PA   (AVET ) AVENTIS CROPSCIENCE SA.
XX
PI   Freyssinet G,  Rang C,  Frutos R;
XX
DR   WPI; 2003-002439/01.
XX
PT   New modified Cry protein, useful as insecticide, comprises at least one
PT   additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS   Disclosure; Page 105; 134pp; French.
XX
CC   The present invention describes a modified Cry protein (I) that is
CC   sensitive to pepsin and comprises at least one additional pepsin cleavage
CC   site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC   proteins by incorporating at least one extra PCS; (b) polynucleotides
CC   (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC   (II) and terminator; (d) expression or transformation vector (III) that
CC   contains CG; (e) host organism (IV) transformed with (III), also, where
CC   the organism is a plant, its parts and seeds; (f) production of (I) by
CC   growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC   against (I). (I) has insecticide activity. (I) can be used as
CC   insecticides, particularly where expressed in transgenic plants. (I) are
CC   sensitive to enzymes in the digestive tract of mammals, so do not persist
CC   in the tract (lack of persistence is required by regulatory authorities
CC   for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC   increase degradation in the digestive tract of insects, so have no effect
CC   on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   78.3%;  Pred. No. 3.9e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2802
              ||||  ||| || || |||||||
Db         24 GAATAAAAATAATAATAAAAAAA 2
```

RESULT 3538
ABK87633/c
ID ABK87633 standard; DNA; 25 BP.
XX
AC ABK87633;
XX
DT 24-SEP-2002 (first entry)
XX
DE BamT15G PCR primer.
XX
KW Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
KW rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
KW viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
OS Unidentified.
XX
PN WO200251999-A1.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-JP011293.
XX
PR 21-DEC-2000; 2000JP-00388739.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (KAZU-) KAZUSA DNA RES INST.
XX
PI Ohara O, Nagase T, Negishi T, Mizushima S, Furusako S;
XX
DR WPI; 2002-519957/55.
XX
PT Human spleen-originated cDNA library-isolated atopic dermatitis-
PT associated gene, which encodes a protein, useful in diagnosis and
PT screening of preventives or remedies for e.g. atopic dermatitis.
XX
PS Example 1; Page 46; 88pp; Japanese.
XX
CC The present invention relates to a new DNA containing a fully defined 568
CC base sequence given in the specification. The polynucleotides and
CC proteins of the invention are useful in diagnosis and screening of
CC preventives or remedies for atopic dermatitis. The invention can also be
CC used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
CC nephritis, arteriosclerosis, allergic diseases, viral diseases,
CC inflammatory colitis, bronchitis and skin diseases. The present nucleic
CC acid sequence represents a PCR primer used in the methods of the
CC invention
XX
SQ Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         24 AAAAAAAAAAAAAAA 10
```

RESULT 3539
ABK87631/c
ID ABK87631 standard; DNA; 25 BP.
XX
AC ABK87631;
XX
DT 24-SEP-2002 (first entry)
XX
DE BamT15A PCR primer.
XX
KW Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
KW rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
KW viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
OS Unidentified.
XX
PN WO200251999-A1.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-JP011293.
XX
PR 21-DEC-2000; 2000JP-00388739.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (KAZU-) KAZUSA DNA RES INST.
XX
PI Ohara O, Nagase T, Negishi T, Mizushima S, Furusako S;
XX
DR WPI; 2002-519957/55.
XX
PT Human spleen-originated cDNA library-isolated atopic dermatitis-
PT associated gene, which encodes a protein, useful in diagnosis and
PT screening of preventives or remedies for e.g. atopic dermatitis.
XX
PS Example 1; Page 45; 88pp; Japanese.
XX
CC The present invention relates to a new DNA containing a fully defined 568
CC base sequence given in the specification. The polynucleotides and
CC proteins of the invention are useful in diagnosis and screening of
CC preventives or remedies for atopic dermatitis. The invention can also be
CC used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
CC nephritis, arteriosclerosis, allergic diseases, viral diseases,
CC inflammatory colitis, bronchitis and skin diseases. The present nucleic
CC acid sequence represents a PCR primer used in the methods of the
CC invention
XX
SQ Sequence 25 BP; 2 A; 5 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         24 AAAAAAAAAAAAAAA 10
```

RESULT 3540
AAC96446
ID AAC96446 standard; DNA; 25 BP.
XX
AC AAC96446;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #48.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX

```
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 5 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 4.1e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||  |  |||| |
Db          1 TTTTTTTTTTTGCTACAACTCT 23


RESULT 3541
AAT38116/c
ID   AAT38116 standard; cDNA; 25 BP.
XX
AC   AAT38116;
XX
DT   09-DEC-1996  (first entry)
XX
DE   NotI-oligo primer.
XX
KW   Tazarotene induced gene 1; TIG1; retinoid; psoriasis; antisporiatic;
KW   fibroblast; keratinocyte; skin raft culture; retinoic acid receptor;
KW   primer; vector; pSPORT; ss.
XX
OS   Synthetic.
XX
PN   WO9623080-A1.
XX
PD   01-AUG-1996.
XX
PF   26-JAN-1996;   96WO-US001339.
XX
PR   27-JAN-1995;   95US-00379280.
XX
PA   (ALLR ) ALLERGAN.
XX
PI   Nagpal S,  Chandraratna RA;
XX
DR   WPI; 1996-362702/36.
XX
PT   Retinoid-inducible polynucleotide, designated Tazarotene Induced Gene
PT   (TGI1\) - having low basal expression, used in assay systems as an
PT   indicator of retinoid action in psoriatic skin cultures.
XX
PS   Example 4; Page 13; 50pp; English.
XX
CC   A NotI-oligo primer (AAT38116) was used to block the poly(A)+ region of
CC   vector pSPORT-1. cDNA derived from mock-treated and AGN-190168- treated
CC   skin raft cultures was ligated into pSPORT-1 and a cDNA library was
CC   created in bacterial host cells. A subtraction procedure and Southern
CC   hybridisation yielded a cDNA clone (AAT38115), designated TIG1
CC   (tazarotene induced gene 1), that corresponds to mRNA that is strongly
CC   induced upon treatment of skin raft cultures with the retinoic acid
CC   receptor beta/gamma selective antipsoriatic synthetic retinoid AGN-190168
XX
SQ   Sequence 25 BP; 0 A; 6 C; 4 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         25 AAAAAAAAAAAAAAA 11


RESULT 3542
AAX40404
ID   AAX40404 standard; DNA; 25 BP.
XX
AC   AAX40404;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Seq ID No:2 of WO9915702.
XX
KW   Nucleic acid normalisation; haptenylated; subtractive hybridization;
KW   normalised library; nucleic acid analysis; ss.
XX
OS   Synthetic.
XX
PN   WO9915702-A1.
XX
PD   01-APR-1999.
XX
PF   24-SEP-1998;   98WO-US019948.
XX
PR   24-SEP-1997;   97US-0059817P.
PR   23-SEP-1998;   98US-00159496.
XX
PA   (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI   Li W,  Jessee J,  Nisson PE;
XX
DR   WPI; 1999-254725/21.
XX
PT   Normalization of nucleic acid libraries.
XX
PS   Example 2; Page 35; 59pp; English.
XX
CC   The invention relates to a new method for normalisation of nucleic acid
CC   molecules that comprises using haptenylated nucleic acid molecules in
CC   subtractive hybridization to remove the more highly abundant molecules.
CC   Normalised libraries produced by the method make all of the nucleic acid
CC   molecules present in the library available for isolation and subsequent
CC   analysis for the study of normal function of individual genes and the
CC   genomes. Using the methods, normalised nucleic acid libraries having a
CC   maximum variation in abundance of the member NAMs no greater than 2- to
CC   10-fold may be produced. The methods provide normalised libraries which
CC   have significantly reduced background
XX
SQ   Sequence 25 BP; 15 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db          1 AAAAAAAAAAAAAAA 15


RESULT 3543
AAC96343/c
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```
ID   AAC96343 standard; DNA; 25 BP.
XX
AC   AAC96343;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #75.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 49; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 4.1e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAA 2797
              |||   | || ||||||||||||
Db         23 TGTACCAGTTAAAAAAAAAAAA 1


RESULT 3544
AAC96433
ID   AAC96433 standard; DNA; 25 BP.
XX
AC   AAC96433;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #35.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 0 A; 7 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 4.1e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||| ||   |  |||
Db          1 TTTTTTTTTTTTCTTCCTCCCTT 23


RESULT 3545
AAC66194/c
ID   AAC66194 standard; DNA; 25 BP.
XX
AC   AAC66194;
XX
DT   14-FEB-2001  (first entry)
XX
DE   PCR primer EcoR1-dt used in trypsin hL identification.
XX
KW   Human; trypsin hL; serine protease; lung disease model animal;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2000253887-A.
XX
PD   19-SEP-2000.
XX
PF   11-MAR-1999;   99JP-00065337.
XX
PR   11-MAR-1999;   99JP-00065337.
XX
PA   (TTPH-) TT PHARMA KK.
XX
DR   WPI; 2000-658814/64.
XX
PT   Novel gene encoding a serine protease and its protein used to screen for
PT   serine protease inhibitors and to prepare lung disease animal models.
XX
PS   Disclosure; Page 7-8; 17pp; Japanese.
XX
CC   Nucleotide sequence AAC66182 encodes human trypsin hL AAB35701, a serine
CC   protease. The invention relates to the human hL gene and protein
CC   sequences, to a recombinant vector containing the nucleotide sequence,
CC   and a host cell containing the vector. Human trypsin hL can be used for
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CC   screening for serine protease inhibitors, in the preparation of a lung
CC   disease model animal, and for the development of an index marker of lung
CC   diseases caused by an anti-trypsin hL antibody. The present sequence
CC   represents a PCR primer used in the identification of trypsin hL
XX
SQ   Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         25 AAAAAAAAAAAAAAA 11


RESULT 3546
AAC96099/c
ID   AAC96099 standard; DNA; 25 BP.
XX
AC   AAC96099;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #66.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 45; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 25;
  Best Local Similarity   78.3%;  Pred. No. 4.1e+03;
  Matches   18;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              || ||  ||  ||||||||||||
Db         23 AGTATCAAAGGAAAAAAAAAAA 1


RESULT 3547
AAT13051/c
ID   AAT13051 standard; DNA; 26 BP.
XX
AC   AAT13051;
XX
DT   25-MAR-2003  (revised)
DT   27-MAY-1996  (first entry)
XX
DE   cDNA primer.
XX
KW   Cotton; fibre; promoter; transgenic plant; crop improvement; primer;
KW   Gossypium; ss.
XX
OS   Synthetic.
XX
PN   US5495070-A.
XX
PD   27-FEB-1996.
XX
PF   18-MAY-1992;   92US-00885970.
XX
PR   04-OCT-1988;   88US-00253243.
PR   21-NOV-1990;   90US-00617239.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John M;
XX
DR   WPI; 1996-139095/14.
XX
PT   New isolated fibre-specific promoters - used for introducing altered-
PT   fibre specific characteristics into plants, partic. cotton.
XX
PS   Example 1; Col 8; 48pp; English.
XX
CC   cDNA was prepd. from cotton fibre cell RNA using the primer given in
CC   AAT13051. cDNA libraries were produced and screened for fibre-specific
CC   clones (see AAT13033-50) and these were in turn used to screen genomic
CC   libraries to identify fibre-specific promoter sequences (see AAT13025-32
CC   and AAT13052-53). (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 3548
AAT39393/c
ID   AAT39393 standard; DNA; 26 BP.
XX
AC   AAT39393;
XX
DT   25-MAR-2003  (revised)
DT   16-DEC-1996  (first entry)
XX
DE   Cotton fibre cDNA first strand synthesis primer.
XX
KW   Cotton fibre; promoter; differential screening; leaf; ovule; root;
KW   flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.
XX
OS   Synthetic.
XX
PN   US5521078-A.
XX
PD   28-MAY-1996.
XX
PF   19-OCT-1994;   94US-00298687.
```

```
XX
PR   04-OCT-1988;   88US-00253243.
PR   21-NOV-1990;   90US-00617239.
PR   18-MAY-1992;   92US-00885970.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John M;
XX
DR   WPI; 1996-267794/27.
XX
PT   Isolation of fibre-specific cotton promoter sequences - using selected
PT   DNA probes to screen genomic DNA fragments, for production of cotton
PT   fibres with improved characteristics.
XX
PS   Example; Col 23; 46pp; English.
XX
CC   Cotton fibre cell-specific promoter sequences were isolated by
CC   differential screening of a cotton plant cDNA library. Of 4788 clones
CC   from a 10 day cell library screened with leaf cDNAs, 800 clones not
CC   present in the leaf were isolated. These were screened with cDNAs from
CC   ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR
CC   analysis was then used to remove cross-hybridising clones. This resulted
CC   in the isolation of 18 cDNA clones specifically expressed in cotton fibre
CC   cells (AAT30242-4 and AAT30253-67). These cDNAs were then used to screen
CC   for homologous genomic sequences (AAT30245-53 and AAT30268) in order to
CC   obtain the corresp. promoter sequences. This primer was used to generate
CC   the first cDNA strand from mRNA isolated from the cotton fibre cells. The
CC   promoters isolated from the fibre cell-specific clones can be used to
CC   generate transgenic cotton plants and lines producing fibres having
CC   altered quantity and quality. (Updated on 25-MAR-2003 to correct PF
CC   field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 3549
AAT43363/c
ID   AAT43363 standard; DNA; 26 BP.
XX
AC   AAT43363;
XX
DT   11-MAR-1997  (first entry)
XX
DE   Cotton fibre first strand cDNA primer.
XX
KW   FbLate; promoter; fibre; transgenic plant; cotton; Gossypium hirsutum;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO9639021-A1.
XX
PD   12-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009449.
XX
PR   06-JUN-1995;   95US-00467504.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   John ME;
XX
DR   WPI; 1997-042726/04.
XX
PT   Plant fibre-specific, developmentally regulated FbLate promoter - useful
PT   for producing transgenic plants, esp. cotton, with altered fibre
PT   properties.
XX
PS   Example 2; Page 15; 79pp; English.
XX
CC   A primer (AAT43363) was used for first strand cDNA synthesis from RNA
CC   obtd. from fibre cells of 23 day-old Coker 312 or 10 day-old Sea Island
CC   cotton bolls. The cDNA was used to construct a cDNA library from which
CC   cDNA clones (see also AAT43361-62) were isolated that corresponded to RNA
CC   prevalent in later fibre development. These clones were used to identify
CC   the FbLate promoter (AAT43360)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 3550
AAT62627/c
ID   AAT62627 standard; cDNA to mRNA; 26 BP.
XX
AC   AAT62627;
XX
DT   25-MAR-2003  (revised)
DT   14-MAY-1997  (first entry)
XX
DE   Primer for cotton fibre-specific cDNA amplification.
XX
KW   cotton; fibre-specific; strength; transgenic plant; anthesis;
KW   developmentally regulated; E6; H6; antisense; sense; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5597718-A.
XX
PD   28-JAN-1997.
XX
PF   20-SEP-1995;   95US-00530797.
XX
PR   04-OCT-1988;   88US-00253243.
PR   21-NOV-1990;   90US-00617239.
PR   18-OCT-1993;   93US-00138814.
XX
PA   (CETU ) AGRACETUS.
XX
PI   Brill WJ,  Umbeck PF,  John ME;
XX
DR   WPI; 1997-108326/10.
XX
PT   Prodn. of transgenic cotton plants - by transformation with the H6 coding
PT   sequence or E6 anti-sense sequence, produces fibre of altered strength.
XX
PS   Example 1; Col 6; 33pp; English.
XX
CC   AAT62627 is a primer used for first strand cDNA synthesis from mRNA
CC   isolated from cotton fibre cells at different stages of development.
CC   Cotton fibre-specific cDNA clones (AAT62609-24) can be used to identify
CC   genomic clones by differential cDNA library screenings. Coding sequences
CC   from these isolated genes are used in sense or antisense orientation to
CC   alter the fibre characteristics, e.g. strength, of transgenic fibre-
CC   producing plants. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 3551
AAT63663/c
ID   AAT63663 standard; DNA; 26 BP.
XX
AC   AAT63663;
XX
DT   25-MAR-2003  (revised)
DT   11-JUN-1997  (first entry)
XX
DE   Primer for cotton fibre-specific cDNA synthesis.
XX
KW   primer; PCR; polymerase chain reaction; cotton fibre; seed floss fibre;
KW   promoter; peroxidase; production; fibre strength; Sea Island;
KW   Gossypium sp; Coker; Kapok; G. barbadense; ss.
XX
OS   Synthetic.
XX
PN   US5608148-A.
XX
PD   04-MAR-1997.
XX
PF   25-JAN-1995;   95US-00378588.
XX
PR   30-SEP-1993;   93US-00130086.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John ME;
XX
DR   WPI; 1997-164559/15.
XX
PT   Transgenic cotton plants with increased fibre strength - are transformed
PT   with construct containing peroxidase gene.
XX
PS   Disclosure; Col 31; 43pp; English.
XX
CC   This primer sequence was used for first strand cDNA synthesis of mRNA
CC   from cotton fibre-specific library. Cotton plants whose genome contains
CC   heterologous genetic construct comprising a seed floss fibre (SFF)-
CC   specific promoter isolated from cotton plants and a coding sequence
CC   encoding a peroxidase are useful for production of cotton with increased
CC   fibre strength. The peroxidase genes are over-expressed in fibre and not
CC   in other plant tissues where it would be harmful to the plant. (Updated
CC   on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 3552
AAT70058/c
ID   AAT70058 standard; cDNA; 26 BP.
XX
AC   AAT70058;
XX
DT   25-MAR-2003  (revised)
DT   20-AUG-1997  (first entry)
XX
DE   Primer for cotton fibre specific cDNA amplification.
XX
KW   cotton; E6; fibre; promoter; transgenic plant; truncated;
KW   heterologous gene expression; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5620882-A.
XX
PD   15-APR-1997.
XX
PF   19-OCT-1994;   94US-00298829.
XX
PR   04-OCT-1988;   88US-00253243.
PR   21-NOV-1990;   90US-00617239.
PR   18-MAY-1992;   92US-00885970.
XX
PA   (CETU ) AGRACETUS INC.
XX
PI   John M;
XX
DR   WPI; 1997-235185/21.
XX
PT   DNA constructs contg. truncated promoter sequence - for fibre-specific
PT   gene expression in cotton plants.
XX
PS   Example 1; Col 8; 48pp; English.
XX
CC   AAT70058 is a primer used to synthesize first strand cDNA from mRNA
CC   isolated from cotton fibre cells at different stages of development.
CC   Claimed DNA constructs comprise a truncated promoter sequence (from one
CC   of AAT70031-38) that promotes preferential gene expression in plant fibre
CC   cells, a protein coding sequence not naturally associated with the
CC   promoter sequence and a 3' termination sequence. The DNA constructs are
CC   useful for expressing foreign genes in fibre-producing plants, esp. to
CC   produce transgenic cotton plants with varied cotton fibre characteristics
CC   and quality. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 15;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||||||||||||
Db         26 AAAAAAAAAAAAAAA 12


RESULT 3553
AAI65862/c
ID   AAI65862 standard; DNA; 30 BP.
XX
AC   AAI65862;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Nucleotide sequence of triplex forming oligonucleotide for Hprt gene.
XX
KW   DNA-modifying molecule; DNA repair-deficient cell; transgenic cell;
KW   disease model; Hprt gene; triplex forming oligonucleotide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "psoralen attached"
XX
PN   WO200173001-A2.
XX
PD   04-OCT-2001.
XX
PF   22-MAR-2001; 2001WO-US009218.
```

XX
PR 24-MAR-2000; 2000US-0191996P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Seidman MM, Majumdar A;
XX
DR WPI; 2001-616491/71.
XX
PT Modifying nucleotide sequence, including recombination of genes in (non-
PT)human cell, comprises introducing DNA-modifying molecule into cell cycle
PT synchronized cell.
XX
PS Example 4; Page 49; 67pp; English.
XX
CC The specification describes a method for modifying a nucleotide sequence
CC in the genome of a cell. The method comprises providing a cell and a DNA-
CC modifying molecule, manipulating the cell to generate a synchronized cell
CC and contacting the synchronized cell with the DNA-modifying molecule
CC under conditions such that a modification in the nucleotide sequence is
CC produced. The method is useful for modifying nucleotide sequences in the
CC genome of a human or non-human cell including a fertilized egg cell from
CC an animal such as sheep, pig, rabbit, cattle and a mouse cell such as
CC blastomere, eight-cell embryo cell, blastocoele, midgestation embryo cell
CC and embryonic stem cell. The cell is preferably DNA repair-deficient. The
CC method is useful for introducing a modification into the genome of a cell
CC for determining the effect of the modification on the cell. The method
CC generates transgenic cells and animals useful as models for diseases, and
CC for screening therapeutic agents. The method also facilitates targeted
CC recombination for producing gene knockout organisms and/or replacement of
CC detective genes with non-defective genes. Further the method is useful
CC for determining the function of a gene of unknown function. AAI65861-62
CC represent triplex forming oligonucleotides, which were used in the method
CC of the invention to modify a fragment of the Hprt gene
XX
SQ Sequence 30 BP; 0 A; 6 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.5%; Score 15; DB 1; Length 30;
Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAA 2803
|| |||| |||| || ||||||
Db 27 AAAAGAAAGAAAAGAAGAAAAAA 5

RESULT 3554
AAN60096/c
ID AAN60096 standard; DNA; 18 BP.
XX
AC AAN60096;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 28-JUN-1991 (first entry)
XX
DE Sequence of probe for novel alpha-factor presegment insulin-like growth
DE factor-I sequences.
XX
KW Saccharomyces cerevisiae; expression vector; heterologous polypeptide;
KW ss.
XX
OS Homo sapiens.
XX
PN EP206783-A.
XX
PD 30-DEC-1986.
XX
PF 20-JUN-1986; 86EP-00304764.
XX
PR 20-JUN-1985; 85US-00747152.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Thill GP, Harpold MM, Tschopp JF;
XX
DR WPI; 1986-341080/52.
XX
PT Expression vectors for Saccharomyces cerevisiae - useful for improving
PT efficiency of heterologous polypeptide secretion.
XX
PS Example; Page 50; 73pp; English.
XX
CC Using the expression vectors of the invention, improved efficiency in the
CC secretion of heterologous polypeptides from transformed S. cerevisiae is
CC possible. The polypeptides include over 200 AA residues. Specific
CC polypeptides include GRF analogues, urokinase, growth hormone, etc.
CC (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1485 AAACCCTGGAGAAAATGG 1502
|| ||||||||||||| |
Db 18 AAGCCCTGGAGAAAATAG 1

RESULT 3555
AAX32947/c
ID AAX32947 standard; DNA; 18 BP.
XX
AC AAX32947;
XX
DT 30-JUN-1999 (first entry)
XX
DE Duplex target sequence Seq ID No: 14.
XX
KW OCH2O linkage; analogue; 2,6-diethylpyridine; DEP; molecular sieve;
KW tetrabutylammonium fluoride; TBAF; tetrahydrofuran; chemical synthesis;
KW THF: thioformacetal linkage; diagnostic agent; ss.
XX
OS Synthetic.
XX
PN US5495009-A.
XX
PD 27-FEB-1996.
XX
PF 24-APR-1992; 92US-00874334.
XX
PR 24-OCT-1989; 89US-00426286.
PR 11-DEC-1989; 89US-00448941.
PR 30-JUL-1990; 90US-00559957.
PR 24-APR-1991; 91US-00690786.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Lin K, Jones B, Matteucci M;
XX
DR WPI; 1996-178794/18.
XX
PT Prodn. of nucleoside dimers with methylenedioxy linkage - by reacting 5'-
PT protected nucleoside 3'-methylthio:methyl ether and 3'-protected
PT nucleoside with bromine.
XX
PS Example 2; Col 25; 27pp; English.
XX
CC The invention relates to a method for linking a first nucleoside or
CC oligonucleotide to a second nucleoside or nucleotide through an OCH2O
CC linkage, starting with a 5'-protected nucleoside or nucleotide which is
CC derivatised in the 3' position with an OCH2SMe group. The method
CC comprises (a) treating the derivatised nucleoside or nucleotide an
CC protected nucleoside or nucleotide with bromine in the presence

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CC   diethylpyridine (DEP) and molecular sieves; and (b) treating the product
CC   with tetrabutylammonium fluoride (TBAF) in tetrahydrofuran (THF). The
CC   OCH2O-linked dimers can be used in the synthesis of oligonucleotide
CC   analogues (containing thioformacetal linkages) e.g. useful as diagnostic
CC   agents (see WO9106629)
XX
SQ   Sequence 18 BP; 13 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2173
              ||||| ||||||| ||||
Db         18 TTTTTCCTCCTTTCTTTT 1


RESULT 3556
AAZ31863/c
ID   AAZ31863 standard; DNA; 18 BP.
XX
AC   AAZ31863;
XX
DT   24-JAN-2000  (first entry)
XX
DE   Human G-alpha-13 antisense inhibitor ISIS# 20738.
XX
KW   G-alpha-13; human; inhibitor; cancer; antisense compound; therapy; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5981732-A.
XX
PD   09-NOV-1999.
XX
PF   04-DEC-1998;   98US-00205860.
XX
PR   04-DEC-1998;   98US-00205860.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 1999-633376/54.
XX
PT   Antisense compound inhibiting expression of human G-alpha-13.
XX
PS   Example 15; Col 38; 38pp; English.
XX
CC   This sequence represents an antisense inhibitor of the invention, and
CC   inhibits the expression of the human G-alpha-13 protein. The antisense
CC   compounds of the invention are of 8 to 30 nucleobases in length, that
CC   inhibits the expression of the human G-alpha-13. The antisense compound
CC   is useful for treating an animal, particularly humans, having or being
CC   prone to a disease or condition associated with the expression of G-alpha
CC   -13, such as cancer
XX
SQ   Sequence 18 BP; 0 A; 11 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         50 CGCGGCGGGGGCGGCGGC 67
              || ||||| ||||||||||
Db         18 CGAGGCGGCGGCGGCGGC 1


RESULT 3557
AAZ46099/c
ID   AAZ46099 standard; DNA; 18 BP.
XX
AC   AAZ46099;
XX
DT   05-MAY-2000  (first entry)
XX
DE   PCR primer used to amplify cDNA encoding murine HPRT.
XX
KW   Forkhead activin signal transducer protein; FAST2; activin signalling;
KW   winged-helix/forkhead domain protein; homeobox gene; goosecoid inducer;
KW   gsc; transforming growth factor-beta signalling; gsc promoter; HPRT;
KW   signal transduction; transcription factor; wound healing; inflammation;
KW   tumour progression; scarring; arthritis; fibrosis; liver fibrosis;
KW   kidney fibrosis; PCR primer; ss.
XX
OS   Mus sp.
XX
PN   WO200004143-A1.
XX
PD   27-JAN-2000.
XX
PF   19-JUL-1999;   99WO-CA000645.
XX
PR   17-JUL-1998;   98CA-02237788.
XX
PA   (HSCR-) HSC RES & DEV LP.
XX
PI   Wrana JL,  Attisano L;
XX
DR   WPI; 2000-171267/15.
XX
PT   New mammalian transcription factor, useful for preventing or treating
PT   disorders associated with transforming growth factor beta or activin
PT   signaling pathways.
XX
PS   Example 1; Page 23; 76pp; English.
XX
CC   PCR primers AAZ46098-99 were used to amplify cDNA encoding murine HPRT,
CC   in the course of the invention. The specification describes a murine
CC   forkhead activin signal transducer (FAST) protein, designated FAST2. The
CC   protein is a winged-helix/forkhead domain protein. The protein is an
CC   inducer of the homeobox gene goosecoid (gsc) by transforming growth
CC   factor (TGF)-beta or activin signaling. FAST2 binds to a nucleotide
CC   sequence in the gsc promoter. The FAST2 protein is useful for modulating
CC   signal transduction in a TGF-beta or activin signaling pathway, which
CC   involves FAST2 as transcription factor, by modulating the formation of
CC   Smad2/Smad4/FAST2 or Smad3/Smad4/FAST2 complex. Inhibition of FAST2
CC   binding to its target DNA site inhibits FAST2 specific TGF-beta
CC   signaling, which is associated with wound healing inflammation, and
CC   tumour progression. Excessive signaling is associated with scarring,
CC   arthritis and fibrosis in numerous diseases, including fibrosis of the
CC   liver and kidney
XX
SQ   Sequence 18 BP; 7 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        847 CCCTGGAAGATTGTCGCT 864
              | |||| ||||||||||
Db         18 CTCTGGTAGATTGTCGCT 1


RESULT 3558
AAA55497/c
ID   AAA55497 standard; DNA; 18 BP.
XX
AC   AAA55497;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF1 antisense oligonucleotide ISIS# 26699.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
```

KW antisense oligonucleotide; phosphorothioate; antiproliferative;
KW anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS Synthetic.
XX
PN WO200020435-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US023171.
XX
PR 06-OCT-1998; 98US-00167109.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Monia BP, Xu XS;
XX
DR WPI; 2000-303732/26.
XX
PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT necrosis factor receptor-associated factor (TRAF), useful for treating
PT diseases associated with TRAF expression such as inflammatory diseases.
XX
PS Example 14; Page 46; 170pp; English.
XX
CC The present invention relates to antisense oligonucleotides (see AAA55496
CC -A55757) which are targeted to nucleic acids encoding a human tumour
CC necrosis factor receptor-associated factor (TRAF). The antisense
CC sequences comprise at least one modified internucleotide linkage, which
CC is a phosphorothioate linkage. The oligonucleotides also include at least
CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC TRAF1-6. Included in the invention is a method for treating a human
CC having a disease associated with the expression of TRAF comprising
CC administering an antisense oligonucleotide. The reduction of jun kinase
CC activation in cells comprises contacting the cells with an antisense
CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC selectin expression in cells or tissues comprises contacting the cells or
CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC The antisense oligonucleotides have antiproliferative and anti-
CC inflammatory activity and are useful for treating disorders associated
CC with cell proliferation and inflammation. The antisense oligonucleotides
CC may also be used as a diagnostic probe for studying gene function
XX
SQ Sequence 18 BP; 2 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 464 CAGCAGGCCTGGCCCGGC 481
||||||.|||.|||||||
Db 18 CAGCAGTCCTCGCCCGGC 1

RESULT 3559
AAA51250
ID AAA51250 standard; DNA; 18 BP.
XX
AC AAA51250;
XX
DT 09-OCT-2000 (first entry)
XX
DE Primer 4 for casein kinase II alpha CTD (4D) mutant cDNA.
XX
KW Casein kinase II interacting protein-1; cell transformation; cytostatic;
KW CKIP-1; osteopathic; antiinflammatory; neuroprotective; vulnerary;
KW C-terminal domain; casein kinase II; primer; mutant; ss.
XX
OS Homo sapiens.
XX
PN WO200036100-A1.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-CA001197.
XX
PR 17-DEC-1998; 98US-0112813P.
XX
PA (UYWO-) UNIV WESTERN ONTARIO.
PA (UYMA-) UNIV MANITOBA.
PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
XX
PI Litchfield DW, Bosc DG;
XX
DR WPI; 2000-431585/37.
XX
PT Nucleic acid encoding a casein kinase II interacting protein-1 (CKIP-1),
PT useful for treating disorders such as cancer, inflammatory diseases, bone
PT resorption, degenerative disorders of the central nervous system and
PT wounds.
XX
PS Example 1; Page 27; 74pp; English.
XX
CC Primers AAA51247-50 were used to amplify a mutant C-terminal domain
CC (CTDs) of casein kinase II (CK2) alpha. The mutant was mutated to replace
CC each phosphorylation site at residues Thr-344, Thr-360, Ser-362 and Ser-
CC 370 with aspartic acid. Primers AAA51247-48 were used to introduce the
CC first mutation. The remaining 3 mutations were introduced using primers
CC AAA51249-50. Constructs containing the alpha subunit CTDs were used as
CC bait in a yeast two hybrid system to identify proteins which interact
CC with CK2. Human casein kinase II interacting protein-1 (CKIP-1) was
CC identified, which possesses a pleckstrin homology (PH) domain as well as
CC proline rich motifs and a potential leucine zipper. The protein functions
CC as an anchoring or targeting protein that localizes some of the cellular
CC casein kinase II to the plasma membrane. CKIP-1 regulates the
CC transformation of cells by regulating the activity or subcellular
CC localization of casein kinase II. CKIP-1 and modulators of CKIP-1 may be
CC useful for treatment of various disorders including cancer, arthropathy,
CC bone resorption, inflammatory disease, degenerative disorders of the
CC central nervous system and wounds
XX
SQ Sequence 18 BP; 2 A; 10 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 252 TCCCCCACCTCTCCTCCG 269
||||||||||| ||| |
Db 1 TCCCCCACCTCTGCTCAG 18

RESULT 3560
AAA63121/c
ID AAA63121 standard; DNA; 18 BP.
XX
AC AAA63121;
XX
DT 07-DEC-2000 (first entry)
XX
DE Antisense oligonucleotide for use in RNase H mapping assay SEQ ID NO: 25.
XX
KW Immunoregulator; antisense oligonucleotide; cancer; tumour cell vaccine;
KW rheumatoid arthritis; autoimmune disease; diabetes mellitus; thyroiditis;
KW ss.
XX
OS Mus sp.
XX
PN WO200034467-A1.
XX
PD 15-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US028096.
XX
PR 04-DEC-1998; 98US-00205995.

```
XX
PA   (ANTI-) ANTIGEN EXPRESS INC.
XX
PI   Xu M,  Qiu G,  Humphreys R;
XX
DR   WPI; 2000-423417/36.
XX
PT   Cancer cell vaccine for treating malignancies, autoimmune disorders and
PT   isolating autodeterminant peptides comprises a regulator of invariant
PT   chain protein expression or immunoregulatory function.
XX
PS   Example 1; Page 46; 94pp; English.
XX
CC   The present sequence is an antisense oligonucleotide which was used in an
CC   RNase mapping experiment. This enables the identification of sites within
CC   the Ii RNA strand which hybridise to antisense DNA. These sites can then
CC   be used as targets for antisense strands which may, using gene therapy,
CC   be used as tumour cell vaccines (for example to treat carcinomas,
CC   melanoma, leukaemia, lymphomas, stomach, breast, colon or rectum, lung,
CC   prostate, bladder, pancreas, brain and ovarian cancers), or they can be
CC   used to treat autoimmune diseases including rheumatoid arthritis,
CC   diabetes mellitus and thyroiditis
XX
SQ   Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2565 GCTCTGTTCTTGGCTTGG 2582
              |||||| |||||||| ||
Db         18 GCTCTGCTCTTGGCTGGG 1


RESULT 3561
AAF85699
ID   AAF85699 standard; DNA; 18 BP.
XX
AC   AAF85699;
XX
DT   13-JUL-2001  (first entry)
XX
DE   Multiple repeated heat process PCR related oligonucleotide #3.
XX
KW   Multiple repeated heat circulation; polymerase chain reaction; PCR;
KW   target DNA production; DNA synthesis; ds.
XX
OS   Unidentified.
XX
PN   CN1278558-A.
XX
PD   03-JAN-2001.
XX
PF   22-JUN-1999;   99CN-00114949.
XX
PR   22-JUN-1999;   99CN-00114949.
XX
PA   (XIAQ/) XIA Q.
XX
PI   Xia Q;
XX
DR   WPI; 2001-245741/26.
XX
PT   Asynchronous chain-extending polymerase chain reaction for producing lots
PT   of target DNA fragments, comprises a multiple repeated heat circulation
PT   process.
XX
PS   Disclosure; Page 3; 4pp; Chinese.
XX
CC   The present invention relates to a kind of two chains asynchronously-
CC   elongated DNA amplification technology in vitro, which is characterized
CC   by that firstly, a pair of specific primers is synthesized according to
CC   the target DNA sequence to be amplified, then a repetitive sequence
CC   complementary oligo-repetitive sequence of 3' target DNA chain whose tail
CC   end is modified and elongation vitality is lost, then the oligo-
CC   repetitive sequence, chain primer, heat-resisting DNA polymerase, dNTP
CC   substrate, template DNA, magnesium ion, polymerase chain reaction (PCR)
CC   buffer solution and ultra-pure water are mixed uniformly and made into a
CC   reaction system. The reaction system then undergoes the processes of high
CC   -temp., low-temp., medium-low temp., medium-temp, and repeated heat
CC   circulation treatment in the heat-circulating instrument to obtain
CC   million copies of specific target DNA fragments. The invention adopts a
CC   multiple repeated heat circulation process, so that it can produce lots
CC   of target DNA fragments. The present sequence was used in the
CC   exemplification of the invention
XX
SQ   Sequence 18 BP; 0 A; 6 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 18;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGCAG 69
              |||||| ||||||||| |
Db          1 CGGCGGCGGCGGCGGCGG 18


RESULT 3562
ABA91529
ID   ABA91529 standard; DNA; 18 BP.
XX
AC   ABA91529;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.
XX
KW   DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        8. .9
FT                   /*tag=  a
FT                   /label= RNA
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 4; Page 49; 72pp; English.
XX
CC   The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC   AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
CC   to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC   oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC   the set had a different number of ribonucleotides, 2 in the present case.
CC   The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC   (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC   minutes. The results showed that 4 ribonucleotides were the minimum
```

CC number for RNA cleavage. The invention provides probes for nucleic acid
CC hybridisation. The probes form a hairpin structure comprising a double-
CC stranded stem and a single-stranded loop, and are capable of both
CC intramolecular and intermolecular hybridisation. The double-stranded stem
CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC can be removed. Arrays and methods for nucleic acid hybridisation using
CC the probes are provided
XX
SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||| |||||||||
Db 1 TTTTTTTAATTTTTTTTT 18

RESULT 3563
ABA91529/c
ID ABA91529 standard; DNA; 18 BP.
XX
AC ABA91529;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.
XX
KW DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 8. .9
FT /*tag= a
FT /label= RNA
XX
PN WO200206531-A2.
XX
PD 24-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US022166.
XX
PR 14-JUL-2000; 2000US-00616761.
PR 30-MAR-2001; 2001US-00823647.
XX
PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI Dattagupta N;
XX
DR WPI; 2002-171819/22.
XX
PT Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.
XX
PS Example 4; Page 49; 72pp; English.
XX
CC The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC the set had a different number of ribonucleotides, 2 in the present case.
CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC minutes. The results showed that 4 ribonucleotides were the minimum
CC number for RNA cleavage. The invention provides probes for nucleic acid
CC hybridisation. The probes form a hairpin structure comprising a double-
CC stranded stem and a single-stranded loop, and are capable of both
CC intramolecular and intermolecular hybridisation. The double-stranded stem
CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC can be removed. Arrays and methods for nucleic acid hybridisation using
CC the probes are provided
XX
SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||| |||||||
Db 18 AAAAAAAAATTAAAAAAA 1

RESULT 3564
ADE27346/c
ID ADE27346 standard; RNA; 19 BP.
XX
AC ADE27346;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:290.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 290; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.

CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 15 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAACTT 2191
||||||||||||||| ||
Db 19 TTTTTTTTTTTTTAGATT 2

RESULT 3565
ADE27636
ID ADE27636 standard; RNA; 19 BP.
XX
AC ADE27636;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:580.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 580; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 2 A; 1 C; 1 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 19;
Best Local Similarity 5.6%; Pred. No. 2.8e+03;
Matches 1; Conservative 15; Mismatches 2; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAACTT 2191
:::::::::::::| ::
Db 1 UUUUUUUUUUUUUAGAUU 18

RESULT 3566
ABK94423/c
ID ABK94423 standard; DNA; 19 BP.
XX
AC ABK94423;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human MLH1 DNA mismatch repair gene, exon 12, PCR primer 12.1F.
XX
KW hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
KW breast and ovarian cancer susceptibility gene; TGDS; human;
KW two-dimensional DNA electrophoresis; tumour suppressor gene;
KW breast cancer; ovarian cancer; tumour.
XX
OS Homo sapiens.
XX
PN WO200236819-A1.
XX
PD 10-MAY-2002.
XX
PF 06-NOV-2000; 2000WO-IB001607.
XX
PR 06-NOV-2000; 2000WO-IB001607.
XX
PA (SCSC-) ACAD APPLIED SCI.
XX
PI Vijg J;
XX
DR WPI; 2002-471507/50.
XX
PT Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT amplification products to 2-dimensional gel electrophoresis to produce a
PT characteristic spot pattern for a specific mutation in either the BRCA1
PT or the hMLH1 gene.
XX
PS Claim 6; Page 21; 57pp; English.
XX
CC The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC comprising subjecting a set of amplification products to two-dimensional
CC DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC detecting mutations in the BRCA1 (breast and ovarian cancer
CC susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
CC mismatch repair gene). The present sequence is a PCR primer specific to
CC hMLH1 used in the method of the invention
XX
SQ Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAAAAA 2797

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                    | ||| ||||||||||||
Db         18 GTATTAAAAAAAAAAAAA 1


RESULT 3567
AAQ20030
ID   AAQ20030 standard; DNA; 19 BP.
XX
AC   AAQ20030;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 116 for targetting HUMIL1B.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group; IL-1;
KW   aziridinylcytosine; cross-linking group; o-xyloso linking group;
KW   human interleukin-1 beta; inverted polarity region; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
FT   modified_base   4
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT   misc_feature    14. .19
FT                   /*tag=  c
FT                   /label= inverted_polarity_region
FT                   /note= "see comments"
FT   modified_base   14
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT   modified_base   18
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT   modified_base   19
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 25; 42pp; English.
XX
CC   This oligomer contains an inverted polarity region formed from an o-
CC   xyloso dimer synthon. Residues 13 and 14 are linked via an o-xyloso group
CC   (i.e. nucleotides that have xylose sugar linked via the o-xylene ring).
CC   The sequence is designed to target the Human interleukin-1 beta gene
CC   beginning at nucleotide 7378 and will covalently cross-link to it via the
CC   N4N4-ethanocytosine group. See also AAQ20026-Q20029
XX
SQ   Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAA 2188
                || ||||||||| |||||
Db          2 TTATTTTTTTTTATTTAA 19


RESULT 3568
AAQ30373
ID   AAQ30373 standard; DNA; 19 BP.
XX
AC   AAQ30373;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer HUM beta 113 for forming triplex with IL-1 target duplex.
XX
KW   Human interleukin - 1 beta gene; herpes simplex; AIDS; modified; HIV;
KW   RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   modified_base   4
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   misc_feature    13. .14
FT                   /*tag=  g
FT                   /note= "o-xyloso dimer synthon linkage"
FT   misc_feature    14. .19
FT                   /*tag=  f
FT                   /label= inverted_polarity_region
FT                   /note= "see comments"
FT   modified_base   14
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   modified_base   18
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   modified_base   19
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
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PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 70; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin -1 beta gene beginning at nucleotide 7378 contg. a purine
CC   rich sequence concd. on one strand of the duplex. The oligomer, and
CC   others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV; HER; HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. The oligomer contains
CC   an inverted polarity region formed from an o-xyloso dimer synthon. The
CC   linking gp. is o-xyloso (nucleotides have the 3' positions of xylose
CC   sugars linked via the o-xylene ring). Two nucleotides are coupled through
CC   a xylene residue to form the dimer synthon. This additional modifications
CC   may render the oligomer stable to nuclease activity. The oligomer is able
CC   to inhibit gene expression, as verified by in vitro systems. See also
CC   AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 19 BP; 5 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAA 2188
              || |||||||||| |||||
Db          2 TTATTTTTTTTTATTTAA 19


RESULT 3569
AAQ30376
ID   AAQ30376 standard; DNA; 19 BP.
XX
AC   AAQ30376;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer HUM beta 116 for forming triplex with IL-1 target duplex.
XX
KW   Human interleukin - 1 beta gene; herpes simplex; AIDS; modified; HIV;
KW   RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
FT   modified_base    4
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   misc_feature     13. .14
FT                    /*tag=  g
FT                    /note= "o-xyloso dimer synthon linkage"
FT   misc_feature     14. .19
FT                    /*tag=  f
FT                    /label= inverted_polarity_region
FT                    /note= "see comments"
FT   modified_base    14
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   modified_base    18
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   modified_base    19
FT                    /*tag=  e
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 70; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin -1 beta gene beginning at nucleotide 7378 contg. a purine
CC   rich sequence concd. on one strand of the duplex. The oligomer, and
CC   others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV; HER; HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. The oligomer contains
CC   an inverted polarity region formed from an o-xyloso dimer synthon. The
CC   linking gp. is o-xyloso (nucleotides have the 3' positions of xylose
CC   sugars linked via the o-xylene ring). Two nucleotides are coupled through
CC   a xylene residue to form the dimer synthon. This additional modifications
CC   may render the oligomer stable to nuclease activity. The oligomer is able
CC   to inhibit gene expression, as verified by in vitro systems. See also
CC   AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 19 BP; 4 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAA 2188
              || |||||||||| |||||
Db          2 TTATTTTTTTTTATTTAA 19


RESULT 3570
AAT32774
ID   AAT32774 standard; DNA; 19 BP.
XX
AC   AAT32774;
```

```
XX
DT   18-FEB-1997  (first entry)
XX
DE   Triple helix-forming oligonucleotide.
XX
KW   Triple helix; triplex formation; Hoogsteen base pairing; plasmid;
KW   purification; double-stranded DNA; homopyrimidine; polypurine; ss.
XX
OS   Synthetic.
XX
PN   WO9618744-A2.
XX
PD   20-JUN-1996.
XX
PF   08-NOV-1995;   95WO-FR001468.
XX
PR   16-DEC-1994;   94FR-00015162.
XX
PA   (RHON ) RHONE POULENC RORER SA.
XX
PI   Crouzet J,  Scherman D,  Wils P;
XX
DR   WPI; 1996-300660/30.
XX
PT   Purificn. of double stranded DNA by triple helix formation - comprises
PT   hybridising immobilised oligo-nucleotide to specific sequence in target
PT   DNA.
XX
PS   Claim 11; Page 22; 34pp; French.
XX
CC   Double-stranded (ds) DNA can be purified from complex mixtures of nucleic
CC   acids, proteins, endotoxins, nucleases, etc. by passing the mixture over
CC   a support to which an oligonucleotide is covalently attached; the
CC   oligonucleotide is able to form a triple helix by hybridisation with a
CC   specific sequence present in the dsDNA. The present sequence is a
CC   preferred oligonucleotide which can form a triple-helix with the
CC   homopurine target sequence in AAT32773. The target sequence may be
CC   present naturally, e.g. in a plasmid origin of replication, or can be
CC   introduced artificially. The method is particularly suited to
CC   purification of plasmid DNA
XX
SQ   Sequence 19 BP; 8 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 3571
AAT43004/c
ID   AAT43004 standard; DNA; 19 BP.
XX
AC   AAT43004;
XX
DT   16-JUL-1997  (first entry)
XX
DE   Rat type L pyruvate kinase promoter element L3.
XX
KW   Glucose-inducible; rat; pyruvate kinase type L; L-PK; promoter;
KW   hyperglycaemia; diabetes; gene therapy; viral vector; defective virus;
KW   hepatocyte nuclear factor 4; HNF4; ss.
XX
OS   Rattus sp.
XX
PN   WO9632489-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-FR000560.
XX
PR   14-APR-1995;   95FR-00004558.
XX
PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
PI   Chen R,  Doiron B,  Kahn A;
XX
DR   WPI; 1996-477139/47.
XX
PT   Recombinant defective virus contg. heterologous gene under control of
PT   glucose inducible promoter - and infected mammalian cells, esp. for gene
PT   therapy of diabetes.
XX
PS   Claim 9; Page 22; 41pp; French.
XX
CC   A new defective recombinant virus contains at least one heterologous gene
CC   under control of an expression signal inducible by glucose or its
CC   analogues. Preferably, the expression signal is derived from the 183 bp
CC   region located 5' of the type L pyruvate kinase (L-PK) gene, especially
CC   containing at least the L4 element (i.e. the binding site for the major
CC   late transcription factor (MLFT)/USF). Preferably, the expression signal
CC   also contains the L3 element (i.e. the present sequence) which is a
CC   binding site for hepatocyte nuclear factor 4. Expression of the
CC   recombinant virus can be controlled by glucose levels, but insulin
CC   production can be stopped immediately by administering glucagon. This
CC   avoids the risk of hypoglycaemia caused by excessive insulin production.
CC   Mammalian cells infected by the virus can be implanted into liver,
CC   spleen, pancreas or intestine, to provide insulin secretion at
CC   predetermined sites. The virus is useful in gene therapy to treat and/or
CC   prevent diseases associated with hyperglycaemia, particularly diabetes,
CC   but more generally can be used to provide controlled expression of a wide
CC   variety of proteins
XX
SQ   Sequence 19 BP; 2 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1455 CTGGAGACCAGAGTCCAG 1472
              |||| | ||||||||||
Db         18 CTGGGGGCCAGAGTCCAG 1


RESULT 3572
AAV05816
ID   AAV05816 standard; cDNA; 19 BP.
XX
AC   AAV05816;
XX
DT   20-MAY-1998  (first entry)
XX
DE   Oligonucleotide #4 for purification of plasmid DNA.
XX
KW   Purification; double-stranded DNA; pharmaceutical purity; gene therapy;
KW   cellular therapy; affinity chromatography; ceramic hydroxyapatite;
KW   immobilised oligonucleotide; triple-helix; marker gene;
KW   origin of replication; ss.
XX
OS   Synthetic.
XX
PN   WO9735002-A1.
XX
PD   25-SEP-1997.
XX
PF   17-MAR-1997;   97WO-FR000472.
XX
PR   21-MAR-1996;   96FR-00003519.
XX
PA   (RHON ) RHONE-POULENC RORER SA.
XX
PI   Wils P,  Ollivier M;
XX
```

```
DR   WPI; 1997-480209/44.
XX
PT   Purification of double-stranded DNA to pharmaceutical purity - using
PT   ceramic hydroxy:apatite and affinity or ion-exchange chromatography,
PT   particularly for plasmids intended for gene therapy.
XX
PS   Disclosure; Page 6; 51pp; French.
XX
CC   This sequence represents an oligonucleotide used in a method of purifying
CC   double-stranded DNA to pharmaceutical purity, especially for use in gene
CC   or cellular therapy. The method comprises at least one stage of
CC   chromatography on a column of ceramic hydroxyapatite (HA), and another
CC   stage comprising an affinity chromatography purification, preferably with
CC   an immobilised oligonucleotide able to form a triple-helix structure.
CC   This sequence is an example of such a triple-helix forming oligomer. The
CC   oligonucleotide preferably binds to a sequence present in the plasmid to
CC   be purified, especially in a marker gene or the origin of replication
XX
SQ   Sequence 19 BP; 8 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 3573
AAZ59024
ID   AAZ59024 standard; DNA; 19 BP.
XX
AC   AAZ59024;
XX
DT   11-APR-2000  (first entry)
XX
DE   Oligonucleotide GA19 for linking to maleimide peptide.
XX
KW   Antitumour; antiviral; antimicrobial; transfer vector; targeting system;
KW   triplex; triple helix; antisense; ribozyme; gene therapy; blood factor;
KW   hormone; tumour suppressor; antigenic peptide; vaccine; immunotherapy;
KW   cancer; protooncogene; ss.
XX
OS   Synthetic.
XX
PN   WO9949067-A1.
XX
PD   30-SEP-1999.
XX
PF   19-MAR-1999;   99WO-FR000643.
XX
PR   24-MAR-1998;   98FR-00003573.
PR   18-MAY-1998;   98US-0085848P.
XX
PA   (RHON ) RHONE-POULENC RORER SA.
XX
PI   Ciolina C,  Scherman D,  Wils P;
XX
DR   WPI; 1999-572204/48.
XX
PT   New nucleic acid transfer vector comprising double-stranded DNA linked to
PT   oligonucleotide, used for gene therapy.
XX
PS   Example 1; Page 30; 72pp; French.
XX
CC   The invention relates to a method of delivering a therapeutic double
CC   stranded DNA to a target cell or tissue by administering the DNA in a
CC   transfer vector. The vector comprises the double-stranded DNA molecule
CC   and at least one oligonucleotide that is linked to a targeting system and
CC   can form a triplex with a specific sequence within target cell or tissue.
CC   This sequence represents an example of an oligonucleotide able to form a
CC   linkage with a trgeting system ewhere the targeting system is a maleimide
CC   peptide-nuclear localisation signal. The vector is used to deliver
CC   therapeutic DNA (including antisense sequences or ribozymes) for gene
CC   therapy, e.g. sequences that encode enzymes, blood factors, hormones,
CC   tumour suppressors, also antigenic peptides for use as vaccines or
CC   immunotherapeutic agents for control of microbial or viral infections, or
CC   cancer
XX
SQ   Sequence 19 BP; 8 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 3574
AAZ59016
ID   AAZ59016 standard; DNA; 19 BP.
XX
AC   AAZ59016;
XX
DT   11-APR-2000  (first entry)
XX
DE   Triple helix forming oligonucleotide target sequence #1.
XX
KW   Antitumour; antiviral; antimicrobial; transfer vector; targeting system;
KW   triplex; triple helix; antisense; ribozyme; gene therapy; blood factor;
KW   hormone; tumour suppressor; antigenic peptide; vaccine; immunotherapy;
KW   cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9949067-A1.
XX
PD   30-SEP-1999.
XX
PF   19-MAR-1999;   99WO-FR000643.
XX
PR   24-MAR-1998;   98FR-00003573.
PR   18-MAY-1998;   98US-0085848P.
XX
PA   (RHON ) RHONE-POULENC RORER SA.
XX
PI   Ciolina C,  Scherman D,  Wils P;
XX
DR   WPI; 1999-572204/48.
XX
PT   New nucleic acid transfer vector comprising double-stranded DNA linked to
PT   oligonucleotide, used for gene therapy.
XX
PS   Claim 10; Page 40; 72pp; French.
XX
CC   The invention relates to a method of delivering a therapeutic double
CC   stranded DNA to a target cell or tissue by administering the DNA in a
CC   transfer vector. The vector comprises the double-stranded DNA molecule
CC   and at least one oligonucleotide that is linked to a targeting system and
CC   can form a triplex with a specific sequence within target cell or tissue.
CC   This sequence represents an example of a target sequence able to form a
CC   triple helix with the oligonucleotides. The vector is used to deliver
CC   therapeutic DNA (including antisense sequences or ribozymes) for gene
CC   therapy, e.g. sequences that encode enzymes, blood factors, hormones,
CC   tumour suppressors, also antigenic peptides for use as vaccines or
CC   immunotherapeutic agents for control of microbial or viral infections, or
CC   cancer
XX
SQ   Sequence 19 BP; 8 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 3575
AAX09077/c
ID   AAX09077 standard; DNA; 19 BP.
XX
AC   AAX09077;
XX
DT   14-JUN-1999  (first entry)
XX
DE   Tumour necrosis factor alpha antisense oligonucleotide.
XX
KW   Tumour necrosis factor alpha; TNF-alpha; antisense oligonucleotide; ASO;
KW   inhibition; expresssion; treatment; disease; disorder; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9901139-A1.
XX
PD   14-JAN-1999.
XX
PF   02-JUL-1998;   98WO-US013711.
XX
PR   03-JUL-1997;   97US-0051705P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Tu G,  Israel Y;
XX
DR   WPI; 1999-105767/09.
XX
PT   Generation of antisense oligonucleotides - by specifically targeting a
PT   GGGA motif found in mRNA sequences.
XX
PS   Example 2; Page 37; 55pp; English.
XX
CC   Antisense oligonucleotides (ASO) for inhibiting a tumour necrosis factor-
CC   alpha (TNF-alpha) gene in an animal, preferably a human, comprise 12-50
CC   nucleotides, 90% of which are complementary to a region of mRNA
CC   containing a GGGA sequence motif. The ASO is used to inhibit expression
CC   of a gene in an animal and for treating the animal when afflicted with a
CC   disease or disorder characterised by the presence of an mRNA from a gene
CC   containing a GGGA motif. The ASO are specifically targeted to a GGGA
CC   sequence motif found in mRNA from a gene. A study of known ASO has shown
CC   that at least half of the most efficacious ASO's contain one or more TCCC
CC   motifs. This ASO comprises a TCCC motif followed by a cytosine residue
CC   and corresponds to a region of the human p53 open reading frame
XX
SQ   Sequence 19 BP; 0 A; 12 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGG 504
              |||||||| |||||| ||
Db         18 GAGCCAGGGGGGAGCAGG 1


RESULT 3576
AAA83538
ID   AAA83538 standard; DNA; 19 BP.
XX
AC   AAA83538;
XX
DT   04-DEC-2000  (first entry)
XX
DE   cdk-we-hu ribozyme binding site #13.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 63; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 2 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        714 AGCACCTGTTGCTGCACG 731
              || |||||||||||| ||
Db          1 AGGACCTGTTGCTGCCCG 18


RESULT 3577
AAF76366
ID   AAF76366 standard; DNA; 19 BP.
XX
AC   AAF76366;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Mutant E. coli J gene RNA-DNA isothermal amplification primer #5.
XX
KW   Linear isothermal amplification; nucleic acid amplification; sequencing;
KW   mutation detection; genotyping; J gene; mutant; DNA-RNA hybrid;
KW   composite primer; ss.
XX
OS   Escherichia coli.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        10
FT                   /*tag=  a
XX
PN   WO200120035-A2.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US025104.
XX
PR   13-SEP-1999;   99US-0153604P.
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```
PR   12-JAN-2000; 2000US-0175780P.
XX
PA   (NUGE-) NUGEN TECHNOLOGIES INC.
XX
PI   Kurn N;
XX
DR   WPI; 2001-244826/25.
XX
PT   Novel linear isothermal nucleic acid amplification of polynucleotide
PT   sequences by using single RNA/DNA composite primer, which forms basis for
PT   amplification of target sequence and optionally a termination sequence.
XX
PS   Example 5; Page 74; 115pp; English.
XX
CC   The invention relates to a novel method for the linear isothermal
CC   amplification of a nucleotide sequence. The method of the invention
CC   involves the use of a composite primer comprising an RNA portion and a 3'
CC   DNA portion. The RNA-DNA composite primer, and optionally a nucelotide
CC   comprising a termination sequence, is hybridised to a template, and the
CC   composite primer is extended with DNA polymerase. The RNA portion of the
CC   composite primer is then cleaved with an enzyme which cleaves RNA from an
CC   RNA/DNA hybrid (e.g., RNAse H), thereby enabling another identical
CC   composite primer to hybridise to the template and undergo primer
CC   extension. This strand displacement method enables multiple copies of DNA
CC   complementary to the target sequence to be produced. Multiple RNA copies
CC   of the target sequence can subsequently be produced using RNA polymerase
CC   and a nucleotide comprising a propromoter and a region which hybridises
CC   to the displaced primer extension product. Transcription is allowed to
CC   occur, producing RNA complementary to the displaced primer extension
CC   product. Linear isothermal amplification is useful for sequencing a
CC   defined nucleic acid target sequence. It may be used for detecting a
CC   mutation in a target nucleotide by analysing the amplified products for
CC   single stranded conformation, where a difference in conformation as
CC   compared with a reference single stranded nucleotide indicates a mutation
CC   in the target nucleotide. The method is also useful for the qualitative
CC   detection of a nucleic acid sequence, for quantitation of the target
CC   nucleic acid sequence, for detection of the presence of defined sequence
CC   alterations, for genotyping, and for the detection of presence of various
CC   pathogens in a single biological sample. The amplified nucleic acid
CC   products are also useful for genotyping, and can be used for microarray
CC   preparation. As the method does not require thermocycling, it can be
CC   easily automated and adapted for high throughput amplification and/or
CC   analysis of nucleic acids. Sequencing based on the amplification methods
CC   are simplified by the ability to perform the reactions isothermally, and
CC   the isothermal reaction is faster than that afforded by thermal cycling.
CC   Various target sequences and polymorphic sites in a single genomic DNA
CC   sample can be amplified simultaneously in a single reaction mixture. The
CC   present sequence represents a composite DNA-RNA primer targetted to a
CC   region of the Escherichia coli J gene which was used in an
CC   exemplification of the invention. Note: The present sequence (designated
CC   SEQ ID NO:5 on page 74) is 2 nucleotides shorter than the SEQ ID NO:5
CC   (AAF76383) given in the sequence list (page 112)
XX
SQ   Sequence 19 BP; 3 A; 5 C; 6 G; 4 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 2.8e+03;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GCCGATGCGTGTCCAGTG 28
              | ||||||| : |||||||
Db          1 GACGATGCGUCTCCAGTG 18


RESULT 3578
AAH58700
ID   AAH58700 standard; DNA; 19 BP.
XX
AC   AAH58700;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cdk-we-hu ribozyme binding site SEQ ID NO:1124.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 153; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 2 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        714 AGCACCTGTTGCTGCACG 731
              || |||||||||||| ||
Db          1 AGGACCTGTTGCTGCCCG 18


RESULT 3579
AAS01754
ID   AAS01754 standard; DNA; 19 BP.
XX
AC   AAS01754;
XX
DT   12-SEP-2001  (first entry)
```

```
XX
DE   5' end of endochitinase transcript PCR primer RTEND.
XX
KW   Glucanase; endochitinase; exochitinase; cell-wall degradation; fungus;
KW   transgenic plant; plant pathogen; bacteria; seafood waste; shell; ss;
KW   chitin; chemical modification; glucan; PCR primer; RTEND.
XX
OS   Fusarium venenatum.
XX
PN   WO200116353-A1.
XX
PD   08-MAR-2001.
XX
PF   30-AUG-2000; 2000WO-US023802.
XX
PR   30-AUG-1999;   99US-0151582P.
PR   11-AUG-2000; 2000US-0224946P.
PR   28-AUG-2000; 2000US-00649747.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Okubara PA,  Blechl AE,  Hohn TM,  Berka RM;
XX
DR   WPI; 2001-218524/22.
XX
PT   Fusarium nucleic acids encoding polypeptides having glucanase,
PT   endochitinase or exochitinase activity, useful for producing transgenic
PT   plants which are resistant to plant pathogens, particularly Fusarium
PT   species.
XX
PS   Disclosure; Page 102; 216pp; English.
XX
CC   The sequence represents a PCR primer used in the production of DNA
CC   encoding the Fusarium fungal enzyme, endochitinase. Glucanase,
CC   endochitinase and exochitinase are polypeptides with cell-wall degrading
CC   activity, derived from Fusarium fungal genes. The associated nucleic
CC   acids can be used to produce transgenic plants which are resistant to
CC   plant pathogens, particularly Fusarium species. They can also be used to
CC   isolate homologous genes from fungi to obtain genes which protect host
CC   cells, including fungi, bacteria and plants against related fungal
CC   pathogens. The polypeptides, especially chitinases and glucanases, are
CC   useful for degrading seafood waste, such as shells that contain chitin,
CC   or for chemical modification of chitin or glucan
XX
SQ   Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        849 CTGGAAGATTGTCGCTCC 866
              ||||||| ||||||| ||
Db          1 CTGGAAGTTTGTCGCACC 18


RESULT 3580
AAS19331
ID   AAS19331 standard; DNA; 19 BP.
XX
AC   AAS19331;
XX
DT   20-MAR-2002  (first entry)
XX
DE   Triple helix forming oligonucleotide used in plasmid purification #2.
XX
KW   ss; DNA purification; triple helix; plasmid purification.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .19
FT                   /*tag=  a
FT                   /bound_moiety= "Binds nucleotides 1-19 of the sequences
FT                   represented in AAS19330 and AAS19332 to form a triple
FT                   helix"
XX
PN   WO200192511-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US017122.
XX
PR   26-MAY-2000; 2000US-00580923.
XX
PA   (AVET ) AVENTIS PHARMA SA.
XX
PI   Crouzet J,  Scherman D,  Wils P,  Blanche F,  Cameron B;
XX
DR   WPI; 2002-097772/13.
XX
PT   Purifying double-stranded (ds) DNA from a solution containing dsDNA and
PT   other components, comprises passing the solution through a support
PT   comprising a covalently coupled oligonucleotide able to form a triple
PT   helix with the dsDNA.
XX
PS   Disclosure; Page 5; 40pp; English.
XX
CC   This invention comprises a method of purifying double-stranded DNA from a
CC   solution containing the double-stranded DNA mixed with other components,
CC   comprising passing the solution through a support comprising a covalently
CC   coupled oligonucleotide capable of forming a triple helix with the double
CC   -stranded DNA by hybridisation with a specific sequence present in the
CC   double-stranded DNA. The method is useful for purifying double-stranded
CC   DNA contained in a solution and mixed with other components. The new
CC   method is a simple, rapid and effective method for DNA purification, and
CC   makes it possible to obtain especially high purities with high yields.
CC   The method enables DNA to be purified from complex mixtures comprising
CC   other nucleic acids, proteins, endotoxins, nucleases and the like. The
CC   supports may be readily recycled, and the DNAs obtained display improved
CC   properties to pharmaceutical safety. Further, the method entails only one
CC   step contrary to prior art. The present sequence represents an
CC   oligonucleotide sequence used to create a triple helix in the DNA
CC   purification method of the invention
XX
SQ   Sequence 19 BP; 8 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1540 AGGAGAGTAGGGAAGGAA 1557
              ||||||| ||||| ||||
Db          2 AGGAGAGGAGGGAGGGAA 19


RESULT 3581
AAD27678
ID   AAD27678 standard; DNA; 19 BP.
XX
AC   AAD27678;
XX
DT   18-APR-2002  (first entry)
XX
DE   RNA/DNA hybrid composite PCR primer #2.
XX
KW   Transcription module; composite primer based amplification;
KW   RNA transcript; single stranded conformation polymorphism;
KW   promoter region; rNTP analogue; PCR primer; RNA/DNA hybrid; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        10
FT                   /*tag=  a
FT                   /note= "RNA"
```

XX
PN WO200200938-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US020660.
XX
PR 26-JUN-2000; 2000US-0213908P.
PR 21-MAR-2001; 2001US-0277748P.
XX
PA (NUGE-) NUGEN TGECHNOLOGIES INC.
XX
PI Kurn N;
XX
DR WPI; 2002-139937/18.
XX
PT Generating multiple copies of desired nucleic acid sequence by linear
PT isothermal amplification of a defined sequence followed by isothermal
PT exponential amplification of the obtained sequence to yield multiple
PT copies.
XX
PS Example 5; Page 86; 121pp; English.
XX
CC The present invention relates to a method for generating multiple copies
CC of desired nucleic acid sequence. The method involves employing two
CC transcription modules, where first module provides linear composite
CC primer based amplification resulting in RNA transcripts and second module
CC provides for further amplification of first module by creating an
CC intermediate product comprising a double stranded promoter region from
CC which transcription can occur. The method is useful for generating
CC multiple copies of a desired nucleic acid sequence. The method is also
CC useful for sequencing target polynucleotide, comprising amplifying the
CC target by the method in the presence of a mixture of rNTP and rNTP
CC analogues so that transcriptions terminated upon incorporation of an rNTP
CC analogue and analysing the amplification products to determine sequence.
CC It can be used for detecting a mutation in target by single stranded
CC conformation polymorphism. It is used for producing a microarray
CC comprising amplifying target polynucleotide by method, and immobilising
CC the amplification products on a substrate to fabricate a microarray
CC comprising the products. The method is used for characterising a desired
CC sequence comprising amplifying target polynucleotide by method and
CC analysing the labelled RNA products. It is also useful for determining
CC gene expression profile in a sample. The present sequence is a RNA/DNA
CC hybrid composite PCR primer used in the first transcription module of a
CC composite-primer based amplification method
XX
SQ Sequence 19 BP; 3 A; 5 C; 6 G; 4 T; 1 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GCCGATGCGTGTCCAGTG 28
|| ||||||| ||||||| ||||||
Db 1 GACGATGCGUCTCCAGTG 18

RESULT 3582
ADD00279
ID ADD00279 standard; RNA; 19 BP.
XX
AC ADD00279;
XX
DT 01-JAN-2004 (first entry)
XX
DE HCV coding region-derived 50% conserved RNA sequence 225.
XX
KW HCV infection; replication; pathogenesis; virucide; vaccine;
KW gene therapy; ds.
XX
OS Hepatitis C virus.
XX
PN WO2003016572-A1.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US021843.
XX
PR 17-AUG-2001; 2001US-0313076P.
PR 20-DEC-2001; 2001US-0344116P.
PR 01-FEB-2002; 2002US-0353750P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Zhao G, Lu J, Glass JI, Martinez A, Yang Y;
XX
DR WPI; 2003-268345/26.
XX
PT New double stranded RNA oligonucleotide, useful for preparing a
PT composition for treating or preventing hepatitis C virus.
XX
PS Disclosure; Page 63; 173pp; English.
XX
CC The invention relates to a novel isolated double stranded RNA
CC oligonucleotide about 19 to about 25 ribonucleotides in length or its
CC equivalent. One strand of the oligonucleotide comprises the same
CC nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC polynucleotide sequence required for hepatitis C virus infection,
CC replication or pathogenesis in vitro or in vivo in a host cell. The
CC oligonucleotide of the invention demonstrates virucide activity and may
CC be useful for preparing a composition or vaccine for treating or
CC preventing hepatitis C virus, as well as during gene therapy procedures.
CC The current sequence is that of the HCV coding region-derived conserved
CC RNA sequence of the invention.
XX
SQ Sequence 19 BP; 6 A; 11 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 437 CACCAGCCGGCGCCCACA 454
||||| ||| ||||||||
Db 2 CACCAACCGCCGCCCACA 19

RESULT 3583
ADD00127
ID ADD00127 standard; RNA; 19 BP.
XX
AC ADD00127;
XX
DT 01-JAN-2004 (first entry)
XX
DE HCV coding region-derived 60% conserved RNA sequence 73.
XX
KW HCV infection; replication; pathogenesis; virucide; vaccine;
KW gene therapy; ds.
XX
OS Hepatitis C virus.
XX
PN WO2003016572-A1.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US021843.
XX
PR 17-AUG-2001; 2001US-0313076P.
PR 20-DEC-2001; 2001US-0344116P.
PR 01-FEB-2002; 2002US-0353750P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Zhao G, Lu J, Glass JI, Martinez A, Yang Y;
XX
DR WPI; 2003-268345/26.

```
XX
PT   New double stranded RNA oligonucleotide, useful for preparing a
PT   composition for treating or preventing hepatitis C virus.
XX
PS   Disclosure; Page 49; 173pp; English.
XX
CC   The invention relates to a novel isolated double stranded RNA
CC   oligonucleotide about 19 to about 25 ribonucleotides in length or its
CC   equivalent. One strand of the oligonucleotide comprises the same
CC   nucleotide sequence as a region of a hepatitis C virus (HCV) target RNA
CC   polynucleotide sequence required for hepatitis C virus infection,
CC   replication or pathogenesis in vitro or in vivo in a host cell. The
CC   oligonucleotide of the invention demonstrates virucide activity and may
CC   be useful for preparing a composition or vaccine for treating or
CC   preventing hepatitis C virus, as well as during gene therapy procedures.
CC   The current sequence is that of the HCV coding region-derived conserved
CC   RNA sequence of the invention.
XX
SQ   Sequence 19 BP; 6 A; 11 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        437 CACCAGCCGGCGCCCACA 454
              ||||| ||| ||||||||
Db          2 CACCAACCGCCGCCCACA 19


RESULT 3584
ADE65640
ID   ADE65640 standard; RNA; 19 BP.
XX
AC   ADE65640;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human c-fos transcript target sequence/siNA upper strand, SEQ ID NO:95.
XX
KW   RNA interference; short interfering nucleic acid; siNA;
KW   short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW   short hairpin RNA; shRNA; expression modulation; gene therapy;
KW   drug screening; diagnosis; therapeutic target identification;
KW   pharmacogenomics; gene function analysis; gene mapping;
KW   central nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; Huntington's disease; epilepsy; dementia;
KW   amyotrophic lateral sclerosis; cancer; proliferative disease; restenosis;
KW   polycystic kidney disease; inflammatory disease; allergic disease;
KW   viral infection; HIV infection; autoimmune disease; transplant rejection;
KW   vasotropic; nootropic; antiparkinsonian; neuroprotective; cytostatic;
KW   antiinflammatory; antiallergic; virucide; anti-HIV; immunosuppressive;
KW   anticonvulsant; nephrotropic; human; c-fos; target sequence; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003070914-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005162.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-679877/64.
XX
PT   New short interfering nucleic acid downregulates expression of the c-fos
PT   gene useful for treatment and diagnosis of diseases, e.g. cancer and
PT   inflammation.
XX
PS   Example 3; SEQ ID NO 95; 145pp; English.
XX
CC   The invention relates to short interfering nucleic acids (siNA) which
CC   downregulate expression of the human c-fos gene by RNA interference. The
CC   siNAs may or may not comprise ribonucleotides and may be double or single
CC   stranded. They further comprise sense and antisense regions, or
CC   alternatively are assembled from a sense oligonucleotide and an antisense
CC   oligonucleotide. Specifically, the siNAs include short interfering RNA
CC   (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC   (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC   deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC   vector or enzymatically synthesised. The invention also relates to kits
CC   for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC   of siNA; and vectors that express siNA. The siNAs are used to modulate
CC   expression of the c-fos gene in cells, tissue explants or organisms
CC   (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC   treatment of a variety of conditions. They may be used for treating
CC   central nervous system lesions and injuries (e.g., Alzheimer's disease,
CC   Parkinson's disease, Huntington's disease, epilepsy, dementia or
CC   amyotrophic lateral sclerosis); various cancers; other proliferative
CC   diseases (e.g., restenosis and polycystic kidney disease); inflammatory
CC   and/or allergic diseases; viral infections (including HIV infection);
CC   autoimmune diseases; and transplant rejection. The siNAs are also useful
CC   for drug screening, diagnosis, therapeutic target identification and
CC   validation, genetic engineering, pharmacogenomics, studying gene
CC   function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC   The present sequence represents the upper strand of a human c-fos-
CC   targeted double-stranded siNA, which is identical to the c-fos transcript
CC   target sequence.
XX
SQ   Sequence 19 BP; 8 A; 3 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+03;
  Matches   12;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1470 CAGCTGATTCTAACAAAA 1487
              ||||:||:: :||||| |
Db          1 CAGCUGAUUUUAACAAUA 18


RESULT 3585
ADE65756/c
ID   ADE65756 standard; RNA; 19 BP.
XX
AC   ADE65756;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human c-fos siNA lower strand, SEQ ID NO:211.
XX
KW   RNA interference; short interfering nucleic acid; siNA;
KW   short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW   short hairpin RNA; shRNA; expression modulation; gene therapy;
KW   drug screening; diagnosis; therapeutic target identification;
KW   pharmacogenomics; gene function analysis; gene mapping;
KW   central nervous system disorder; Alzheimer's disease;
KW   Parkinson's disease; Huntington's disease; epilepsy; dementia;
KW   amyotrophic lateral sclerosis; cancer; proliferative disease; restenosis;
KW   polycystic kidney disease; inflammatory disease; allergic disease;
KW   viral infection; HIV infection; autoimmune disease; transplant rejection;
KW   vasotropic; nootropic; antiparkinsonian; neuroprotective; cytostatic;
KW   antiinflammatory; antiallergic; virucide; anti-HIV; immunosuppressive;
KW   anticonvulsant; nephrotropic; human; c-fos; ss.
XX
OS   Homo sapiens.
XX
```

```
PN   WO2003070914-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005162.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-679877/64.
XX
PT   New short interfering nucleic acid downregulates expression of the c-fos
PT   gene useful for treatment and diagnosis of diseases, e.g. cancer and
PT   inflammation.
XX
PS   Example 3; SEQ ID NO 211; 145pp; English.
XX
CC   The invention relates to short interfering nucleic acids (siNA) which
CC   downregulate expression of the human c-fos gene by RNA interference. The
CC   siNAs may or may not comprise ribonucleotides and may be double or single
CC   stranded. They further comprise sense and antisense regions, or
CC   alternatively are assembled from a sense oligonucleotide and an antisense
CC   oligonucleotide. Specifically, the siNAs include short interfering RNA
CC   (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC   (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC   deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC   vector or enzymatically synthesised. The invention also relates to kits
CC   for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC   of siNA; and vectors that express siNA. The siNAs are used to modulate
CC   expression of the c-fos gene in cells, tissue explants or organisms
CC   (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC   treatment of a variety of conditions. They may be used for treating
CC   central nervous system lesions and injuries (e.g., Alzheimer's disease,
CC   Parkinson's disease, Huntington's disease, epilepsy, dementia or
CC   amyotrophic lateral sclerosis); various cancers; other proliferative
CC   diseases (e.g., restenosis and polycystic kidney disease); inflammatory
CC   and/or allergic diseases; viral infections (including HIV infection);
CC   autoimmune diseases; and transplant rejection. The siNAs are also useful
CC   for drug screening, diagnosis, therapeutic target identification and
CC   validation, genetic engineering, pharmacogenomics, studying gene
CC   function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC   The present sequence represents the lower strand of a human c-fos-
CC   targeted double-stranded siNA.
XX
SQ   Sequence 19 BP; 6 A; 2 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 2.8e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1470 CAGCTGATTCTAACAAAA 1487
              |||||||| |||||| |
Db         19 CAGCTGATTTTAACAATA 2


RESULT 3586
AAQ68872
ID   AAQ68872 standard; DNA; 20 BP.
XX
AC   AAQ68872;
XX
DT   25-MAR-2003  (revised)
DT   31-MAY-1995  (first entry)
XX
DE   Oligonucleotide (SA12/m1) used as control in antisense therapy.
XX
KW   Oligonucleotide; antisense; self paired; nuclease resistant;
KW   dermatological disorders; viral infection; cancer; atopical dermatitis;
KW   psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
KW   hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
KW   elastase; bone marrow graft; ss.
XX
OS   Synthetic.
XX
PN   FR2703053-A1.
XX
PD   30-SEP-1994.
XX
PF   26-MAR-1993;   93FR-00003514.
XX
PR   26-MAR-1993;   93FR-00003514.
XX
PA   (GEST ) GENSET.
XX
PI   Vasseur M,  Blumenfeld M,  Meguenni S,  Poddevin B;
XX
DR   WPI; 1994-312170/39.
XX
PT   New oligo:nucleotide(s) self paired at one or both ends - have improved
PT   resistance to nuclease(s) and reduced toxicity, useful as anti:sense
PT   molecules for treating dermatological disorders, virus infections,
PT   cancer, etc.
XX
PS   Example 1; Fig 4a; 40pp; French.
XX
CC   New hooked or semi-hooked oligonucleotides (see AAQ68869-71, AAQ68873,
CC   AAQ68875, AAQ68877, AAQ68879 and AAQ68880) are useful as therapeutic
CC   antisense molecules for treating dermatological disorders (e.g. atopical
CC   dermatitis, psoriasis, melanoma, T cell lymphoma etc.) viral infections
CC   (e.g. herpes simplex, papilloma, hepatitis or HIV); or cancer (when
CC   directed against an oncogene), due to their ability to hybridise with
CC   target nucleic acid. They can be used ex vivo, e.g., to treat bone marrow
CC   grafts. They can also be used for diagnosis or in cosmetics e.g. to block
CC   mRNA coding proteins involved in the ageing process such as collagenase
CC   or elastase. This linear antisense oligonucleotide is used as a control
CC   to see whether the hooked and semi-hooked oligonucleotides exhibit a
CC   greater resistance to exonucleases than linear oligonucleotides. (Updated
CC   on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct
CC   PA field.)
XX
SQ   Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||||||||| | |||
Db          1 AAAAAAAAAAAATAGAAA 18


RESULT 3587
AAA94536/c
ID   AAA94536 standard; DNA; 20 BP.
XX
AC   AAA94536;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antisense oligonucleotide #20976 targeted to human G-alpha-S1.
XX
KW   G-alpha-S1; infection; inflammation; tumour; antisense; human;
KW   phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KW   Gs-alpha short form; ss.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally the internucleotide linkages are
FT                   phosphorothioate"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
XX
PN   US6110664-A.
XX
PD   29-AUG-2000.
XX
PF   25-JUN-1999;   99US-00344914.
XX
PR   25-JUN-1999;   99US-00344914.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-586346/55.
XX
PT   New antisense compounds for modulating the expression of G-alpha-S1,
PT   especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
PT   prevent or delay infection, inflammation or tumor formation.
XX
PS   Claim 3; Col 40; 37pp; English.
XX
CC   The present invention relates to antisense compounds 8-30 bases long
CC   targeted to a coding region, a stop codon, or a 3' untranslated region of
CC   human G-alpha-S1 (see AAA94451). The antisense compounds specifically
CC   hybridize with and inhibit the expression of human G-alpha-S1. The
CC   antisense compounds are useful for diagnostics, therapeutics and
CC   prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC   formation. Particularly, the antisense oligonucleotides are useful for
CC   treating humans prone to a disease or condition associated with
CC   expression of G-alpha-S1. The present sequence an antisense
CC   oligonucleotide targeted to the 3' untranslated region of human G-alpha-
CC   S1
XX
SQ   Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAA 1520
              ||||||| | ||||||||
Db         20 AGAAACAAATGAAATAAA 3


RESULT 3588
AAH91454
ID   AAH91454 standard; DNA; 20 BP.
XX
AC   AAH91454;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human inflammatory bowel disease associated polymorphic site #529.
XX
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW   chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    12
FT                   /*tag=  a
FT                   /note= "SNP, optionally insertion or deletion at this
FT                   position"
XX
PN   WO200142511-A2.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US033632.
XX
PR   10-DEC-1999;   99US-0170257P.
PR   10-APR-2000; 2000US-0196046P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI   Daly M,  Hudson TJ,  Lander ES,  Rioux J,  Siminovitch K;
XX
DR   WPI; 2001-367874/38.
XX
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay.
XX
PS   Claim 1; Page 61; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention
XX
SQ   Sequence 20 BP; 17 A; 0 C; 2 G; 0 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||| ||| |||
Db          1 AAAAAGAAAAANAAAGAAA 19


RESULT 3589
ABQ96037
ID   ABQ96037 standard; DNA; 20 BP.
XX
AC   ABQ96037;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Tumour suppression-related oligonucleotide #1688.
XX
KW   Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW   tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW   viral infection; cell degeneration disease; neurodegeneration; ds;
KW   Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   FR2819824-A1.
XX
PD   26-JUL-2002.
XX
PF   23-JAN-2001; 2001FR-00000899.
XX
```

PR 23-JAN-2001; 2001FR-00000899.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Telerman A, Amson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 468; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral
CC resistance. (I) are useful as probes or primers for detecting,
CC identifying, measuring and/or amplifying nucleic acid sequences, as
CC antisense reagents and for recombinant production of polypeptides. (I),
CC polypeptides (II) encoded by (I), vector containing (I), cells containing
CC these vectors and antibodies (Ab) against (II) are all useful for
CC treatment/prevention of viral, tumour and cell degeneration diseases
CC (especially neurodegeneration, such as Alzheimer's disease and
CC schizophrenia). Analysing the expression of (I) is also useful for
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC (I) are used for studying the aetiology of these diseases (also immune
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC in the specification
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||.|||||||.||.||
Db 1 AAAACAAAAAAAAGAANAA 19

RESULT 3590
ABZ85668/c
ID ABZ85668 standard; DNA; 20 BP.
XX
AC ABZ85668;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 910; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2803
|||.||||||||||.|||
Db 20 AAAGAAAAAAAAAAGAAA 3

RESULT 3591
ABZ89545
ID ABZ89545 standard; DNA; 20 BP.
XX
AC ABZ89545;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4787; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAA 2798
|||| ||||||||||||
Db 3 AATTTTAAAAAAAAAAAA 20

RESULT 3592
ABZ90649
ID ABZ90649 standard; DNA; 20 BP.
XX
AC ABZ90649;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5891; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 14 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAA 2801
|| ||||||||||||||
Db 3 TGTCAAAAAAAAAAAAAA 20

RESULT 3593
AAC82909/c
ID AAC82909 standard; DNA; 20 BP.
XX
AC AAC82909;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human beta-actin derived oligonucleotide #2.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at

```
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 0 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||| ||||||| ||||
Db         18 ACCTTAAAAAAAAAAAAA 1


RESULT 3594
AAC82923/c
ID   AAC82923 standard; DNA; 20 BP.
XX
AC   AAC82923;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #7.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 2 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              | ||| ||||||||||||
Db         18 GCATTAAAAAAAAAAAAA 1


RESULT 3595
AAC82911/c
ID   AAC82911 standard; DNA; 20 BP.
XX
AC   AAC82911;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #4.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 1 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||| ||||||| ||||
Db         18 ACCTTAAAAAAAAAAAAA 1


RESULT 3596
AAC82908/c
ID   AAC82908 standard; DNA; 20 BP.
```

```
XX
AC   AAC82908;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human beta-actin derived oligonucleotide #1.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||| ||||||| ||||
Db         18 ACCTTAAAAAAAAAAAAA 1


RESULT 3597
AAQ20027/c
ID   AAQ20027 standard; DNA; 20 BP.
XX
AC   AAQ20027;
XX
DT   01-APR-1992  (first entry)
XX
DE   Cross-linking oligomer 112 for targetting HUMIL1B.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group; IL-1;
KW   aziridinylcytosine; cross-linking group; o-xyloso linking group;
KW   human interleukin-1 beta; inverted polarity region; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
FT   modified_base   4
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   misc_feature    14. .20
FT                   /*tag=  c
FT                   /label= inverted_polarity_region
FT                   /note= "see comments"
FT   modified_base   14
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  e
FT                   /mod_base= m5c
FT   modified_base   19
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 4; Page 25; 42pp; English.
XX
CC   This oligomer contains an inverted polarity region formed from an o-
CC   xyloso dimer synthon. Residues 13 and 14 are linked via an o-xyloso group
CC   (i.e. nucleotides that have xylose sugar linked via the o-xylene ring).
CC   The sequence is designed to target the Human interleukin-1 beta gene
CC   beginning at nucleotide 7378 and will covalently cross-link to it via the
CC   N4N4-ethanocytosine group. See also AAQ20026-Q20030
XX
SQ   Sequence 20 BP; 1 A; 4 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||||| |||||||||| ||
Db         19 TGAAAGAAAAAAAAAGAA 2


RESULT 3598
AAQ30371/c
ID   AAQ30371 standard; DNA; 20 BP.
XX
AC   AAQ30371;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer HUM beta 111 for forming triplex with IL-1 target duplex.
XX
KW   Human interleukin - 1 beta gene; herpes simplex; AIDS; modified; HIV;
KW   RSV; HPV; malignancy; hepatitis; inflammation; ss.
```

```
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   modified_base   4
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   misc_feature    13. .14
FT                   /*tag=  g
FT                   /note= "o-xyloso dimer synthon linkage"
FT   misc_feature    14. .20
FT                   /*tag=  f
FT                   /label= inverted_polarity_region
FT                   /note= "see comments"
FT   modified_base   14
FT                   /*tag=  c
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   19
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 70; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin -1 beta gene beginning at nucleotide 7378 contg. a purine
CC   rich sequence concd. on one strand of the duplex. The oligomer, and
CC   others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV; HER; HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. The oligomer contains
CC   an inverted polarity region formed from an o-xyloso dimer synthon. The
CC   linking gp. is o-xyloso (nucleotides have the 3' positions of xylose
CC   sugars linked via the o-xylene ring). Two nucleotides are coupled through
CC   a xylene residue to form the dimer synthon. This additional modifications
CC   may render the oligomer stable to nuclease activity. The oligomer is able
CC   to inhibit gene expression, as verified by in vitro systems. See also
CC   AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 20 BP; 2 A; 3 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||||| ||||||||| ||
Db         19 TGAAAGAAAAAAAAAGAA 2


RESULT 3599
AAQ30372/c
ID   AAQ30372 standard; DNA; 20 BP.
XX
AC   AAQ30372;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer HUM beta 112 for forming triplex with IL-1 target duplex.
XX
KW   Human interleukin - 1 beta gene; herpes simplex; AIDS; modified; HIV;
KW   RSV; HPV; malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N4 N4 ethanocytosine"
FT   modified_base   4
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   misc_feature    13. .14
FT                   /*tag=  g
FT                   /note= "o-xyloso dimer synthon linkage"
FT   misc_feature    14. .20
FT                   /*tag=  f
FT                   /label= inverted_polarity_region
FT                   /note= "see comments"
FT   modified_base   14
FT                   /*tag=  c
FT                   /mod_base= m5c
FT   modified_base   18
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   19
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
```

```
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 70; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin -1 beta gene beginning at nucleotide 7378 contg. a purine
CC   rich sequence concd. on one strand of the duplex. The oligomer, and
CC   others like it are useful in diagnosis and therapy of diseases
CC   characterised by specific DNA duplex targets, e.g. HPV; HER; HIV,
CC   hepatitis B, herpes, malignant tumours and inflammation. The triple
CC   helices form under mild conditions thus assays may be carried out without
CC   subjecting the test specimen to harsh conditions. The oligomer contains
CC   an inverted polarity region formed from an o-xyloso dimer synthon. The
CC   linking gp. is o-xyloso (nucleotides have the 3' positions of xylose
CC   sugars linked via the o-xylene ring). Two nucleotides are coupled through
CC   a xylene residue to form the dimer synthon. This additional modifications
CC   may render the oligomer stable to nuclease activity. The oligomer is able
CC   to inhibit gene expression, as verified by in vitro systems. See also
CC   AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 20 BP; 1 A; 4 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||||| ||||||||| ||
Db         19 TGAAAGAAAAAAAAAGAA 2

RESULT 3600
AAQ54136
ID   AAQ54136 standard; DNA; 20 BP.
XX
AC   AAQ54136;
XX
DT   25-MAR-2003  (revised)
DT   15-JUN-1994  (first entry)
XX
DE   Multiplex vector 10 primer Plex 10E.
XX
KW   Simultaneous sequencing; ss.
XX
OS   Synthetic.
XX
PN   WO9324654-A1.
XX
PD   09-DEC-1993.
XX
PF   01-JUN-1993;   93WO-EP001376.
XX
PR   02-JUN-1992;   92DE-04218152.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI   Sagner G,  Blum H,  Domdey H;
XX
DR   WPI; 1993-405842/50.
XX
PT   Simultaneously sequencing many nucleic acid fragments - by cloning in
PT   vector after attachment of double strands adaptors, and sequencing
PT   selected clones, for high cloning efficiency with only one vector.
XX
PS   Example 3; Page 23; 47pp; German.
XX
CC   The sequence is that of a primer, Plex 10E, which was used in the
CC   sequencing of Multiplex vector 10 as part of a method of simultaneously
CC   sequencing nucleic acids. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 6 A; 0 C; 6 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2530 TATATACAGGGTATTAAG 2547
              |||||| ||||||||| |
Db          1 TATATATAGGGTATTAGG 18

RESULT 3601
AAQ68869/c
ID   AAQ68869 standard; DNA; 20 BP.
XX
AC   AAQ68869;
XX
DT   25-MAR-2003  (revised)
DT   22-MAY-1995  (first entry)
XX
DE   Self paired oligonucleotide (SA12) used in antisense therapy.
XX
KW   Oligonucleotide; antisense; self paired; nuclease resistant;
KW   dermatological disorders; viral infection; cancer; atopical dermatitis;
KW   psoriasis; melanoma; T cell lymphoma; herpes simplex; papilloma;
KW   hepatitis; HIV; human immunodeficiency virus; oncogene; collagenase;
KW   elastase; bone marrow graft; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_structure  13. .20
FT                   /*tag=  a
FT                   /label= Hairpin loop.
XX
PN   FR2703053-A1.
XX
PD   30-SEP-1994.
XX
PF   26-MAR-1993;   93FR-00003514.
XX
PR   26-MAR-1993;   93FR-00003514.
XX
PA   (GEST ) GENSET.
XX
PI   Vasseur M,  Blumenfeld M,  Meguenni S,  Poddevin B;
XX
DR   WPI; 1994-312170/39.
XX
PT   New oligo:nucleotide(s) self paired at one or both ends - have improved
PT   resistance to nuclease(s) and reduced toxicity, useful as anti:sense
PT   molecules for treating dermatological disorders, virus infections,
PT   cancer, etc.
XX
PS   Example 1; Fig 4a; 40pp; French.
XX
CC   The new hooked or semi-hooked oligonucleotides (see AAQ68869-71,
CC   AAQ68873, AAQ68875, AAQ68877, AAQ68879 and AAQ68880) are useful as
CC   therapeutic antisense molecules for treating dermatological disorders
CC   (e.g. atopical dermatitis, psoriasis, melanoma, T cell lymphoma etc.)
CC   viral infections (e.g. herpes simplex, papilloma, hepatitis or HIV); or
CC   cancer (when directed against an oncogene), due to their ability to
CC   hybridise with target nucleic acid. They can be used ex vivo, e.g., to
CC   treat bone marrow grafts. They can also be used for diagnosis or in
CC   cosmetics e.g. to block mRNA coding proteins involved in the ageing
CC   process such as collagenase or elastase. Compared with linear antisense
CC   molecules, the hooked or semi-hooked oligonucleotides are more resistant
CC   to exonucleases and less toxic because they are less likely to hybridise
CC   with partially complementary non-target sequences. (Updated on 25-MAR-
CC   2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
```

```
XX
SQ   Sequence 20 BP; 15 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTT 2176
              |||| | ||||||||||||
Db         18 TTTCGCTTTTTTTTTTTT 1


RESULT 3602
AAT44460
ID   AAT44460 standard; DNA; 20 BP.
XX
AC   AAT44460;
XX
DT   30-JAN-1997  (first entry)
XX
DE   5' primer for laminin B1 chain gene amplification.
XX
KW   primer; PCR; polymerase chain reaction; quantification; control; laminin;
KW   A; B; B1; beta-actin; sensitive; ss.
XX
OS   Synthetic.
XX
PN   US5543509-A.
XX
PD   06-AUG-1996.
XX
PF   14-AUG-1992;   92US-00929204.
XX
PR   14-AUG-1992;   92US-00929204.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Horikoshi S,  Klotman PE,  Bruggeman LA;
XX
DR   WPI; 1996-370683/37.
XX
PT   PCR amplification using control template and specific laminin and beta-
PT   actin primers - useful for quantifying laminin and beta-actin mRNA in
PT   samples.
XX
PS   Claim 4; Col 9; 13pp; English.
XX
CC   Quantification of human and murine laminin mRNA transcripts of the A, B1
CC   and B2 chains and beta-actin mRNA comprises utilising partic. PCR primers
CC   and control cRNA. These primers and control cRNA overcome the problem of
CC   insufficient biopsy material contg. laminin and beta-actin genes combined
CC   with their low transcription levels. A known quantity of "control
CC   complementary RNA" (cRNA) (transcribed from template DNA; AAT44466) is
CC   placed in the same reaction with cellular mRNA from cells suspected of
CC   expressing laminin and/or beta-actin. All primer pairs produce a 166 bp
CC   control PCR product. AAT44460-61 are a primer pair specific for the
CC   laminin B1 gene and produce a 408 bp mRNA PCR product
XX
SQ   Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1113 ACTTTGCCTATGTCTGTG 1130
              |||| ||||||| |||||
Db          3 ACTTCGCCTATGACTGTG 20


RESULT 3603
AAT13503
ID   AAT13503 standard; DNA; 20 BP.
XX
AC   AAT13503;
XX
DT   20-NOV-1996  (first entry)
XX
DE   PCR primer (TSK8B) for Xp/Yp PAR1 proximal target sequence.
XX
KW   Human; Xp/Yp; pseudoautosomal region; PAR1; telomere repeat array;
KW   primer; genomic DNA; characterisation; amplification; PCR;
KW   internal repeat unit; detection; disease predisposition; abnormal;
KW   cell growth; cell division; diagnosis; family relationship;
KW   telomere mapping; human chromosome; flanking sequence;
KW   cancer identification; polymerase chain reaction; ss.
XX
OS   Homo sapiens.
XX
PN   GB2294322-A.
XX
PD   24-APR-1996.
XX
PF   19-OCT-1995;   95GB-00021447.
XX
PR   21-OCT-1994;   94GB-00021234.
PR   21-MAY-1995;   95GB-00010639.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Baird DM,  Royle NJ,  Jeffreys AJ;
XX
DR   WPI; 1996-190531/20.
XX
PT   Characterising genomic DNA by amplifying selected internal repeat units -
PT   in telomere repeat array used for, e.g. disease diagnosis, determn. of
PT   family relationships, telomere mapping, etc.
XX
PS   Claim 18; Page 52; 68pp; English.
XX
CC   The present sequence is a PCR primer for a sequence proximal to the human
CC   Xp/Yp pseudoautosomal region (PAR1) telomere repeat array, produced using
CC   sequence information obtd. from 32 Caucasian and 21 African DNAs. The
CC   sequence was found to contain 20 substitution polymorphisms, and a 10 bp
CC   deletion/insertion polymorphism found only in African DNAs. Claimed type
CC   specific primers, which hybridise to loci contained in the sequence, can
CC   be used for the characterisation of a genomic DNA test sample by
CC   amplifying selected internal repeat units in a telomere repeat array.
CC   This characterisation is useful in the detection of inherited or acquired
CC   disease predisposition, abnormal cell division or growth diagnosis (e.g.
CC   cancer), individual and family relationship identification and telomere
CC   mapping of human chromosomes from DNA flanking sequences
XX
SQ   Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1800 CTCTGAAAGTGGTGCTAT 1817
              ||||||||||||  ||||
Db          3 CTCTGAAAGTGGACCTAT 20


RESULT 3604
AAX32946/c
ID   AAX32946 standard; RNA; 20 BP.
XX
AC   AAX32946;
XX
DT   30-JUN-1999  (first entry)
XX
DE   Seq ID No: 13 of US5495009.
XX
KW   OCH2O linkage; analogue; 2,6-diethylpyridine; DEP; molecular sieve;
KW   tetrabutylammonium fluoride; TBAF; tetrahydrofuran; chemical synthesis;
KW   THF: thioformacetal linkage; diagnostic agent; ss.
```

XX
OS Synthetic.
XX
PN US5495009-A.
XX
PD 27-FEB-1996.
XX
PF 24-APR-1992; 92US-00874334.
XX
PR 24-OCT-1989; 89US-00426286.
PR 11-DEC-1989; 89US-00448941.
PR 30-JUL-1990; 90US-00559957.
PR 24-APR-1991; 91US-00690786.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Lin K, Jones B, Matteucci M;
XX
DR WPI; 1996-178794/18.
XX
PT Prodn. of nucleoside dimers with methylenedioxy linkage - by reacting 5'-
PT protected nucleoside 3'-methylthio:methyl ether and 3'-protected
PT nucleoside with bromine.
XX
PS Example 2; Col 27; 27pp; English.
XX
CC The invention relates to a method for linking a first nucleoside or
CC oligonucleotide to a second nucleoside or nucleotide through an OCH2O
CC linkage, starting with a 5'-protected nucleoside or nucleotide which is
CC derivatised in the 3' position with an OCH2SMe group. The method
CC comprises (a) treating the derivatised nucleoside or nucleotide and a 3'-
CC protected nucleoside or nucleotide with bromine in the presence of 2,6-
CC diethylpyridine (DEP) and molecular sieves; and (b) treating the product
CC with tetrabutylammonium fluoride (TBAF) in tetrahydrofuran (THF). The
CC OCH2O-linked dimers can be used in the synthesis of oligonucleotide
CC analogues (containing thioformacetal linkages) e.g. useful as diagnostic
CC agents (see WO9106629)
XX
SQ Sequence 20 BP; 13 A; 0 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2156 TTTTTTCTCCTTTTTTTT 2173
||||| ||||||| ||||
Db 19 TTTTTCCTCCTTTCTTTT 2

RESULT 3605
AAT73396
ID AAT73396 standard; DNA; 20 BP.
XX
AC AAT73396;
XX
DT 01-OCT-1997 (first entry)
XX
DE S. pneumoniae HSP72 primer OCCR3.
XX
KW Streptococcus pneumoniae; S. pyogenes; S. agalactiae; genome; HSP72;
KW open reading frame; heat shock protein 72; DnaJ; DnaK; chimaeric; FucI;
KW E. coli; Lactococcus lactis; antibody; vaccine; infection; human; PCR;
KW polymerase chain reaction; amplication; primer; ss.
XX
OS Synthetic.
XX
PN WO9640928-A1.
XX
PD 19-DEC-1996.
XX
PF 17-MAY-1996; 96WO-CA000322.
XX
PR 07-JUN-1995; 95US-00472534.
PR 04-AUG-1995; 95US-0001805P.
XX
PA (IAFB-) IAF BIOVAC INC.
XX
PI Hamel J, Brodeur B, Martin D, Rioux C;
XX
DR WPI; 1997-052328/05.
XX
PT Streptococcal heat shock proteins and corresponding DNA sequences - used
PT in the production of a vaccine to treating and preventing strain-specific
PT Streptococcal infection.
XX
PS Example 9; Page 75; 156pp; English.
XX
CC Primers AAT73395-6 were used to amplify a 782 bp fragment of the gene
CC encoding the heat shock protein 72 (HSP72) from S. pneumoniae (AAT73391).
CC The amplified region starts at base 332 downstream of the ATG initiation
CC codon of the S. pneumoniae HSP72 gene (AAT73388). This region was chosen
CC as it is well conserved between Gram +ve bacterial HSP70 genes
CC characterised so far. The product was used to screen S. pyogenes and S.
CC agalactiae DNA libraries to isolate the corresponding HSP70 genes from
CC these species (see AAT73389 and AAT73390). The HSP72 protein and its
CC fragments, or antibodies specific to HSP72, are used in pharmaceutical
CC compositions, pref. a vaccine, for treating or preventing infection by S.
CC pneumoniae or related bacteria in humans, e.g. S.pyogenes or S.
CC agalactiae
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 883 ATACAAAGTGACAGTGGC 900
|||| |||||||| ||||
Db 2 ATACCAAGTGACAATGGC 19

RESULT 3606
AAX80654/c
ID AAX80654 standard; DNA; 20 BP.
XX
AC AAX80654;
XX
DT 29-SEP-1999 (first entry)
XX
DE Primer2 for mutant glpK gene analysis.
XX
KW Glycerol kinase; glycerol; recombinant organism; E.coli FM5; PCR; primer;
KW glpK; RJFm10; plasmid pRN102-1; gene analysis; electro-transformation;
KW ss.
XX
OS Synthetic.
XX
PN WO9928480-A1.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US025551.
XX
PR 02-DEC-1997; 97US-00982783.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (GEMV) GENENCOR INT INC.
XX
PI Nair RV, Payne MS, Trimbur DE, Valle F;
XX
DR WPI; 1999-385384/32.
XX
PT Recombinant organisms containing G3PDH and or G3P phosphatase.
XX
PS Example 5; Page 77; 84pp; English.
XX

```
CC   The present sequence is a synthetic PCR primer which is used for mutant
CC   glpK gene analysis. This mutant, RJF10m was constructed by the electro-
CC   transformation of E.coli FM5 with the non-replicative integration plasmid
CC   pRN102-1. Such transformants are chloramphenicol-resistant and kanamycin-
CC   sensitive. These glycerol kinase mutants of E.coli FM5 are used for the
CC   production of glycerol from glucose
XX
SQ   Sequence 20 BP; 10 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         18 AGTGATTTTTTTCTCCAT 1


RESULT 3607
AAZ46525/c
ID   AAZ46525 standard; DNA; 20 BP.
XX
AC   AAZ46525;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Mouse CACNA1F exon 40N-48N amplifying forward primer.
XX
KW   Retinal calcium channel; RCC gene; alpha1F-subunit; retinal disorder;
KW   myopia; nystagmus; strabismus; calcium-regulated development pathway;
KW   eye disorder; mouse; CACNA1F; CSNB; PCR primer; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO9963078-A2.
XX
PD   09-DEC-1999.
XX
PF   02-JUN-1999;   99WO-CA000514.
XX
PR   02-JUN-1998;   98US-0087635P.
XX
PA   (UYTE-) UNIV TECHNOLOGIES INT INC.
XX
PI   Bech-Hansen T,  Naylor MJ;
XX
DR   WPI; 2000-097327/08.
XX
PT   New isolated mammalian retinal calcium channel gene, used to develop
PT   products for the diagnosis and treatment of incomplete congenital
PT   stationary night blindness and related disorders.
XX
PS   Example 4; Page 27; 55pp; English.
XX
CC   The invention provides a DNA molecule comprising a sequence of
CC   nucleotides encoding an alpha1F-subunit of a mammalian retinal calcium
CC   channel (RCC), including a human alpha1F-subunit, a murine alpha1F-
CC   subunit and orthologs of the human and murine alpha1F-subunits. The RCC
CC   gene may be used to develop products for diagnostic tests, for incomplete
CC   CSMB and risk assessment in affected families. The RCC gene can provide
CC   information as to the basic defect in this retinal conditions, which
CC   could lead to effective methods for treatment or cure of the disorder. As
CC   the associated features of myopia, nystagmus and strabismus frequently
CC   observed in patients with incomplete CSNB may be caused by calcium-
CC   regulated development pathways, identification of the RCC gene may help
CC   to elucidate the molecular details of eye development and which may lead
CC   to treatment for related eye disorders or diseases. Sequences AAZ46522-
CC   540 represent PCR primers used for the isolation of murine CACNA1F
CC   (alpha1F- subunit of RCC gene) ortholog
XX
SQ   Sequence 20 BP; 10 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1790 TTCTTTCCTTCTCTGAAA 1807
              |||||||||||||| | ||
Db         18 TTCTTTCCTTCTCCGGAA 1


RESULT 3608
AAA55739
ID   AAA55739 standard; DNA; 20 BP.
XX
AC   AAA55739;
XX
DT   30-AUG-2000  (first entry)
XX
DE   TRAF1 antisense oligonucleotide ISIS# 101890.
XX
KW   Tumour necrosis factor receptor-associated factor; TRAF; human;
KW   antisense oligonucleotide; phosphorothioate; antiproliferative;
KW   anti-inflammatory; E-selectin; jun kinase; ss.
XX
OS   Synthetic.
XX
PN   WO200020435-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999;   99WO-US023171.
XX
PR   06-OCT-1998;   98US-00167109.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Monia BP,  Xu XS;
XX
DR   WPI; 2000-303732/26.
XX
PT   Antisense oligonucleotides targeted to nucleic acids encoding human tumor
PT   necrosis factor receptor-associated factor (TRAF), useful for treating
PT   diseases associated with TRAF expression such as inflammatory diseases.
XX
PS   Example 33; Page 100; 170pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (see AAA55496
CC   -A55757) which are targeted to nucleic acids encoding a human tumour
CC   necrosis factor receptor-associated factor (TRAF). The antisense
CC   sequences comprise at least one modified internucleotide linkage, which
CC   is a phosphorothioate linkage. The oligonucleotides also include at least
CC   one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
CC   Sequences AAA55490-A55495 represent nucleotide sequences encoding human
CC   TRAF1-6. Included in the invention is a method for treating a human
CC   having a disease associated with the expression of TRAF comprising
CC   administering an antisense oligonucleotide. The reduction of jun kinase
CC   activation in cells comprises contacting the cells with an antisense
CC   oligonucleotide targeted to TRAF-6. A method for the reduction of E-
CC   selectin expression in cells or tissues comprises contacting the cells or
CC   tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
CC   The antisense oligonucleotides have antiproliferative and anti-
CC   inflammatory activity and are useful for treating disorders associated
CC   with cell proliferation and inflammation. The antisense oligonucleotides
CC   may also be used as a diagnostic probe for studying gene function
XX
SQ   Sequence 20 BP; 3 A; 4 C; 12 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        483 GCCAGAGCCAGGAGGGAG 500
              ||||| |||||| |||||
Db          2 GCCAGGGCCAGGTGGGAG 19
```

```
RESULT 3609
AAA60337/c
ID   AAA60337 standard; DNA; 20 BP.
XX
AC   AAA60337;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Human HPC2 cDNA exon 18 mutation screening primer SEQ ID NO: 158.
XX
KW   Human; mouse; prostate cancer predisposing gene; HPC2;
KW   human chromosome 17p; gene therapy; peptide therapy; drug design;
KW   PCR primer; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200027864-A1.
XX
PD   18-MAY-2000.
XX
PF   05-NOV-1999;   99WO-US026055.
XX
PR   06-NOV-1998;   98US-0107468P.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Tavtigian SV,  Teng DHF,  Simard J,  Rommens JM;
XX
DR   WPI; 2000-376481/32.
XX
PT   Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies,
PT   useful for treatment and diagnosis of prostate cancer.
XX
PS   Example 5; Page 61; 157pp; English.
XX
CC   The present sequence is a primer used in the isolation of the human and
CC   murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC   version of the gene is found on chromosome 17p. Some alleles cause a
CC   predisposition to cancer, particularly prostate cancer. This gene and its
CC   protein can be used in peptide and gene therapy for cancer patients, as
CC   well as being useful as diagnostic tools (both for cancer sufferers and
CC   those with a predisposition to the disease) and in the production of
CC   cancer drugs
XX
SQ   Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        894 CAGTGGCTGAAGTACAGA 911
              || |||||||||| |||||
Db         19 CATTGGCTGAAGGACAGA 2


RESULT 3610
AAA60341/c
ID   AAA60341 standard; DNA; 20 BP.
XX
AC   AAA60341;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Human HPC2 cDNA exon 19 mutation screening primer SEQ ID NO: 162.
XX
KW   Human; mouse; prostate cancer predisposing gene; HPC2;
KW   human chromosome 17p; gene therapy; peptide therapy; drug design;
KW   PCR primer; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200027864-A1.
XX
PD   18-MAY-2000.
XX
PF   05-NOV-1999;   99WO-US026055.
XX
PR   06-NOV-1998;   98US-0107468P.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Tavtigian SV,  Teng DHF,  Simard J,  Rommens JM;
XX
DR   WPI; 2000-376481/32.
XX
PT   Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies,
PT   useful for treatment and diagnosis of prostate cancer.
XX
PS   Example 5; Page 61; 157pp; English.
XX
CC   The present sequence is a primer used in the isolation of the human and
CC   murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC   version of the gene is found on chromosome 17p. Some alleles cause a
CC   predisposition to cancer, particularly prostate cancer. This gene and its
CC   protein can be used in peptide and gene therapy for cancer patients, as
CC   well as being useful as diagnostic tools (both for cancer sufferers and
CC   those with a predisposition to the disease) and in the production of
CC   cancer drugs
XX
SQ   Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        894 CAGTGGCTGAAGTACAGA 911
              || |||||||||| |||||
Db         19 CATTGGCTGAAGGACAGA 2


RESULT 3611
AAA94534/c
ID   AAA94534 standard; DNA; 20 BP.
XX
AC   AAA94534;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antisense oligonucleotide #20974 targeted to human G-alpha-S1.
XX
KW   G-alpha-S1; infection; inflammation; tumour; antisense; human;
KW   phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KW   Gs-alpha short form; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally the internucleotide linkages are
FT                   phosphorothioate"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
XX
PN   US6110664-A.
```

```
XX
PD   29-AUG-2000.
XX
PF   25-JUN-1999;   99US-00344914.
XX
PR   25-JUN-1999;   99US-00344914.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-586346/55.
XX
PT   New antisense compounds for modulating the expression of G-alpha-S1,
PT   especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
PT   prevent or delay infection, inflammation or tumor formation.
XX
PS   Claim 3; Col 40; 37pp; English.
XX
CC   The present invention relates to antisense compounds 8-30 bases long
CC   targeted to a coding region, a stop codon, or a 3' untranslated region of
CC   human G-alpha-S1 (see AAA94451). The antisense compounds specifically
CC   hybridize with and inhibit the expression of human G-alpha-S1. The
CC   antisense compounds are useful for diagnostics, therapeutics and
CC   prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC   formation. Particularly, the antisense oligonucleotides are useful for
CC   treating humans prone to a disease or condition associated with
CC   expression of G-alpha-S1. The present sequence an antisense
CC   oligonucleotide targeted to the 3' untranslated region of human G-alpha-
CC   S1
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAA 1520
              ||||||| | ||||||||
Db         18 AGAAACAAATGAAATAAA 1


RESULT 3612
AAA94535
ID   AAA94535 standard; DNA; 20 BP.
XX
AC   AAA94535;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antisense oligonucleotide #20975 targeted to human G-alpha-S1.
XX
KW   G-alpha-S1; infection; inflammation; tumour; antisense; human;
KW   phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KW   Gs-alpha short form; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally the internucleotide linkages are
FT                   phosphorothioate"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
XX
PN   US6110664-A.
XX
PD   29-AUG-2000.
XX
PF   25-JUN-1999;   99US-00344914.
XX
PR   25-JUN-1999;   99US-00344914.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-586346/55.
XX
PT   New antisense compounds for modulating the expression of G-alpha-S1,
PT   especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
PT   prevent or delay infection, inflammation or tumor formation.
XX
PS   Claim 3; Col 40; 37pp; English.
XX
CC   The present invention relates to antisense compounds 8-30 bases long
CC   targeted to a coding region, a stop codon, or a 3' untranslated region of
CC   human G-alpha-S1 (see AAA94451). The antisense compounds specifically
CC   hybridize with and inhibit the expression of human G-alpha-S1. The
CC   antisense compounds are useful for diagnostics, therapeutics and
CC   prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC   formation. Particularly, the antisense oligonucleotides are useful for
CC   treating humans prone to a disease or condition associated with
CC   expression of G-alpha-S1. The present sequence an antisense
CC   oligonucleotide targeted to the 3' untranslated region of human G-alpha-
CC   S1
XX
SQ   Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2266 ATTTATTTCAGATGTTTC 2283
              |||||||||| ||||||
Db          1 ATTTATTTCATTTGTTTC 18


RESULT 3613
AAA94535/c
ID   AAA94535 standard; DNA; 20 BP.
XX
AC   AAA94535;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antisense oligonucleotide #20975 targeted to human G-alpha-S1.
XX
KW   G-alpha-S1; infection; inflammation; tumour; antisense; human;
KW   phosphorothioate; 2'-methoxyethyl; MOE; 5-methylcytidine;
KW   Gs-alpha short form; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Optionally the internucleotide linkages are
FT                   phosphorothioate"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
FT   modified_base   16. .20
```

```
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Optionally the nucleotides are 2'-methoxyethyl
FT                   and cytidine residues are 5-methylcytidines"
XX
PN   US6110664-A.
XX
PD   29-AUG-2000.
XX
PF   25-JUN-1999;   99US-00344914.
XX
PR   25-JUN-1999;   99US-00344914.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-586346/55.
XX
PT   New antisense compounds for modulating the expression of G-alpha-S1,
PT   especially useful for diagnostics, therapeutics and prophylaxis, e.g. to
PT   prevent or delay infection, inflammation or tumor formation.
XX
PS   Claim 3; Col 40; 37pp; English.
XX
CC   The present invention relates to antisense compounds 8-30 bases long
CC   targeted to a coding region, a stop codon, or a 3' untranslated region of
CC   human G-alpha-S1 (see AAA94451). The antisense compounds specifically
CC   hybridize with and inhibit the expression of human G-alpha-S1. The
CC   antisense compounds are useful for diagnostics, therapeutics and
CC   prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC   formation. Particularly, the antisense oligonucleotides are useful for
CC   treating humans prone to a disease or condition associated with
CC   expression of G-alpha-S1. The present sequence an antisense
CC   oligonucleotide targeted to the 3' untranslated region of human G-alpha-
CC   S1
XX
SQ   Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAA 1520
              ||||||| | ||||||||
Db         19 AGAAACAAATGAAATAAA 2


RESULT 3614
AAA11308
ID   AAA11308 standard; DNA; 20 BP.
XX
AC   AAA11308;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human TRPC7 gene intron 12/exon 13 junction.
XX
KW   Transmembrane protein; TRPC7; brain; transient receptor potential; TRP;
KW   calcium channel function; human; gene therapy; periodic psychosis;
KW   mutation; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   intron          1. .10
FT                   /*tag=  a
FT                   /number= 12
FT   exon            11. .20
FT                   /*tag=  b
FT                   /number= 13
XX
PN   WO200029571-A1.
XX
PD   25-MAY-2000.
XX
PF   11-NOV-1999;   99WO-JP006289.
XX
PR   12-NOV-1998;   98JP-00321200.
XX
PA   (EIKE ) EIKEN KAGAKU KK.
XX
PI   Shimizu N,  Nagamine K;
XX
DR   WPI; 2000-387784/33.
XX
PT   Nucleic acids encoding transmembrane protein TRPC7 expressed in brain and
PT   homologous to transient receptor potential protein useful in the of
PT   treatment of associated diseases such as periodic psychosis.
XX
PS   Example 7; Page 38; 77pp; Japanese.
XX
CC   The invention relates to the isolation of a nucleic acid (AAA11284)
CC   coding for a transmembrane protein TRPC7 (AAY92944) which is expressed in
CC   brain and is homologous to transient receptor potential (TRP) protein.
CC   This suggests that the TRPC7 protein may have a calcium channel function.
CC   The genomic sequence has been shown to contain 31 introns. This sequence
CC   represents an exon/intron junction from the genomic TRPC7 sequence. The
CC   DNA and protein can be used in the diagnosis and treatment of disorders
CC   associated with TRPC7, especially the screening, monitoring and treatment
CC   (by gene therapy) of periodic psychosis, which appears to be associated
CC   with mutations in the TRPC7 gene
XX
SQ   Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        478 CGGCCGCCAGAGCCAGGA 495
              ||| | ||||||||||||
Db          1 CGGTCCCCAGAGCCAGGA 18


RESULT 3615
AAZ60521/c
ID   AAZ60521 standard; DNA; 20 BP.
XX
AC   AAZ60521;
XX
DT   05-MAY-2000  (first entry)
XX
DE   PCR primer CATATGN used to amplify a bacterial CAT gene.
XX
KW   CAT gene; MLV; retroviral vector; gag gene; env gene; gene therapy;
KW   replication-competent retrovirus; murine leukemia virus; pol gene;
KW   PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200000629-A1.
XX
PD   06-JAN-2000.
XX
PF   24-JUN-1999;   99WO-KR000334.
XX
PR   26-JUN-1998;   98KR-00024478.
PR   22-JUN-1999;   99KR-00023398.
XX
PA   (VIRO-) VIROMED LTD.
XX
PI   Kim S,  Yu SS,  Kim J;
XX
DR   WPI; 2000-170923/15.
XX
PT   Novel high efficiency retroviral vectors lacking viral coding sequences
```

```
PT   useful for gene therapy.
XX
PS   Example 1; Page 57; 68pp; English.
XX
CC   PCR primers AAZ60521-22 were used to amplify a bacterial CAT gene. The
CC   amplified fragment was inserted into the murine leukemia virus (MLV)-
CC   based retroviral vectors of the invention, and used to test gene
CC   expression from the vectors. The specification describes MLV-based
CC   retroviral vectors in which the viral coding sequences (specifically gag,
CC   env and pol) are completely deleted. The vectors also contain a
CC   heterologous intron and/or a heterologous splicing acceptor which is
CC   inserted into the upstream position of a cloning site for a foreign gene.
CC   The retroviral vectors are used for gene therapy. The vectors also allow
CC   foreign genes to be expressed both stably and efficiently, in high
CC   amounts, and allow the cloning of larger sequences. In the vectors of the
CC   invention, the formation of replication-competent retrovirus through
CC   homologous recombination, due to the presence of viral coding sequences
CC   in the vector, is not possible, as all retroviral coding sequences are
CC   deleted
XX
SQ   Sequence 20 BP; 10 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         20 AGTGATTTTTTTCTCCAT 3


RESULT 3616
AAA50702/c
ID   AAA50702 standard; DNA; 20 BP.
XX
AC   AAA50702;
XX
DT   01-SEP-2000  (first entry)
XX
DE   Sense strand encoding a topoisomerase type II recognition peptide.
XX
KW   Type II topoisomerase; identify; detect; eukaryote; intron; ss.
XX
OS   Synthetic.
XX
PN   EP997536-A2.
XX
PD   03-MAY-2000.
XX
PF   24-SEP-1999;   99EP-00118075.
XX
PR   24-SEP-1998;   98JP-00270337.
XX
PA   (MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
XX
PI   Yamamoto S,  Atsumi M,  Kasai H,  Hamada T,  Nakamura S;
XX
DR   WPI; 2000-295087/26.
XX
PT   Identification and detection of eukaryotes by probing an intron-
PT   containing region in a type II topisomerase gene.
XX
PS   Disclosure; Page 4; 30pp; English.
XX
CC   The present invention relates to the identification of a eukaryote based
CC   on the sequence of a type II topoisomerase gene intron containing region.
CC   The method comprises amplifying the eukaryote DNA by PCR or cDNA cloning,
CC   comprising a primer or probe having a nucleotide sequence encoding a
CC   specific polypeptide. The present sequence represents a nucleotide
CC   sequence encoding a polypeptide recognised by the primers used in the
CC   invention. Those peptides used to create primers for use in the method
CC   were selected by comparing the amino acid sequences of the type II
CC   topoisomerase of organisms belonging to the Animalia, Plantae, Protista
CC   and Fungi kingdoms. The regions containing conserved amino acid sequences
CC   for the respective eukaryotes were chosen, and included regions with the
CC   fewest possible degenerate codons. The method is based on the
CC   identification and detection of DNA sequences in introns. These non-
CC   coding regions are subject to a faster mutation rate than coding regions
CC   and are therefore less conserved, making them very useful in the
CC   identification of closely related organisms. The method is useful in the
CC   detection and identification of eukaryotes
XX
SQ   Sequence 20 BP; 10 A; 0 C; 4 G; 0 T; 0 U; 6 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   68.4%;  Pred. No. 3.1e+03;
  Matches   13;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              | ||:|| ||:||:||:||
Db         19 CNCCYTTRTTYTTYTTYTT 1


RESULT 3617
AAA80354/c
ID   AAA80354 standard; DNA; 20 BP.
XX
AC   AAA80354;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human ASTH1I 5' region polymorphic site, SEQ ID NO:100 (b).
XX
KW   ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KW   bronchial hyperreactivity; ets family; transcription factor;
KW   splice variant; genetic predisposition; polymorphism; antibody;
KW   drug screening; prophylaxis; therapy; diagnosis;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(10. .11,TTA)
FT                   /*tag=  a
XX
PN   US6087485-A.
XX
PD   11-JUL-2000.
XX
PF   21-JAN-1998;   98US-00009913.
XX
PR   21-JAN-1997;   97US-0035663P.
PR   01-JUL-1997;   97US-0051432P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  North M,  Cardon L,  Buckler A;
PI   Brooks-Wilson AR,  Carey AH;
XX
DR   WPI; 2000-505109/45.
XX
PT   New nucleic acids other than naturally occurring chromosomes encoding
PT   ASTH1 protein, for e.g. screening compositions that modulate expression
PT   or function of ASTH1 proteins or as diagnostics for genetic
PT   predisposition to asthma.
XX
PS   Example; Col 41-42; 131pp; English.
XX
CC   The invention relates to the ASTH1 locus on the short arm of human
CC   chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
CC   are associated with a genetic predisposition to asthma and bronchial
CC   hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
CC   directions with the ASTH1 locus, and have similar patterns of expression
CC   and common sequence motifs. They are both expressed in trachea, lung and
CC   several other tissues. ASTH1I and ASTH1J are novel members of the ets
CC   family of transcription factors, which have been implicated in the
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CC   activation of a variety of genes including the TCRa gene and cytokine
CC   genes known to be important in the aetiology of asthma. Both ASTH1I and
CC   ASTH1J mRNAs are alternatively spliced. Alternative splicing of
CC   transcripts has no effect on the open reading frame of ASTH1J, as the
CC   exons involved are all 5' to the start codon in exon b. In contrast,
CC   alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
CC   isoforms. The invention also encompasses mouse asth1j protein. The ASTH1
CC   nucleic acids are useful as diagnostics to identify a hereditary
CC   predisposition to asthma, as probes for identifying ASTH1 related genes,
CC   for identifying expression of the gene in a biological specimen, and for
CC   generating genetically modified non-human animals or site specific gene
CC   modifications in cell lines. The encoded ASTH1 proteins are useful as
CC   immunogens to raise specific antibodies; in drug screening for
CC   compositions that mimic or modulate activity or expression of ASTH1I
CC   and/or ASTH1J (including altered forms of these proteins); and as a
CC   therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC   ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
CC   antibodies are useful in the identification of individuals predisposed to
CC   development of asthma, and for modulation of gene activity in vivo for
CC   prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
CC   proteins or active fragments thereof may be used to modulate or reduce
CC   bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC   represent polymorphic sites within the ASTH1J or ASTH1I genes
XX
SQ   Sequence 20 BP; 8 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1968 TATTTACCTTGAAAAAAA 1985
              ||||| |||| |||||||
Db         20 TATTTTCCTTAAAAAAAA 3


RESULT 3618
AAF81969/c
ID   AAF81969 standard; DNA; 20 BP.
XX
AC   AAF81969;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Escherichia coli FM5 glpK mutant PCR primer SEQ ID NO:9.
XX
KW   Bioconversion; 1,3-propanediol; 3-hydroxypropionaldehyde; fermentation;
KW   carbon; PCR primer; mutant; ss.
XX
OS   Escherichia coli.
OS   Synthetic.
XX
PN   WO200112833-A2.
XX
PD   22-FEB-2001.
XX
PF   18-AUG-2000; 2000WO-US022874.
XX
PR   18-AUG-1999;   99US-0149534P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (GEMV ) GENENCOR INT INC.
XX
PI   Emptage M,  Haynie S,  Laffend L,  Pucci J,  Whited G;
XX
DR   WPI; 2001-307889/32.
XX
PT   Novel nucleic acid fragment encoding a non-specific catalytic activity
PT   for the bioconversion of 3-hydroxypropionaldehyde to 1,3-propanediol.
XX
PS   Example 2; Page 92; 109pp; English.
XX
CC   The present invention an isolated nucleic acid fragment (I) encoding a
CC   non-specific catalytic activity for the conversion of 3-
CC   hydroxypropionaldehyde to 1,3-propanediol. Also described are: (1) a
CC   polypeptide (II) encoded by (I); (2) a chimeric gene (III) comprising (I)
CC   operably linked to suitable regulatory sequences; (3) a microorganism
CC   (IV) transformed with (III), where (IV) is selected from Citrobacter,
CC   Enterobacter, Clostridium, Klebsiella, Aerobacter, Lactobacillus,
CC   Aspergillus, Saccharomyces, Schizosaccharomyces, Zygosaccharomyces,
CC   Pichia, Kluyveromyces, Candida, Hansenula, Debaromyces, Mucor,
CC   Torulopsis, Methylobacter, Salmonella, Bacillus, Streptomyces and
CC   Pseudomonas; (4) a recombinant microorganism (V), useful for the
CC   production of 1,3-propanediol; (5) a vector pDT29 (VI) comprising a set
CC   of genes dhaR, orfY, dhaT, orfX, orfW, dhaB1, dhaB2, dhaB3 and orfZ with
CC   a 12145 base pair sequence (AAF81961); and (6) a vector pKP32 (VII)
CC   comprising dhaR, orfY, orfX, orfW, dhaB1, dhaB2, dhaB3 and orfZ with a
CC   sequence (AAF81961). (V) e.g. Escherichia coli, is useful for the
CC   bioproduction of 1,3-propanediol by contacting (V) with a carbon source,
CC   and optionally recovering the 1,3-propanediol produced. A fermentable
CC   carbon source can be directly converted to 1,3-propanediol at
CC   significantly higher titre resulting in improved economics, and an
CC   improved process for the production of 1,3-propanediol from glucose. The
CC   present sequence represents a PCR primer used to amplify an Escherichia
CC   coli FM5 glpK mutant, which is used in an example from the present
CC   invention
XX
SQ   Sequence 20 BP; 10 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         18 AGTGATTTTTTTCTCCAT 1


RESULT 3619
AAH02131
ID   AAH02131 standard; DNA; 20 BP.
XX
AC   AAH02131;
XX
DT   24-JUL-2001  (first entry)
XX
DE   C. difficile cdtA toxin gene detection nucleotide SEQ ID NO:2124.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ss.
XX
OS   Clostridium difficile.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
```

```
PS   Claim 21; Page 1497; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 20 BP; 4 A; 1 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2243 AGGTACTGAAGCTTTATT 2260
              ||||||| || ||||||
Db          2 AGGTACTGTAGGTTTATT 19


RESULT 3620
AAH25642
ID   AAH25642 standard; DNA; 20 BP.
XX
AC   AAH25642;
XX
DT   05-SEP-2001  (first entry)
XX
DE   Antisense oligonucleotide for zinc finger protein-217 coding region.
XX
KW   Antisense oligonucleotide; zinc finger protein-217; infection;
KW   inflammation; tumour formation; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /note= "all cytidines are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   6. .15
FT                   /*tag=  c
FT                   /note= "2'-deoxynucleotides"
FT   modified_base   16. .20
FT                   /*tag=  d
FT                   /note= "2'-methoxyethyl nucleotides"
XX
PN   US6242590-B1.
XX
PD   05-JUN-2001.
XX
PF   28-APR-2000; 2000US-00560594.
XX
PR   28-APR-2000; 2000US-00560594.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2001-373821/39.
XX
PT   New antisense oligonucleotides for modulating the expression of zinc
PT   finger protein-217, particularly useful for preventing, delaying or
PT   treating infection, inflammation or tumor formation.
XX
PS   Claim 1; Col 41; 41pp; English.
XX
CC   Antisense oligonucleotides AAH25596-AAH25675 are targeted to various
CC   regions of the human zinc finger protein-217 gene, and inhibit expression
CC   of this gene. The antisense compounds are useful for diagnostics,
CC   therapeutics, prophylaxis, or as research reagents or kits. The antisense
CC   oligonucleotides are useful for treating an animal, particularly a human,
CC   suspected of having or being prone to a disease or condition associated
CC   with the expression of zinc finger protein-217. In particular, the
CC   antisense oligonucleotides are useful for preventing, delaying or
CC   treating infection, inflammation or tumour formation
XX
SQ   Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2115 TGGTTTTAGGAAACTTGT 2132
              ||||||||||||||| | |
Db          1 TGGTTTTAGGAAACATCT 18


RESULT 3621
AAS10558
ID   AAS10558 standard; DNA; 20 BP.
XX
AC   AAS10558;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human caspase 3 antisense oligonucleotide 108882.
XX
KW   Human; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;
KW   viral infection; haematopoietic disorder; autoimmune disorder;
KW   atherosclerosis; neurological disorder; antisense; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate internucleotide linkages.
FT                   Some bases especially bases 1-5 and bases 16-20 are 2'-
FT                   methoxyethyl (2'-MOE) bases, bases 6-15 are 2'-
FT                   deoxynucleotides and all cytidine bases are 5'-
FT                   methylcytidines"
XX
PN   WO200153310-A1.
XX
PD   26-JUL-2001.
XX
PF   11-JAN-2001; 2001WO-US000888.
XX
PR   18-JAN-2000; 2000US-00484617.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Zhang H,  Cowsert LM;
```

XX
DR WPI; 2001-442252/47.
XX
PT New antisense compound to inhibit caspase 3 is useful for treating
PT hepatitis and atherosclerosis.
XX
PS Example 15; Page 84; 127pp; English.
XX
CC The present sequence for human caspase 3 antisense oligonucleotide 108882
CC is 1 of various novel antisense oligonucleotides (AAS10517-AAS10676)
CC described in the present invention. Also described are methods of using
CC these compounds for the modulation of caspase 3 expression. The caspase 3
CC antisense oligonucleotides specifically hybridise with and inhibit the
CC expression of caspase 3. Antisense compounds targeted to caspase 3 are
CC useful to inhibit caspase 3 expression in cells or tissues and to
CC modulate apoptosis. The caspase 3 antisense oligonucleotides are useful
CC for treating disorders associated with expression of caspase 3. Such
CC disorders include hyperproliferative disorders (e.g. cancer), viral
CC infections (e.g. hepatitis), haematopoietic disorders, autoimmune
CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
CC disease)
XX
SQ Sequence 20 BP; 6 A; 3 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2394 ATTTATGCGTAATTTAAT 2411
||||||.|.|||||||||
Db 1 ATTTATTCCTAATTTAAT 18

RESULT 3622
AAH42680/c
ID AAH42680 standard; DNA; 20 BP.
XX
AC AAH42680;
XX
DT 01-OCT-2001 (first entry)
XX
DE Primer and probe for the human endoderm cell marker aldolase B.
XX
KW Human; embryo-derived cell; EBD cell; ectodermal cell; mesodermal cell;
KW endodermal cell; nestin; vimentin; myf6; flk1; alpha-1 fetoprotein;
KW myosin light-chain 2 ventricular isoform; GATA-4; cell culture;
KW tissue transplantation; tissue engineering; drug discovery; gene therapy;
KW transplantation therapy; Parkinson's disease; spinal cord injury;
KW amyotrophic lateral sclerosis; stroke; motor neuron injury; diabetes;
KW brain injury; ischemia; cardiac disease; skeletal disease; eye disease;
KW smooth muscles disease; liver disease; pancreas disease; cell marker;
KW vascular disease; artificial chromosome; probe; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200153465-A1.
XX
PD 26-JUL-2001.
XX
PF 22-JAN-2001; 2001WO-US002230.
XX
PR 21-JAN-2000; 2000US-0177287P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Shamblott MJ, Gearhart JD;
XX
DR WPI; 2001-476113/51.
XX
PT Human embryo-derived cell culture comprising cells that simultaneously
PT express polypeptide or mRNA markers that are characteristic of at least 2
PT cell types, useful in tissue transplantation, drug discovery, gene
PT therapy.
XX
PS Example 7; Page 75; 107pp; English.
XX
CC The specification describes a human embryo-derived (EBD) cell culture
CC that comprises cells which simultaneously express polypeptide or mRNA
CC markers that are characteristic of at least 2 different cell types. The
CC cell types are ectodermal, mesodermal, and/or endodermal cells. The
CC markers include nestin, vimentin, myf6, myosin light-chain 2 ventricular
CC isoform, flk1, alpha-1 fetoprotein and GATA-4. The EBD cells are useful
CC in cell culture, tissue transplantation, tissue engineering, drug
CC discovery and gene therapy. They are especially useful in transplantation
CC therapies for the treatment of Parkinson's disease, amyotrophic lateral
CC sclerosis, stroke, injury to motor neurons, including spinal cord injury,
CC and diabetes. Human EBD cells can be implanted into the central nervous
CC system for the treatment of disease or physical brain injury, such as
CC ischemia or chemical injury, as well as to treat diseases of cardiac,
CC skeletal or smooth muscles, liver, pancreas, eyes, vascular diseases, to
CC repopulate bone marrow, in organotypic co-culture, in the biosynthetic
CC production of macromolecules, and in the construction and testing of
CC human artificial chromosomes. AAH42612-85 represent PCR primers and
CC probes for markers of human cells. They were used to examine the mRNA
CC expression profiles of human cells
XX
SQ Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2025 TGGTAGGAGGCAAAGGTT 2042
||||||.||||||||||
Db 19 TGGTAGAGGGCAAAGGTT 2

RESULT 3623
ABN84466
ID ABN84466 standard; DNA; 20 BP.
XX
AC ABN84466;
XX
DT 21-OCT-2002 (first entry)
XX
DE Alpha-amylase-2A forward PCR primer.
XX
KW Alpha-amylase; enzyme; islet of Langerhans; endocrine; stem cell;
KW cell differentiation; diabetes; antidiabetic; cell therapy; PCR; primer;
KW ss.
XX
OS Mus sp.
XX
PN WO200259278-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002361.
XX
PR 24-JAN-2001; 2001US-0264107P.
PR 06-FEB-2001; 2001US-0266917P.
PR 18-OCT-2001; 2001US-0344548P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lumelsky NL, Blondel O, Mc Kay RD, Kim J;
XX
DR WPI; 2002-599773/64.
XX
PT Differentiating embryonic stem cells from endocrine cells, for treating a
PT pancreatic endocrine disorder, e.g. type I or type II diabetes, comprises
PT culturing endocrine cells in an expansion medium containing a growth
PT factor.
XX
PS Example 1; Page 42; 76pp; English.
XX

```
CC   The invention provides a method of differentiating embryonic stem cells
CC   to endocrine cells. The method involves generating embryoid bodies from a
CC   culture of undifferentiated embryonic stem cells, selecting endocrine
CC   precursor cells (EPCs), expanding the EPCs by culturing in an expansion
CC   medium that comprises a growth factor, and differentiating the expanded
CC   EPCs in a differentiation medium. The present sequence is a forward PCR
CC   primer for alpha-amylase-2A. Use with the primer given in ABN84467
CC   generates a product of 300 bp. A primer set (see ABN84454-71) was used in
CC   an example of the invention for RT-PCR analysis of endocrine pancreatic
CC   gene expression in mouse embryos at stages 1 and 5. The results suggested
CC   that the culture conditions used to generate pancreatic endocrine cells
CC   supported the differentiation of pancreatic cells. Pancreatic endocrine
CC   cells generated in vitro can be used as a model system to study the cells
CC   of the islets of Langerhans, to study the kinetics and pharmacology of
CC   insulin release, to study agents that affect insulin secretion, and for
CC   the development of artificial islet and artificial pancreas tissues for
CC   use in the treatment of pancreatic endocrine disorders, particularly type
CC   I or type II diabetes
XX
SQ   Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGTCACC 2334
              ||||||| |||||||||
Db          3 TTGTTGCACCTTGTCACC 20


RESULT 3624
ABA83519
ID   ABA83519 standard; DNA; 20 BP.
XX
AC   ABA83519;
XX
DT   08-FEB-2002  (first entry)
XX
DE   Human MP-1 antisense oligonucleotide SEQ ID NO 78.
XX
KW   Human; mouse; rat; antisense gene therapy; MP-1; MAP kinase Partner 1;
KW   antiinflammatory; cytostatic; antimicrobial; infection; tumour;
KW   phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone linkage, all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-MOE wings"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-MOE wings"
XX
PN   US6306606-B1.
XX
PD   23-OCT-2001.
XX
PF   22-NOV-2000; 2000US-00721822.
XX
PR   22-NOV-2000; 2000US-00721822.
XX
PA   (ISIS-) ISIS PHARM INC.
PA   (UYVI-) UNIV VIRGINIA.
XX
PI   Weber MJ,  Wyatt J,  Cowsert LM;
XX
DR   WPI; 2002-040199/05.
XX
PT   New antisense oligonucleotides for modulating the expression of MP-1 (MAP
PT   kinase partner 1), for preventing, delaying or treating infection,
PT   inflammation or tumor formation, especially in humans.
XX
PS   Claim 1; Col 41-42; 47pp; English.
XX
CC   The invention relates to an antisense compound (ABA83459-ABA83576) which
CC   is up to 30 nucleobases in length and that inhibits the expression of MP-
CC   1 (MAP kinase Partner 1) in cells or tissues comprising contacting the
CC   cells or tissues in vitro with the antisense compound so that expression
CC   of MP-1 is inhibited. The antisense compounds have potential
CC   antiinflammatory, cytostatic and antimicrobial activity. The antisense
CC   compounds are useful for diagnostics, therapeutics, prophylaxis or as
CC   research reagents or kits. The antisense oligonucleotides are useful in
CC   gene therapy for treating an animal, particularly a human, suspected of
CC   having or being prone to a disease or condition associated with the
CC   expression of MP-1. In particular, the antisense oligonucleotides are
CC   useful for preventing, delaying or treating infection, inflammation or
CC   tumour formation. The present sequence is that of a human MP-1 antisense
CC   oligonucleotide, comprising a chimeric oligonucleotide gapmer 20
CC   nucleotides in length, composed of a central gap region of ten 2'-
CC   deoxynucleotides flanked by five nucleotide 2'-MOE wings
XX
SQ   Sequence 20 BP; 5 A; 2 C; 3 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2379 GAGTGTACAGATTTTATT 2396
              || ||||| |||||||||
Db          1 GATTGTACTGATTTTATT 18


RESULT 3625
AAD31950
ID   AAD31950 standard; DNA; 20 BP.
XX
AC   AAD31950;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human microtubule associated protein 2C (MAP2C) DNA.
XX
KW   Microbial virulence factor; genetic predisposition; Alzheimer's disease;
KW   Parkinson's disease; schizophrenia; frontotemporal lobe dementia; human;
KW   hereditary multi-infarct dementia; primary X-linked mental retardation;
KW   dementia; myopathy; familial British dementia; psychiatric disorder;
KW   transgenic animal; microtubule associated protein 2C; MAP2C; enzyme; ds.
XX
OS   Homo sapiens.
XX
PN   WO200214546-A1.
XX
PD   21-FEB-2002.
XX
PF   15-FEB-2001; 2001WO-IB000189.
XX
PR   16-AUG-2000; 2000WO-IB001127.
XX
PA   (FRIT/) FRITZSCHE M.
XX
PI   Fritzsche M;
XX
DR   WPI; 2002-241910/29.
XX
PT   Use of DNA sequence having fragment of nucleic acid encoding putative
PT   microbial virulence factor useful for identification of disease e.g.
PT   Alzheimer's disease, caused by mutations or for genetic predisposition.
```

```
XX
PS   Example 1; Page 46; 52pp; English.
XX
CC   The present invention relates to the use of a DNA sequence comprising a
CC   fragment of a nucleic acid encoding a putative microbial virulence factor
CC   for the identification of a disease caused by mutations or for a genetic
CC   predisposition. The invention also relates to a method for identification
CC   of a disease which comprises detecting the presence of a mutation within
CC   a nucleic acid sequence of the fragment of virulence factor in a tissue-
CC   or blood sample of a subject, where the tissue sample is a foetal graft
CC   for neurotransplantation and where the sequence is inserted in the 3' UTR
CC   (untranslated region) of the gene and mutation is found in the
CC   polyadenylation signal of G1. The method is useful for identification of
CC   a disease caused by mutation or for their genetic predisposition where
CC   the disease is human disease which is from Alzheimer's disease,
CC   Parkinson's disease, schizophrenia, myopathy, other forms of dementias
CC   (frontotemporal lobe dementia, autosomal dominant Parkinson Lewy-Body
CC   dementia, hereditary multi-infarct dementia, familial British dementia,
CC   primary X-linked mental retardation) and where the human disease
CC   constitutes a predisposition or a genetic variation, the pathological
CC   manifestation of which is triggered by medicaments or drugs which is
CC   preferably cannabis, where the manifestation comprises any forms of
CC   dementia, schizophrenia or related psychiatric disorders. The invention
CC   also relates to transgenic animals (e.g. comprising a non-functional
CC   endogenous cannabinoid receptor (CB1) gene) which are useful for the
CC   identifying or screening of compounds that have an effect on the
CC   activity, expression or regulation of the translated protein (e.g. CB1
CC   protein). The present sequence is a DNA encoding human microtubule
CC   associated protein 2C (MAP2C) used in the exemplification of the
CC   invention
XX
SQ   Sequence 20 BP; 12 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1505 AAACACAGGAAATAAAAT 1522
              |||| ||| |||||||||
Db          1 AAACTCAGAAAATAAAAT 18


RESULT 3626
AAD31912
ID   AAD31912 standard; DNA; 20 BP.
XX
AC   AAD31912;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Borrelia burgdorferi microtubule associated protein 2C (MAP2C) DNA.
XX
KW   Microbial virulence factor; genetic predisposition; Alzheimer's disease;
KW   Parkinson's disease; schizophrenia; frontotemporal lobe dementia;
KW   hereditary multi-infarct dementia; primary X-linked mental retardation;
KW   dementia; myopathy; familial British dementia; psychiatric disorder;
KW   transgenic animal; microtubule associated protein 2C; MAP2C; ds.
XX
OS   Borrelia burgdorferi.
XX
PN   WO200214546-A1.
XX
PD   21-FEB-2002.
XX
PF   15-FEB-2001; 2001WO-IB000189.
XX
PR   16-AUG-2000; 2000WO-IB001127.
XX
PA   (FRIT/) FRITZSCHE M.
XX
PI   Fritzsche M;
XX
DR   WPI; 2002-241910/29.
XX
PT   Use of DNA sequence having fragment of nucleic acid encoding putative
PT   microbial virulence factor useful for identification of disease e.g.
PT   Alzheimer's disease, caused by mutations or for genetic predisposition.
XX
PS   Claim 6; Page 28; 52pp; English.
XX
CC   The present invention relates to the use of a DNA sequence comprising a
CC   fragment of a nucleic acid encoding a putative microbial virulence factor
CC   for the identification of a disease caused by mutations or for a genetic
CC   predisposition. The invention also relates to a method for identification
CC   of a disease which comprises detecting the presence of a mutation within
CC   a nucleic acid sequence of the fragment of virulence factor in a tissue-
CC   or blood sample of a subject, where the tissue sample is a foetal graft
CC   for neurotransplantation and where the sequence is inserted in the 3' UTR
CC   (untranslated region) of the gene and mutation is found in the
CC   polyadenylation signal of G1. The method is useful for identification of
CC   a disease caused by mutation or for their genetic predisposition where
CC   the disease is human disease which is from Alzheimer's disease,
CC   Parkinson's disease, schizophrenia, myopathy, other forms of dementias
CC   (frontotemporal lobe dementia, autosomal dominant Parkinson Lewy-Body
CC   dementia, hereditary multi-infarct dementia, familial British dementia,
CC   primary X-linked mental retardation) and where the human disease
CC   constitutes a predisposition or a genetic variation, the pathological
CC   manifestation of which is triggered by medicaments or drugs which is
CC   preferably cannabis, where the manifestation comprises any forms of
CC   dementia, schizophrenia or related psychiatric disorders. The invention
CC   also relates to transgenic animals (e.g. comprising a non-functional
CC   endogenous cannabinoid receptor (CB1) gene) which are useful for the
CC   identifying or screening of compounds that have an effect on the
CC   activity, expression or regulation of the translated protein (e.g. CB1
CC   protein). The present sequence is a DNA encoding Borrelia burgdorferi
CC   microtubule associated protein 2C (MAP2C), virulence factor protein. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 20 BP; 12 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1505 AAACACAGGAAATAAAAT 1522
              |||| ||| |||||||||
Db          1 AAACTCAGAAAATAAAAT 18


RESULT 3627
ABS53426/c
ID   ABS53426 standard; DNA; 20 BP.
XX
AC   ABS53426;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human Jun-B PCR primer #2.
XX
KW   Human; primer; PCR; ss; nuclear mRNA extraction; Jun-B; gene chip;
KW   microarray.
XX
OS   Homo sapiens.
XX
PN   WO200266637-A2.
XX
PD   29-AUG-2002.
XX
PF   25-OCT-2001; 2001WO-US049498.
XX
PR   31-OCT-2000; 2000US-0244672P.
PR   26-JUL-2001; 2001US-0308038P.
XX
PA   (HITB ) HITACHI CHEM RES CENT INC.
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (HITA ) HITACHI LTD.
```

XX
PI Mitsuhashi M;
XX
DR WPI; 2002-674939/72.
XX
PT Detecting gene expression in a cell for analysis of gene chips or for
PT producing cDNA libraries, comprises permeabilizing the cells that are
PT captured on a filter or membrane, dissolving the isolated nuclei and
PT recovering the mRNA.
XX
PS Example 10; Page 14; 27pp; English.
XX
CC This invention relates to a novel method for isolating nuclear RNA and
CC detecting gene expression in a cell. The method comprises treating the
CC cells that are captured on a membrane with a cell membrane permeation
CC solution, such as NP-40, to increase their cell membrane permeability,
CC dissolving the nuclei after washing the cytoplasm and recovering the
CC mRNA. The method is useful for analysis of gene chips and microarrays,
CC diagnostic analysis by PCR, production of cDNA libraries, Northern blots
CC or differential display or subtraction library techniques. It is also
CC useful for detecting newly synthesised RNA without contamination from RNA
CC that is being degraded in the cytoplasm. The method of the invention
CC enables the treatment of a large number of specimens with only 2-3
CC minutes extra time required. Further, the method can be incorporated into
CC an automated system. The present sequence represents a human Jun-B mRNA
CC specific PCR primer used to quantitate UVC induced Jun-B gene expression
CC in an example of the method of the invention
XX
SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 775 CCCTCTGAACCTCCCCTG 792
|| ||||||| |||||||
Db 19 CCTTCTGAACGTCCCCTG 2

RESULT 3628
AAS99076/c
ID AAS99076 standard; DNA; 20 BP.
XX
AC AAS99076;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human prostate cancer predisposing gene (HPC2) PCR primer #72.
XX
KW Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;
KW gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
KW sequencing primer; PCR primer.
XX
OS Homo sapiens.
XX
PN WO200185911-A2.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014602.
XX
PR 05-MAY-2000; 2000US-00564805.
XX
PA (MYRI-) MYRIAD GENETICS INC.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX
DR WPI; 2002-066599/09.
XX
PT Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
PT for prostate cancer, is useful in gene therapy techniques to restore HPC2
PT normal levels by which neoplastic growth is suppressed in recipient cell.
XX
PS Example 8; Page 74; 239pp; English.
XX
CC The invention relates to a human prostate cancer predisposing gene coding
CC for an HPC2 polypeptide. The DNA and protein sequences are useful as
CC diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in
CC a suspected mutant HPC2 allele by comparing the sequence of the suspected
CC mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also
CC useful for detecting an alteration in HPC2, where the alteration is
CC associated with cancer in a human. The method involves analysing an HPC2
CC gene or an HPC2 gene expression product from a tissue of the human. The
CC HPC2 gene is useful as a marker for prostate cancer and can be used in
CC gene therapy techniques to suppress neoplastic growth of recipient cells
CC which carry the mutant HPC2 allele. The sequences represent primers used
CC in the methods of the invention, cDNA encoding human and mouse HPC2 and
CC cDNA encoding HPC2 paralogues and orthologues
XX
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 894 CAGTGGCTGAAGTACAGA 911
|| ||||||||| |||||
Db 19 CATTGGCTGAAGGACAGA 2

RESULT 3629
AAS99072/c
ID AAS99072 standard; DNA; 20 BP.
XX
AC AAS99072;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human prostate cancer predisposing gene (HPC2) PCR primer #68.
XX
KW Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;
KW gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
KW sequencing primer; PCR primer.
XX
OS Homo sapiens.
XX
PN WO200185911-A2.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014602.
XX
PR 05-MAY-2000; 2000US-00564805.
XX
PA (MYRI-) MYRIAD GENETICS INC.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX
DR WPI; 2002-066599/09.
XX
PT Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
PT for prostate cancer, is useful in gene therapy techniques to restore HPC2
PT normal levels by which neoplastic growth is suppressed in recipient cell.
XX
PS Example 8; Page 74; 239pp; English.
XX
CC The invention relates to a human prostate cancer predisposing gene coding
CC for an HPC2 polypeptide. The DNA and protein sequences are useful as
CC diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in
CC a suspected mutant HPC2 allele by comparing the sequence of the suspected
CC mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also
CC useful for detecting an alteration in HPC2, where the alteration is
CC associated with cancer in a human. The method involves analysing an HPC2
CC gene or an HPC2 gene expression product from a tissue of the human. The

```
CC   HPC2 gene is useful as a marker for prostate cancer and can be used in
CC   gene therapy techniques to suppress neoplastic growth of recipient cells
CC   which carry the mutant HPC2 allele. The sequences represent primers used
CC   in the methods of the invention, cDNA encoding human and mouse HPC2 and
CC   cDNA encoding HPC2 paralogues and orthologues
XX
SQ   Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        894 CAGTGGCTGAAGTACAGA 911
              || |||||||||| |||||
Db         19 CATTGGCTGAAGGACAGA 2


RESULT 3630
ABN81300
ID   ABN81300 standard; DNA; 20 BP.
XX
AC   ABN81300;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Ancyclobacter formate dehydrogenase related PCR primer SEQ ID NO 7.
XX
KW   Ancylobacter; formate dehydrogenase; enzyme; formic acid; industrial;
KW   PCR; primer; ss.
XX
OS   Ancylobacter aquaticus.
XX
PN   WO200246427-A1.
XX
PD   13-JUN-2002.
XX
PF   04-DEC-2001; 2001WO-JP010569.
XX
PR   04-DEC-2000; 2000JP-00368838.
XX
PA   (KANF ) KANEKA CORP.
XX
PI   Takaoka Y,  Nanba H;
XX
DR   WPI; 2002-500448/53.
XX
PT   Soil microorganism-originated formate dehydrogenase with e.g. specific
PT   activity, broad and stable functioning temperature and pH ranges, which
PT   is applicable in industrial production of formic acid.
XX
PS   Example 4; Page 46; 51pp; Japanese.
XX
CC   The invention relates to a formate dehydrogenase (ABB77565) with high
CC   specific activity, a small Km value for formic acid and NAD, being stable
CC   over a broad temperature range and a broad pH range, having a broad
CC   functioning pH and temperature range and being suitable for industrial
CC   production of formic acid. The dehydrogenase has specific activity, small
CC   Km values for formic acid and NAD, which produces only formic acid
CC   without accumulation of carbon dioxide in the system. The present
CC   sequence is that of a formate dehydrogenase related PCR primer, useful in
CC   examples of the invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1084 AGAAGGTGAAGCTGTTCA 1101
              ||| | ||||||||||||
Db          2 AGACGCTGAAGCTGTTCA 19


RESULT 3631
ABZ30368/c
ID   ABZ30368 standard; DNA; 20 BP.
XX
AC   ABZ30368;
XX
DT   30-JAN-2003  (first entry)
XX
DE   Candida albicans GRACE strain PCR primer SEQ ID NO 4519.
XX
KW   Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW   signal transduction; DNA replication; cell division; growth;
KW   proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS   Candida albicans.
XX
PN   WO200253728-A2.
XX
PD   11-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-US049486.
XX
PR   29-DEC-2000; 2000US-0259128P.
PR   20-FEB-2001; 2001US-00792024.
PR   22-AUG-2001; 2001US-0314050P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Roemer T,  Jiang B,  Boone C,  Bussey H,  Ohlsen KL;
XX
DR   WPI; 2002-566694/60.
XX
PT   Constructing strains for identifying gene products as effective targets
PT   for therapeutic intervention, by inactivating in the strain one allele of
PT   a gene and placing other allele of the gene under conditional expression.
XX
PS   Claim 36; SEQ ID NO 4519; 167pp + Sequence Listing; English.
XX
CC   The invention relates to constructing (M1) a strain of diploid fungal
CC   cells in which both alleles of a gene are modified, comprising modifying
CC   one allele by insertion or replacement by a cassette having an
CC   expressible selectable marker and modifying other allele by
CC   recombination, of a promoter replacement fragment with a heterologous
CC   promoter, so that expression of the second allele is regulated by the
CC   promoter. (M1) is useful for constructing a strain of diploid fungal
CC   cells in which both alleles of a gene are modified. The diploid fungal
CC   cells having both alleles modified are useful for identifying a gene that
CC   is essential to the survival or growth of a fungus, a gene that
CC   contributes to the virulence and/or pathogenicity of a fungus, a gene
CC   that contributes to the resistance of a diploid fungus to an antifungal
CC   agent, an antifungal agent that inhibits the growth of a diploid fungus
CC   and for identifying a therapeutic agent for treatment of a mammalian
CC   disease. (M1) is useful for identifying a compound which modulates the
CC   activity of a gene product, preferably enzymatic activity, carbon
CC   compound catabolism, biosynthetic, transporter, transcriptional,
CC   translational, signal transduction, DNA replication and cell division
CC   activity. The method is useful for identifying a compound having the
CC   ability to inhibit growth or proliferation of C. albicans cells and for
CC   treating infection by C. albicans. The present sequence is that of a PCR
CC   primer used in the method of the invention. Note: The sequence data for
CC   this patent is not represented in the printed specification but is based
CC   on sequence information supplied to Derwent by the European Patent Office
XX
SQ   Sequence 20 BP; 3 A; 1 C; 12 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        533 GGCCTACTGCCCCACCTC 550
              | |||||| |||||||||
Db         20 GACCTACTCCCCCACCTC 3
```

```
RESULT 3632
AAD44835
ID   AAD44835 standard; DNA; 20 BP.
XX
AC   AAD44835;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Human raf kinase related antisense oligonucleotide #14.
XX
KW   Raf kinase; hyperproliferation; neovascularisation; ocular angiogenesis;
KW   therapy; cancer; cytostatic; anti-angiogenic; vascular; ophthalmological;
KW   antisense; ss.
XX
OS   Unidentified.
XX
PN   US6410518-B1.
XX
PD   25-JUN-2002.
XX
PF   18-FEB-2000; 2000US-00506073.
XX
PR   31-MAY-1994;   94US-00250856.
PR   31-MAY-1995;   95WO-US007111.
PR   26-NOV-1996;   96US-00756806.
PR   07-JUL-1997;   97US-00888982.
PR   06-JUL-1998;   98WO-US013961.
PR   28-AUG-1998;   98US-00143214.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP;
XX
DR   WPI; 2002-597918/64.
XX
PT   Treating cancer, angiogenesis or neovascularization by administering
PT   antisense oligonucleotides targeted to human raf sequences.
XX
PS   Disclosure; Col 59; 41pp; English.
XX
CC   The present invention relates to novel antisense oligonucleotides which
CC   are targetted to nucleic acids encoding human raf proteins and capable of
CC   inhibiting raf expression. The invention also relates to methods of
CC   inhibiting hyperproliferation of cells which involves contacting the
CC   hyperproliferating cells with a therapeutically effective amount of an
CC   oligonucleotide of the invention. The method is useful for treating
CC   cancer, angiogenesis or neovascularisation, especially ocular
CC   angiogenesis or neovascularisation. The present DNA sequence is human raf
CC   kinase related antisense oligonucleotide
XX
SQ   Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        505 GCTGCCCTCGCACCACGG 522
              |||||||||  ||||||  |
Db          3 GCTGCCCTCACACCACTG 20


RESULT 3633
ABI93269
ID   ABI93269 standard; DNA; 20 BP.
XX
AC   ABI93269;
XX
DT   15-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#356 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency;.Turner Syndrome; obesity; cancer;
KW   oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US010958.
XX
PR   14-APR-2000; 2000US-0197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch.
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention
XX
SQ   Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         26 GTGACCCGGACAGCAAGG 43
              ||||||  ||||||||  ||
Db          3 GTGACCAGGACAGCACGG 20


RESULT 3634
ABI96918
ID   ABI96918 standard; DNA; 20 BP.
XX
AC   ABI96918;
XX
DT   16-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#4005 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
```

KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1046 CGGAAAGCCGCTCATGTG 1063
||||||| |||| ||||
Db 2 CGGAAAGCAGCTCGTGTG 19

RESULT 3635
ABK47115/c
ID ABK47115 standard; DNA; 20 BP.
XX
AC ABK47115;
XX
DT 05-JUN-2002 (first entry)
XX
DE Mouse R1-OS-B1-B2 forward PCR primer.
XX
KW PCR; primer; ss; nucleic acid library; immune response; asthma;
KW airway hyperresponsiveness; bronchoalveolar manifestation;
KW signature sequence; SS; chronic obstructive pulmonary disease; COPD;
KW allergic disease; rhinitis; atopic dermatitis; urticaria;
KW autoimmune disease; multiple sclerosis; inflammatory bowel disease;
KW allograft rejection; infectious disease.
XX
OS Mus sp.
XX
PN WO200214366-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-NL000610.
XX
PR 16-AUG-2000; 2000EP-00202867.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Groot PC, Van Bergenhenegouwen BJ, Van Oosterhout AJM;
XX
DR WPI; 2002-241888/29.
XX
PT Nucleic acid library comprising genes which are capable of initiation,
PT progression and suppression of an immune response, especially an immune
PT response observed with airway hyper-responsiveness of asthma.
XX
PS Example 8; Page 76; 120pp; English.
XX
CC The invention relates to a nucleic acid library comprising genes or their
CC fragments which are capable of modulating an immune response observed
CC with airway hyperresponsiveness and/or bronchoalveolar manifestations of
CC asthma. Also included are a method for modulating an immune response of
CC an individual comprising modulating a gene comprising a nucleic acid at
CC least functionally equivalent to a nucleic acid identifiable by a
CC signature sequence (SS) given in the specification such as R1-SO-R1-A11,
CC StO1-A10, SvO2-1-C11, StO1-A12, and R1-SO-R1-B7, a substance (for use as
CC a medicament) capable of modulating a gene comprising a nucleic acid at
CC least functionally equivalent to a nucleic acid identifiable by SS and
CC the use of a proteinaceous substance derived from a nucleic acid at least
CC functionally equivalent to a nucleic acid identifiable by SS for the
CC production of an antagonist (for use as a medicament) against the
CC substance. The antagonist and substance are useful for the treatment of
CC an immune response observed with airway hyperresponsiveness and/or
CC bronchoalveolar manifestations of asthma. The method is useful for
CC modulating the above immune response, where the gene encodes a gene
CC product capable of modulating the immune response. The substance is
CC useful for treating an immune response, particularly asthma, chronic
CC obstructive pulmonary disease (COPD), allergic diseases (rhinitis, atopic
CC dermatitis, urticaria), autoimmune diseases (e.g. multiple sclerosis),
CC inflammatory bowel disease, allograft rejection and infectious disease.
CC The present sequence is a PCR primer used to amplify and/or characterise
CC a mouse signature sequence of the invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1290 CCAGCAGGCTCGCCCCAG 1307
|||||||||| || |||
Db 18 CCAGCAGGCTCCCCTCAG 1

RESULT 3636
ABZ93604/c
ID ABZ93604 standard; DNA; 20 BP.
XX
AC ABZ93604;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

```
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 8846; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 12 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1544 GAGTAGGGAAGGAACAGG 1561
              | ||||||||||||  |||
Db         20 GGGTAGGGAAGGAAGAGG 3


RESULT 3637
ABZ89084
ID   ABZ89084 standard; DNA; 20 BP.
XX
AC   ABZ89084;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
```

```
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4326; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              || ||  ||||||||||||
Db          3 GAGAAGAAAAAAAAAAAA 20


RESULT 3638
ABZ90035/c
ID   ABZ90035 standard; DNA; 20 BP.
XX
AC   ABZ90035;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
```

XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5277; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1983 AAAGAAAAGTGTGTATCT 2000
||||||| |||||| |||
Db 18 AAAGAAATGTGTGTTTCT 1

RESULT 3639
ABZ90375
ID ABZ90375 standard; DNA; 20 BP.
XX
AC ABZ90375;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5617; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||| |||||| |||||||
Db 1 AAACAAAAAACAAAAAAA 18

RESULT 3640
ABZ90375/c
ID ABZ90375 standard; DNA; 20 BP.
XX
AC ABZ90375;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.

```
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
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PA   (EPIG-) EPIGENESIS PHARM INC.
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PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
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PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5617; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
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CC   use in antisense gene therapy. The composition is useful for treating or
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CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 16 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||| |||||| |||
Db         18 TTTTTTTGTTTTTTGTTT 1


RESULT 3641
ABZ99051
ID   ABZ99051 standard; DNA; 20 BP.
XX
AC   ABZ99051;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human PDE4C oligonucleotide sequence.
```

```
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 14293; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||| |||||| |
Db          1 TTTTTTTTTCTTTTTTGA 18


RESULT 3642
ABZ99051/c
ID   ABZ99051 standard; DNA; 20 BP.
XX
AC   ABZ99051;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human PDE4C oligonucleotide sequence.
```

```
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
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PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 14293; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
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CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              | |||||| |||||||||
Db         18 TCAAAAAAGAAAAAAAAA 1


RESULT 3643
ABZ86258
ID   ABZ86258 standard; DNA; 20 BP.
XX
AC   ABZ86258;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
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PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 1500; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1555 GAACAGGACTGCAAAAAT 1572
              ||||||||||  |||||
Db          2 GAACAGGACTGACAAAAT 19


RESULT 3644
ADA66499/c
ID   ADA66499 standard; DNA; 20 BP.
XX
AC   ADA66499;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Transforming growth factor-beta 3 antisense oligonucleotide, SEQ ID 58.
```

```
XX
KW   Cytostatic; antirheumatic; antiarthritic; gynecological;
KW   antiarteriosclerotic; Transforming Growth Factor beta-3; TGF beta-3;
KW   hyperproliferative disorder; cancers; atherosclerosis;
KW   rheumatoid arthritis; preeclampsia; fibrosis; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 5 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2003008544-A2.
XX
PD   30-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-US022423.
XX
PR   14-JUL-2001; 2001US-00906158.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Freier SM;
XX
DR   WPI; 2003-229569/22.
XX
PT   Novel antisense compound which is targeted to nucleic acid encoding
PT   transforming growth factor beta-3, and inhibits expression of TGF-beta 3,
PT   useful for treating a condition associated with TGF-beta 3, e.g. cancer.
XX
PS   Claim 3; Page 87; 154pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADA66459-
CC   ADA66609), which inhibit Transforming Growth Factor (TGF) beta-3
CC   expression. The oligonucleotides are useful for inhibiting the expression
CC   of TGF-beta3 in cells or tissues, and for treating an animal having a
CC   disease condition associated with TGF-beta3, e.g. a hyperproliferative
CC   disorder such as cancers of lung, liver, colon, oesophagus, pancreas,
CC   breast, skin or haematopoietic, atherosclerosis, rheumatoid arthritis,
CC   preeclampsia and fibrosis.
XX
SQ   Sequence 20 BP; 6 A; 4 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        835 CTTCTGCTCAGTCCCTGG 852
              ||||||||||| |||| |
Db         20 CTTCTGCTCAGGCCCTTG 3


RESULT 3645
ABV72400/c
ID   ABV72400 standard; DNA; 20 BP.
XX
AC   ABV72400;
XX
DT   29-JAN-2003  (first entry)
XX
DE   PCR primer used to amplify Human Artemis gene exon 6.
XX
KW   Human; Artemis gene; DNA repair factor; metallo beta-lactamase; RS-SCID;
KW   chromosome 10; severe combined immunodeficiency; SCIDl; cancer; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200277228-A1.
XX
PD   03-OCT-2002.
XX
PF   22-MAR-2001; 2001WO-IB000546.
XX
PR   22-MAR-2001; 2001WO-IB000546.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   De Villartay J,  Moshous D,  Fischer A;
XX
DR   WPI; 2003-029937/02.
XX
PT   New isolated nucleic acid molecule of the Artemis gene, useful for
PT   diagnosing or treating SCID or cancer.
XX
PS   Example 1; Page 65; 71pp; English.
XX
CC   PCR primers ABV72389-ABV72416 were used to amplify exons of the human
CC   Artemis gene. This gene encodes a V(D)J recombination and/or DNA repair
CC   factor that belongs to the metallo beta-lactamase superfamily, and whose
CC   mutations give rise to the human RS-SCID condition. The gene is localised
CC   to chromosome 10. The Artemis gene or its nucleic acid is useful for
CC   diagnosing or treating severe combined immunodeficiencies (SCIDs) or
CC   cancer
XX
SQ   Sequence 20 BP; 9 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2480 TTTTAATGGTGATGGGGT 2497
              ||||| ||| ||||||||
Db         20 TTTTAGTGGAGATGGGGT 3


RESULT 3646
ACD42151
ID   ACD42151 standard; DNA; 20 BP.
XX
AC   ACD42151;
XX
DT   05-SEP-2003  (first entry)
XX
DE   Human raf-associated antisense oligonucleotide #13.
XX
KW   Antisense; c-raf; a-raf; b-raf; protein kinase; cancer; ss;
KW   signal transduction; cell proliferation; lung carcinoma; cytostatic;
KW   antisense gene therapy; chemotherapeutic agent; angiogenesis;
KW   hyperproliferative condition; neovascularisation; ocular angiogenesis.
XX
OS   Unidentified.
XX
PN   US2003032607-A1.
XX
PD   13-FEB-2003.
XX
PF   25-JAN-2002; 2002US-00057550.
XX
PR   31-MAY-1994;   94US-00250856.
PR   31-MAY-1995;   95WO-US007111.
PR   26-NOV-1996;   96US-00756806.
PR   07-JUL-1997;   97US-00888982.
PR   06-JUL-1998;   98WO-US013961.
PR   28-AUG-1998;   98US-00143214.
PR   18-FEB-2000; 2000US-00506073.
XX
PA   (MONI/) MONIA B P.
XX
PI   Monia BP;
XX
```

```
DR   WPI; 2003-503332/47.
XX
PT   Novel antisense oligonucleotide which is targeted to mRNA encoding human
PT   raf and which is capable of inhibiting raf expression, useful for
PT   treating or preventing hyperproliferative conditions such as cancer.
XX
PS   Disclosure; Page 31; 42pp; English.
XX
CC   The invention relates to an oligonucleotide 8-50 nucleotides in length
CC   which is targeted to mRNA encoding human c-raf, a-raf or b-raf (raf is a
CC   protein kinase playing a regulatory role in signal transduction,
CC   regulating cell proliferation and has been implicated in lung carcinoma),
CC   and which is capable of inhibiting raf expression. Also included is a
CC   composition comprising the oligonucleotide and a pharmaceutically
CC   acceptable carrier. The antisense oligonucleotide is useful for
CC   inhibiting the expression of human raf in human cells or tissues, by
CC   contacting the human cells or tissues with the oligo. The oligo. is also
CC   is useful for treating or preventing a disease or condition associated
CC   with the expression of raf by administering it in combination with a
CC   chemotherapeutic agent to a human or cells of the human, where the
CC   expression of raf is abnormal expression, and the condition is a
CC   hyperproliferative condition such as cancer, angiogenesis or
CC   neovascularisation (preferably ocular angiogenesis or
CC   neovascularisation). The oligo. is also useful for inhibiting
CC   hyperproliferation of cells. The oligos. are also useful as tools, for
CC   example for detecting and determining the role of raf expression in
CC   various cell functions and physiological processes and conditions and for
CC   diagnosing conditions associated with raf expression and for research
CC   purposes. The present sequence is an antisense oligonucleotide included
CC   in the sequence listing but not mentioned elsewhere in the specification
XX
SQ   Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        505 GCTGCCCTCGCACCACGG 522
              ||||||||| |||||| |
Db          3 GCTGCCCTCACACCACTG 20


RESULT 3647
ABT34147
ID   ABT34147 standard; DNA; 20 BP.
XX
AC   ABT34147;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human short heterodimer partner-1 expression oligo SEQ ID No 22.
XX
KW   Antiarteriosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
KW   antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
KW   short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
KW   cardiovascular disease; infection; inflammation; tumour formation; human;
KW   antisense; ds.
XX
OS   Unidentified.
XX
PN   WO2003012033-A2.
XX
PD   13-FEB-2003.
XX
PF   17-JUL-2002; 2002WO-US023245.
XX
PR   31-JUL-2001; 2001US-00919197.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-248161/24.
XX
PT   New antisense oligonucleotide targeted to a nucleic acid encoding short
PT   heterodimer partner-1, useful for treating diseases involving abnormal
PT   lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
PT   diseases.
XX
PS   Claim 3; Page 93; 121pp; English.
XX
CC   The invention relates to a novel compound of 8 - 50 nucleobases in length
CC   targeted to a nucleic acid molecule encoding a short heterodimer partner-
CC   1. The novel compound specifically hybridizes with a nucleic acid
CC   molecule encoding the short heterodimer partner-1, and inhibits the
CC   expression of the nucleic acid molecule. The compound, and a composition
CC   comprising it are useful for treating a disease or condition associated
CC   with the short heterodimer partner-1, particularly a condition involving
CC   abnormal lipid or cholesterol metabolism such as atherosclerosis or a
CC   cardiovascular disease. They are also useful in research and diagnostics
CC   for modulating the expression of short heterodimer partner-1. They can
CC   also be useful prophylactically in preventing or delaying infection,
CC   inflammation or tumour formation. This polynucleotide sequence represents
CC   a human antisense oligo relating to the heterodimer partner-1 of the
CC   invention
XX
SQ   Sequence 20 BP; 4 A; 10 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        432 CCCTGCACCAGCCGGCGC 449
              ||||||| |||||| |||
Db          3 CCCTGCAGCAGCCGCCGC 20


RESULT 3648
ABZ68360
ID   ABZ68360 standard; DNA; 20 BP.
XX
AC   ABZ68360;
XX
DT   22-APR-2003  (first entry)
XX
DE   Primer XpYpB2 used for determining telomere length.
XX
KW   Telomere; cancer; age; telomerase; male infertility; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003000927-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-GB002855.
XX
PR   23-JUN-2001; 2001GB-00015451.
PR   21-SEP-2001; 2001GB-00022755.
XX
PA   (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
PI   Baird DM;
XX
DR   WPI; 2003-175294/17.
XX
PT   Determining telomere length of mammalian chromosomal DNA by annealing and
PT   covalently binding telorettes, useful in assessing a potential anti-
PT   cancer treatment and/or assessing, treating or diagnosing male
PT   infertility.
XX
PS   Claim 23; Page 36; 50pp; English.
XX
CC   The present sequence represents a primer, which is used in the method of
CC   the invention for determining telomere length. The method comprises
CC   annealing the 3' end of a single-stranded oligonucleotide to a single-
```

```
CC   stranded overhang comprising TTAGGG repeat sequences, and covalently
CC   binding the oligonucleotide to the 5' end of the C-rich telomeric strand
CC   forming a ligation product. This ligation product is amplified to form a
CC   primer extension product, whose length is then detected. The method is
CC   useful in assessing potential anti-cancer treatments and cancer-related
CC   procedures. It can also be used in assessing telomere dynamics with age,
CC   effect of modulating telomerase activity, and in assessing, treating or
CC   diagnosing male infertility
XX
SQ   Sequence 20 BP; 6 A; 4 C; 5 G; 4 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1801 TCTGAAAGTGGTGCTATAAG 1820
              ||||||||||| |:|| ||
Db          1 TCTGAAAGTGGACCWATCAG 20


RESULT 3649
ACC70832
ID   ACC70832 standard; DNA; 20 BP.
XX
AC   ACC70832;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Thiobacillus halogen-tolerant formate dehydrogenase PCR primer #4.
XX
KW   Halogen-tolerant formate dehydrogenase; enzyme; PCR; primer; ss.
XX
OS   Thiobacillus sp.
XX
PN   WO2003031626-A1.
XX
PD   17-APR-2003.
XX
PF   09-OCT-2002; 2002WO-JP010460.
XX
PR   09-OCT-2001; 2001JP-00312043.
XX
PA   (KANF ) KANEKA CORP.
XX
PI   Nanba H,  Takaoka Y;
XX
DR   WPI; 2003-363368/34.
XX
PT   New halogen-tolerant formate dehydrogenase, useful as enzyme for
PT   regeneration of coenzyme in enzymatic reductions, is derived from
PT   Thiobacillus.
XX
PS   Example 4; Page 54; 102pp; Japanese.
XX
CC   The present invention relates to a novel halogen-tolerant formate
CC   dehydrogenase (ABR56300) from Thiobacillus sp. The enzyme is useful in
CC   industrial scale batch or continuous enzymatic reactions, including those
CC   using immobilised enzyme or a membrane reactor. In particular, the enzyme
CC   is efficient for the regeneration of coenzyme in enzymatic reductions,
CC   especially of alpha-haloketones such as ethyl 4-chloroacetoacetate, (1S)-
CC   3-chloro-2-oxo-1-benzylpropylcarbamic acid tert-butyl ester, 1-
CC   (benzoyloxy)-3-chloro-2-propanone and 2-chloroacetophenone. The present
CC   sequence is a PCR primer, which was used in an example from the invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1084 AGAAGGTGAAGCTGTTCA 1101
              ||| | ||||||||||||
Db          2 AGACGCTGAAGCTGTTCA 19


RESULT 3650
ACC47022/c
ID   ACC47022 standard; DNA; 20 BP.
XX
AC   ACC47022;
XX
DT   05-JUN-2003  (first entry)
XX
DE   Mouse phospholipase A2 antisense oligonucleotide SEQ ID NO:119.
XX
KW   Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW   phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW   antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW   psoriasis; diabetes; ss.
XX
OS   Mus musculus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN   WO200297133-A1.
XX
PD   05-DEC-2002.
XX
PF   21-MAY-2002; 2002WO-US016135.
XX
PR   25-MAY-2001; 2001US-00865866.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Wyatt JR;
XX
DR   WPI; 2003-140495/13.
XX
PT   New compound that hybridizes with and inhibits the expression of
PT   Phospholipase A2, group IIA, useful for preparing a composition for
PT   treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
PS   Example 15; Page 90; 135pp; English.
XX
CC   The present invention describes a compound (I) comprising 8-50
CC   nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC   3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC   A2, group IIA (synovial), where the compound specifically hybridises with
CC   and inhibits the expression of phospholipase A2, group IIA (synovial).
CC   Also described: (1) a composition comprising the compound and a carrier
CC   or diluent; (2) a method of inhibiting the expression of phospholipase
CC   A2, group IIA in cells or tissues; and (3) a method of treating an animal
CC   having a disease or condition associated with phospholipase A2, group IIA
CC   (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
CC   antipsoriatic activities, and can be used in vaccines and in gene
CC   therapy. The compound (I) can be used for preparing a composition for
CC   treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC   present sequence represents a mouse phospholipase A2 group IIA (synovial)
CC   chimeric phosphorothioate antisense oligonucleotide, which is used in an
CC   example from the present invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;
```

```
  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1482 ACAAAACCCTGGAGAAAA 1499
              |||| | ||||||||||
Db         19 ACAAGAGCCTGGAGAAAA 2


RESULT 3651
AAD47544/c
ID   AAD47544 standard; DNA; 20 BP.
XX
AC   AAD47544;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human Artemis exon 6 amplifying PCR primer, Ex6R1.
XX
KW   Human; ARTEMIS protein; V(D)J recombination; DNA repair; gene therapy;
KW   severe combined immunodeficiency; SCID; cancer; exon 6; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200277026-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-IB001737.
XX
PR   22-MAR-2001; 2001WO-IB000546.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   De Villartay J,  Moshous D,  Fischer A;
XX
DR   WPI; 2003-018886/01.
XX
PT   New ARTEMIS nucleic acid coding for a protein involved in V(D)J
PT   recombination and/or DNA repair, useful for treating and diagnosing
PT   severe combined immunodeficiencies (SCID) or cancer.
XX
PS   Example 1; Page 68; 71pp; English.
XX
CC   The invention relates to an Artemis nucleic acid coding for a protein
CC   involved in V(D)J recombination and/or DNA repair. Sequences of the
CC   invention are useful for treating severe combined immunodeficiencies
CC   (SCID) or cancer. They are also useful for diagnosing a patient,
CC   including a prenatal diagnosis with SCID, a predisposition to cancer, an
CC   immune deficiency or a carriage of a mutation increasing the risk of
CC   progeny to have such a disease. Peptides of the invention are used for
CC   preparing antibodies. The invention is useful in gene therapy. The
CC   present sequence is a PCR primer used to amplify human Artemis exon 6 DNA
XX
SQ   Sequence 20 BP; 9 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2480 TTTTAATGGTGATGGGGT 2497
              ||||| ||| ||||||||
Db         20 TTTTAGTGGAGATGGGGT 3


RESULT 3652
AAD55496/c
ID   AAD55496 standard; DNA; 20 BP.
XX
AC   AAD55496;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human FGFR-3 antisense oligonucleotide, ISIS #125202.
XX
KW   Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
KW   developmental disorder; hyperproliferative disorder; antisense therapy;
KW   FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidine residues
FT                    are 5-methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2 -methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2003023004-A2.
XX
PD   20-MAR-2003.
XX
PF   06-SEP-2002; 2002WO-US028549.
XX
PR   10-SEP-2001; 2001US-00953047.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Wyatt JR;
XX
DR   WPI; 2003-313244/30.
XX
PT   Novel compound targeted to a nucleic acid molecule encoding fibroblast
PT   growth factor receptor 3, useful for inhibiting the expression of the
PT   receptor and for treating an animal having cancer or developmental
PT   disorder.
XX
PS   Claim 3; Page 79; 120pp; English.
XX
CC   The invention relates to antisense compounds targetted to a nucleic acid
CC   molecule encoding fibroblast growth factor (FGF) receptor 3 (also known
CC   as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense
CC   compounds of the invention are useful for treating diseases or conditions
CC   associated with FGFR-3 such as developmental disorders or
CC   hyperproliferative disorders, especially cancer of colorectal, bladder,
CC   bone, lung, cervical, breast or skin. They are useful as research
CC   reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools
CC   in differential and/or combinatorial analyses to elucidate expression
CC   patterns of a portion of the genes expressed within cells and tissues.
CC   They are also useful in antisense therapy. The present sequence is an
CC   antisense oligonucleotide targetted to human FGFR-3
XX
SQ   Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        506 CTGCCCTCGCACCACGGG 523
              ||||| | ||||||||||
Db         20 CTGCCTTTGCACCACGGG 3


RESULT 3653
AAL53965/c
ID   AAL53965 standard; DNA; 20 BP.
XX
```

```
AC   AAL53965;
XX
DT   18-FEB-2003  (first entry)
XX
DE   DNA mutation detection related oligo, SEQ ID No 15.
XX
KW   Detecting; point mutation; hybridising; target DNA; duplex; RNase H;
KW   single nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   US2002142308-A1.
XX
PD   03-OCT-2002.
XX
PF   30-MAR-2001; 2001US-00823634.
XX
PR   30-MAR-2001; 2001US-00823634.
XX
PA   (DATT/) DATTAGUPTA N.
PA   (TSEN/) TSENG T.
XX
PI   Dattagupta N,  Tseng T;
XX
DR   WPI; 2003-102506/09.
XX
PT   Detecting point mutation in DNA strand, by hybridizing target DNA strand
PT   having mutation with test DNA strand to form duplex, contacting the
PT   duplex with RNase H and determining the cleavage of test strand by RNase
PT   H.
XX
PS   Example 5; Fig 4; 26pp; English.
XX
CC   The invention relates to a novel method for detecting a point mutation in
CC   a DNA strand. The novel method comprises hybridising a target DNA strand
CC   containing or suspected of containing a point mutation with a test
CC   nucleic acid strand complementary to the DNA strand to form a target DNA
CC   strand/test nucleic acid strand duplex, contacting the duplex with an
CC   RNase H, and determining whether the ribonucleotide residues within the
CC   nucleotide sequence are cleaved by RNase H. The method is useful for
CC   detecting a point mutation in a DNA strand, where the point mutation to
CC   be detected is a single nucleotide polymorphism, preferably a
CC   polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian
CC   or human genome. The method is useful to detect any nucleic acids from
CC   any species of organisms such as Acintobacter, Bacillus, Candida,
CC   Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
CC   This polynucleotide sequence represents an oligo relating to the mutation
CC   detecting method of the invention
XX
SQ   Sequence 20 BP; 16 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTT 2172
              ||||||| |||||||||
Db         18 TTTTTTTAACCTTTTTTT 1


RESULT 3654
ACF57337
ID   ACF57337 standard; DNA; 20 BP.
XX
AC   ACF57337;
XX
DT   16-OCT-2003  (first entry)
XX
DE   Human atlastin exon 10 intronic acceptor splice site.
XX
KW   Human; atlastin; chromosome 14; 14q22.1; hereditary spastic paraplegia;
KW   HSP; neuroprotective; gene therapy; intronic splice site; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003026566-A2.
XX
PD   03-APR-2003.
XX
PF   13-SEP-2002; 2002WO-US029165.
XX
PR   21-SEP-2001; 2001US-0323997P.
PR   12-SEP-2002; 2002US-00242008.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Fink JK,  Zhao X;
XX
DR   WPI; 2003-371871/35.
XX
PT   New atlastin gene, useful for preparing a composition for treating
PT   Hereditary Spastic Paraplegia (HSP) or for identifying subjects who have,
PT   or at risk of developing, HSP.
XX
PS   Example 6; Page 102; 111pp; English.
XX
CC   The present invention describes human atlastin, which is located to
CC   chromosome 14 (more specifically to 14q22.1). Also described: (1) an
CC   isolated atlastin polypeptide; (2) identifying subjects who have, or are
CC   at risk of developing, hereditary spastic paraplegia (HSP); (3) a kit for
CC   determining if a subject has, or at risk of developing, HSP; (4) a
CC   computer readable medium encoding a representation of the atlastin
CC   nucleic acid sequence or polypeptide; (6) identifying subjects at risk of
CC   carrying an allele for HSP; and (7) treating a patient with HSP. Atlastin
CC   has neuroprotective activity and can be used in gene therapy. The
CC   atlastin nucleic acid is useful for preparing a composition for treating
CC   HSP or for identifying subjects who have, or at risk of developing, HSP.
CC   The present sequence represents an atlastin intronic splice site
CC   oligonucleotide, which is given in an example from the present invention
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              | ||||| ||||||||||
Db          2 TCTTTTTCTTTTTTTTTA 19


RESULT 3655
ACF04230
ID   ACF04230 standard; DNA; 20 BP.
XX
AC   ACF04230;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Murine embryonic cell line amylase-2A PCR primer #1.
XX
KW   Embryonic stem cell; ES cell; mouse; differentiation; nerve cell;
KW   pancreatic islet cell; cell transplant therapy; antidiabetic;
KW   neuroprotective; nootropic; PCR; primer; ss.
XX
OS   Mus sp.
XX
PN   WO2003062405-A2.
XX
PD   31-JUL-2003.
XX
PF   27-JAN-2003; 2003WO-JP000699.
XX
PR   25-JAN-2002; 2002US-00054789.
XX
```

PA (OKUM-) OKUMA CONTACTLENS KENKYUSHO YG.
PA (INOU/) INOUE K.
XX
PI Inoue K, Kim D, Gu Y, Ishii M;
XX
DR WPI; 2003-598750/56.
XX
PT Inducing differentiation of mammalian embryonic stem (ES) cells into
PT functioning cells, for treating e.g. diabetes, comprises culturing ES
PT cells in a medium containing leukemia inhibitor factor and basic
PT fibroblast growth factor.
XX
PS Example 1; Page 63; 70pp; English.
XX
CC The present invention relates to a method of inducing differentiation of
CC mammalian embryonic stem cells into functioning cells, which comprises
CC culturing embryonic stem cells in a medium comprising leukaemia inhibitor
CC factor and basic fibroblast growth factor. In particular, the invention
CC relates to the differentiation of murine embryonic stem cells. The method
CC is useful for inducing differentiation of mammalian embryonic stem cells
CC into functioning cells. Other methods are useful for treating a mammalian
CC patient having disorders in pancreatic function, and in nerve function.
CC The cells are pancreatic islet like cell clusters and nerve like cells.
CC Functioning cells induced from embryonic stem cells using the present
CC method may be used for treating disorders in pancreatic islet function
CC (e.g. diabetes), neuronal degeneration (e.g. Alzheimer's disease and
CC Creutzfeldt-Jakob disease) or spinal cord disorders. The functioning
CC cells are useful not only for cell transplant therapy, but for in vitro
CC screening of various new drugs which affect or restore islet or nerve
CC function, and for safety evaluation of new drugs. The present sequence is
CC a PCR primer used in the exemplification of the invention
XX
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGTCACC 2334
              ||||||| |||||||||
Db          3 TTGTTGCACCTTGTCACC 20
```

RESULT 3656
ACH66496
ID ACH66496 standard; DNA; 20 BP.
XX
AC ACH66496;
XX
DT 16-OCT-2003 (first entry)
XX
DE Sense PCR primer used to amplify FADD.
XX
KW PCR; primer; ss; genomic DNA; gDNA; untranslated region; UTR;
KW DNA high-density microarray; biosite; large scale production; gDNA probe;
KW microarray; Type II primer.
XX
OS *Homo sapiens*.
XX
PN US2003073085-A1.
XX
PD 17-APR-2003.
XX
PF 05-OCT-2001; 2001US-00972469.
XX
PR 05-OCT-2001; 2001US-00972469.
XX
PA (LAIF/) LAI F.
PA (ZHOU/) ZHOU D.
XX
PI Lai F, Zhou D;
XX
DR WPI; 2003-555942/52.
XX
PT Amplifying expressed genetic sequences from genomic DNA of mammalian or
PT higher order plant species for printing on DNA microarrays, involves
PT using the 3' untranslated region of the gene sequence.
XX
PS Disclosure; Page 7; 15pp; English.
XX
CC The invention discloses a method for amplifying expressed genetic
CC sequences from genomic DNA (gDNA) from mammalian or higher order plant
CC species. The method involves identifying a 3' untranslated region (UTR)
CC of a gDNA sequence, designing probe, performing PCR, separating the
CC product by size differentiation and performing a second PCR to amplify
CC the predetermined sequence. Also claimed is a biological analysis device,
CC comprising a substrate and an array of a set of expressed genetic
CC sequences, located on the substrate, which are generated by the method
CC above and a DNA high-density microarray comprising a substrate upon which
CC are deposited an array of biosites of genomic DNA fragments having the
CC sequence of at least one exon, and absent polyadenine and vector
CC sequences, where the genomic DNA fragments have a sequence length of from
CC about 75-2000 nucleotides. The method is efficient for amplifying gene
CC sequences, enables large-scale production of gDNA sequences, generates
CC large quantities of gDNA probes, which enables greater efficiency for
CC printing in microarray formats, fabricates high-density DNA arrays of
CC enhanced, widely varying genetic content and abstains from using RNA-
CC derived sequences by simple PCR amplifications without cloning. The
CC method produces amplified sequences that have greater specificity and
CC size consistency than that observed with cDNA fragments, and allows for
CC greater signal sensitivity than oligonucleotides. The sequence presented
CC is a Type II gene specific primer
XX
SQ Sequence 20 BP; 5 A; 1 C; 9 G; 5 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        999 TGCGGGAGAAGTTGGACA 1016
              |||||||| ||||||| |
Db          1 TGCGGGAGTAGTTGGAAA 18
```

RESULT 3657
ADC65824/c
ID ADC65824 standard; DNA; 20 BP.
XX
AC ADC65824;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mouse TGF-beta receptor II targeted antisense oligonucleotide #23.
XX
KW mouse; antisense oligonucleotide;
KW transforming growth factor beta receptor II; TGF-beta receptor II;
KW hyperproliferative disorder; breast cancer; autoimmune disorder;
KW rheumatoid arthritis; 2'-O-methoxyethyl gapmer;
KW phosphorothioate backbone; ss; murine.
XX
OS Mus musculus.
XX
PN WO2003000656-A2.
XX
PD 03-JAN-2003.
XX
PF 19-JUN-2002; 2002WO-US019665.
XX
PR 21-JUN-2001; 2001US-00888361.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Murray SF, Wyatt JR;
XX
DR WPI; 2003-175279/17.
XX

```
PT   New compound having a sequence targeted to a nucleic acid encoding
PT   Transforming growth factor beta-receptor II, useful for preparing a
PT   composition for treating hyperproliferative disorder e.g., lung, liver,
PT   colon or gastric cancer.
XX
PS   Example 15; SEQ ID NO 120; 141pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acid encoding transforming growth factor beta (TGF-beta)
CC   receptor II. The antisense oligonucleotides of the invention are useful
CC   for treating: hyperproliferative disorders (e.g. breast cancer), or an
CC   autoimmune disorder (e.g. rheumatoid arthritis). The present DNA sequence
CC   represents a 2'-O-methoxyethyl gapmer oligonucleotide with a
CC   phosphorothioate backbone that is targeted to mouse TGF-beta receptor II.
XX
SQ   Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 20;
  Best Local Similarity   88.9%;  Pred. No. 3.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1175 CCTCATCTTGGAGGACGA 1192
              | ||||| ||||||||||
Db         20 CATCATCCTGGAGGACGA 3


RESULT 3658
AAQ65146
ID   AAQ65146 standard; DNA; 21 BP.
XX
AC   AAQ65146;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KW   inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-02104649.
XX
PR   25-AUG-1992;   92JP-00248796.
PR   03-MAR-1993;   93JP-00042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Seki M,  Honda Y,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT   genome - are useful as antiviral agents.
XX
PS   Claim 5; Page 165; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound i.e.
CC   it has a base sequence of 15-30 bases which is included within the 49
CC   bases from G at position 127 to C at position 175 of AAQ64913 and which
CC   contains at least 7 bases from C at position 147 to C at position 153.
CC   The antisense oligonucleotide is useful for inhibiting translation of HCV
CC   genes
XX
SQ   Sequence 21 BP; 2 A; 5 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       113 GGCTGGGGGGGATCCTGGA 130
             ||| |||||| |||||||
Db         3 GGCAGGGGGGGTCCTGGA 20


RESULT 3659
AAT05742
ID   AAT05742 standard; DNA; 21 BP.
XX
AC   AAT05742;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   21-MAR-1996  (first entry)
XX
DE   Plant consensus splice site.
XX
KW   Crystal protein; toxin; Bacillus thuringiensis var. tenebrionis; Btt;
KW   insecticide; insect resistance; disease resistance; transgenic plant;
KW   crop improvement; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    20. .21
FT                   /*tag=  a
FT                   /function= "consensus splice site"
XX
PN   EP682115-A1.
XX
PD   15-NOV-1995.
XX
PF   07-SEP-1989;   95EP-00201374.
XX
PR   09-SEP-1988;   88US-00242482.
XX
PA   (MYCO ) MYCOGEN PLANT SCI INC.
XX
PI   Adang MJ,  Rocheleau TA,  Merlo DJ,  Murray EE;
XX
DR   WPI; 1995-384255/50.
XX
PT   Synthetic gene for B.thuringiensis insecticidal protein - designed for
PT   high level expression in plants to improve protection against insect
PT   pests.
XX
PS   Claim 11; Page 31; 38pp; English.
XX
CC   The plant consensus splice site (AAT05742) was searched for, and found to
CC   be not present, in a Bacillus thuringiensis subsp. tenebrionis synthetic
CC   crystal protein gene (AAT05738). Its presence might have had a
CC   destabilising effect on the gene. (Updated on 25-MAR-2003 to correct PF
CC   field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 21 BP; 1 A; 2 C; 2 G; 11 T; 0 U; 5 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   65.0%;  Pred. No. 3.4e+03;
  Matches   13;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2519 TTTTATTCATATATATACAG 2538
              ||||:|| :|:|:|:| |||
Db          1 TTTTRTTTRTRTRTRTGCAG 20


RESULT 3660
AAT76513/c
ID   AAT76513 standard; DNA; 21 BP.
XX
AC   AAT76513;
XX
DT   16-SEP-1997  (first entry)
```

XX
DE Endothelial nitric oxide antisense oligonucleotide.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US009306.
XX
PR 07-JUN-1995; 95US-00474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW, Metzger WJ;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject.
XX
PS Example 5; Page 43; 71pp; English.
XX
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for endothelial nitric oxide. The method can be used to treat airway
CC diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary
CC disease, bronchitis and other airway diseases characterised by an
CC inflammatory response. By eliminating adenosine from the antisense ON,
CC its liberation upon antisense degradation is prevented, thereby
CC preventing adenosine-induced bronchoconstriction in patients with hyper-
CC reactive airways
XX
SQ Sequence 21 BP; 0 A; 8 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        436 GCACCAGCCGGCGCCCAC 453
              | ||| ||||||||||||
Db         18 GGACCCGCCGGCGCCCAC 1
```

RESULT 3661
AAZ26632/c
ID AAZ26632 standard; DNA; 21 BP.
XX
AC AAZ26632;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 821.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 15 A; 2 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       2171 TTTTTTTTTTTTTTTAA 2188
              |||||||||||  ||||
Db         21 TTTTTTTTTTTAGTTAA 4
```

RESULT 3662
AAZ26714/c
ID AAZ26714 standard; DNA; 21 BP.
XX
AC AAZ26714;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 903.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.

```
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||| | |||
Db         21 TTTTTTTTTTTTATGTTA 4


RESULT 3663
AAX56816/c
ID   AAX56816 standard; DNA; 21 BP.
XX
AC   AAX56816;
XX
DT   14-JUL-1999  (first entry)
XX
DE   WO9922023 probe 52.
XX
KW   Microorganism; hybridisation; probe; identification; detection; bacteria;
KW   milk; water; automated; ss.
XX
OS   Synthetic.
XX
PN   WO9922023-A2.
XX
PD   06-MAY-1999.
XX
PF   29-OCT-1998;   98WO-EP006863.
XX
PR   29-OCT-1997;   97DE-01047731.
XX
PA   (MIRA-) MIRA DIAGNOSTICA GMBH.
XX
PI   Leiser M,  Epping B;
XX
DR   WPI; 1999-303024/25.
XX
PT   Identifying specific microorganisms present in a mixture.
XX
PS   Claim 1; Page 9; 19pp; German.
XX
CC   This invention describes the detection of specific microorganisms from
CC   various taxa, in a sample containing several different microorganisms by
CC   nucleic acid hybridization, using as probes, 62 specific oligonucleotides
CC   (represented in AAX56765-X56826) with at least one oligonucleotide being
CC   able to hybridize to each microorganism. The method is useful for
CC   detecting and identifying bacteria in milk and water. The method, which
CC   may be fully automated, allows simultaneous detection and unequivocal
CC   identification of bacteria from different taxa
XX
SQ   Sequence 21 BP; 7 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        168 TGTTGTGGAAAATAACCG 185
              ||||||||  ||||||||
Db         21 TGTTGTGGTTAATAACCG 4


RESULT 3664
AAX54304/c
ID   AAX54304 standard; DNA; 21 BP.
XX
AC   AAX54304;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Endothelial nitric oxide synthase antisense oligonucleotide.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 61; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
```

```
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 21 BP; 0 A; 8 C; 10 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        436 GCACCAGCCGGCGCCCAC 453
              | ||| ||||||||||||
Db         18 GGACCCGCCGGCGCCCAC 1


RESULT 3665
AAA33748/c
ID   AAA33748 standard; DNA; 21 BP.
XX
AC   AAA33748;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Low adenosine antisense oligonucleotide SEQ ID NO:1437.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Claim 18; Page 444; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 21 BP; 0 A; 8 C; 10 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        436 GCACCAGCCGGCGCCCAC 453
              | ||| ||||||||||||
Db         18 GGACCCGCCGGCGCCCAC 1


RESULT 3666
AAF19870/c
ID   AAF19870 standard; DNA; 21 BP.
XX
AC   AAF19870;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human endothelial nitric oxide synthase polynucleotide fragment #1437.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
```

```
PS   Claim 14; Page 251; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 21 BP; 0 A; 8 C; 10 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        436 GCACCAGCCGGCGCCCAC 453
              | ||| ||||||||||||
Db         18 GGACCCGCCGGCGCCCAC 1


RESULT 3667
AAC86173/c
ID   AAC86173 standard; cDNA; 21 BP.
XX
AC   AAC86173;
XX
DT   19-SEP-2001  (first entry)
XX
DE   Tyr300 primer #1.
XX
KW   Melanoma-specific promoter; human; tyrosinase gene; Tyr300; M box;
KW   activator; transgene expression; gene therapy; tumour; melanoma;
KW   polymerase chain reaction; primer; amplify; PCR; ss.
XX
OS   Synthetic.
XX
PN   WO200138488-A2.
XX
PD   31-MAY-2001.
XX
PF   22-NOV-2000; 2000WO-US032203.
XX
PR   23-NOV-1999;   99US-0167085P.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI   Vile R,  Gough M;
XX
DR   WPI; 2001-367671/38.
XX
PT   Novel nucleic acid construct for cell type-specific expression of
PT   therapeutic transgene, comprising a cell type-specific promoter operably
PT   linked to therapeutic gene, and amplification promoter element.
XX
PS   Example 1; Page 29; 33pp; English.
XX
CC   The sequences given in AAC86173-74 are primers which were used to
CC   identify the minimal melanoma-specific promoter of the human tyrosinase
CC   gene. The identified fragment corresponding to bases -300 to -1 and is
CC   designated Tyr300. Tyr300 is a subsequence of the 5' untranslated region
CC   of the human tyrosinase gene and contains at least four positive DNA
CC   binding elements as one as one negative element. The M box, found at -107
CC   to -97 is a conserved element found in other melanocyte-specific
CC   promoters. When Tyr300 is incorporated into a recombinant construct, it
CC   functions as a highly selective activator for transgene expression in
CC   melanoma cells. Constructs such as these are useful for gene therapy of
CC   tumours such as melanoma, cancers, genetic diseases and other ailments
CC   amenable to gene therapy
XX
SQ   Sequence 21 BP; 11 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 21;
  Best Local Similarity   88.9%;  Pred. No. 3.4e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTT 2167
              | ||||||||||||||| |
Db         18 AGTGATTTTTTTCTCCAT 1


RESULT 3668
ABK65637
ID   ABK65637 standard; DNA; 21 BP.
XX
AC   ABK65637;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human single nucleotide polymorphism #257.
XX
KW   Human; single nucleotide polymorphism; SNP; sickle cell anaemia;
KW   agammaglobulinaemia; diabetes insipidus; Lesch-Nyhan syndrome;
KW   muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease;
KW   familial hypercholesterolaemia; polycystic kidney disease; cancer;
KW   hereditary spherocytosis; Von Willebrand's disease; tuberous sclerosis;
KW   hereditary haemorrhagic telangiectasia; familial colonic polyposis;
KW   Ehlers-Danlos syndrome; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; inflammation; nervous system disorder;
KW   infection; rheumatoid arthritis; multiple sclerosis; diabetes;
KW   systemic lupus erythematosus; Graves disease; longevity; obesity;
KW   baldness; fertility; forensic; paternity testing; ss.
XX
OS   Homo sapiens.
XX
PN   US2002037508-A1.
XX
PD   28-MAR-2002.
XX
PF   18-JAN-2001; 2001US-00765081.
XX
PR   19-JAN-2000; 2000US-0176861P.
XX
PA   (CARG/) CARGILL M.
PA   (IREL/) IRELAND J S.
PA   (LAND/) LANDER E S.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2002-315108/35.
XX
PT   Nucleic acid comprising single nucleotide polymorphisms, useful in
PT   forensics, paternity testing and diagnosis of disease.
XX
```

PS Claim 1; Page 68; 96pp; English.
XX
CC The invention relates to a nucleic acid comprising single nucleotide
CC polymorphisms (SNPs) associated with diseases. The nucleic acids
CC comprising the SNPs and probes and primers for detecting them may be used
CC in assays for the diagnosis of diseases associated with SNPs (such as
CC sickle cell anaemia, agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolaemia, polycystic kidney disease, hereditary
CC spherocytosis, Von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, and acute intermittent porphyria,
CC symptoms of, or susceptibility to, multifactorial diseases of which a
CC component is or may be genetic, such as autoimmune diseases,
CC inflammation, cancer, diseases of the nervous system, and infection by
CC pathogenic microorganisms, autoimmune diseases including rheumatoid
CC arthritis, multiple sclerosis, diabetes (insulin-dependent and non-
CC independent), systemic lupus erythematosus and Graves disease, cancers
CC including cancers of the bladder, brain, breast, colon, oesophagus,
CC kidney, leukaemia, liver, lung, oral cavity, ovary, pancreas, prostate,
CC skin, stomach and uterus, longevity, appearance (e.g., baldness,
CC obesity), strength, speed, endurance, fertility, and susceptibility or
CC receptivity to particular drugs or therapeutic treatments), in forensics
CC and in paternity testing. ABK65381-ABK65841 represent human single
CC nucleotide polymorphisms of the invention
XX
SQ Sequence 21 BP; 3 A; 6 C; 10 G; 1 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 638 GCCGCGGGCCTGGCCGAG 655
|| ||||| |||||||||
Db 3 GCAGCGGGRCTGGCCGAG 20

RESULT 3669
ABZ95564/c
ID ABZ95564 standard; DNA; 21 BP.
XX
AC ABZ95564;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human endothelial nitric oxide synthase antisense fragment no.1428.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 10806; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 0 A; 8 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 436 GCACCAGCCGGCGCCCAC 453
| ||| ||||||||||||
Db 18 GGACCCGCCGGCGCCCAC 1

RESULT 3670
ACC79539
ID ACC79539 standard; DNA; 21 BP.
XX
AC ACC79539;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human TCH169 PCR primer SEQ ID NO:3.
XX
KW Human; TCH169; dicarboxylate transport; hepatotropic; cytostatic;
KW nephrotropic; vasotropic; antidiabetic; liver disease; hepatitis;
KW hepatic sclerosis; alcohol-related liver disease; prostate disease;
KW prostatitis; prostatic hypertrophy; spleen disease; spleen hyperactivity;
KW kidney disease; nephritis; kidney failure; nephritis; dropsy; diabetes;
KW diabetes-associated renal disease; metabolic disease; hyperlipaemia;
KW circulatory disease; arteriosclerosis; cancer; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003025168-A1.
XX
PD 27-MAR-2003.
XX
PF 13-SEP-2002; 2002WO-JP009444.
XX
PR 17-SEP-2001; 2001JP-00281992.
PR 02-OCT-2001; 2001JP-00306873.
PR 16-APR-2002; 2002JP-00113279.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Nakanishi A, Uno Y, Sagiya Y;
XX
DR WPI; 2003-313352/30.

XX
PT Protein TCH169 with dicarboxylate transport activity for treatment and
PT diagnosis of diseases including liver disease, cancer and circulatory
PT disorders.
XX
PS Example 2; Page 103; 132pp; Japanese.
XX
CC The present invention describes protein TCH169 and its salts having
CC dicarboxylate transport activity. TCH169 has hepatotropic, cytostatic,
CC nephrotropic, vasotropic and antidiabetic activities. The TCH169 protein
CC and polynucleotide can be used in the treatment, prevention and diagnosis
CC of liver disease (such as hepatitis, hepatic sclerosis and alcohol-
CC related liver disease); prostate disease (such as prostatitis and
CC prostatic hypertrophy); spleen disease (such as spleen hyperactivity);
CC kidney disease (such as nephritis, kidney failure, nephritis, dropsy and
CC diabetes-associated renal disease); metabolic disease (such as diabetes);
CC circulatory disease (such as hyperlipaemia and arteriosclerosis); and
CC cancer (such as non-small cell lung cancer, liver cancer, renal cancer,
CC ovarian cancer, prostate cancer, stomach cancer, pancreatic cancer,
CC breast cancer, colon cancer, bladder cancer and womb cancer). The present
CC sequence represents a PCR primer for human TCH169, which is used in an
CC example from the present invention
XX
SQ Sequence 21 BP; 4 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2656 AGGTGAGTGTGCAGTACA 2673
||||| |||| |||||||
Db 4 AGGTGTGTGTCCAGTACA 21

RESULT 3671
AAV26091/c
ID AAV26091 standard; DNA; 22 BP.
XX
AC AAV26091;
XX
DT 27-AUG-1998 (first entry)
XX
DE Mandarin mb2ch1 gene PCR primer.
XX
KW Orange; mandarin; detection; chloroplast DNA; identification; fruit;
KW citrus; plant; food product; olive oil; fruit juice; PCR primer; ss.
XX
OS Synthetic.
OS Citrus reticulata.
XX
PN WO9814607-A1.
XX
PD 09-APR-1998.
XX
PF 30-SEP-1997; 97WO-GB002688.
XX
PR 02-OCT-1996; 96GB-00020498.
PR 20-NOV-1996; 96GB-00024083.
XX
PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.
XX
PI Knight AI;
XX
DR WPI; 1998-240104/21.
XX
PT Detection of particular plant species, especially in food products - by
PT extracting chloroplast DNA from the product and detecting a sequence
PT which is characteristic of the plant species.
XX
PS Claim 20; Page 19; 31pp; English.
XX
CC AAV26085-V26096 are PCR primers used in a method of detecting a
CC particular plant species in a product, in this case orange and mandarin.
CC The method involves extracting chloroplast DNA from the product and
CC analysing the DNA to detect a sequence which is characteristic of the
CC particular plant species. The example used is a method for detecting the
CC presence of C. reticulata (mandarin) in a sample containing C. sinensis
CC (orange) which involves extracting DNA from the sample, carrying out an
CC amplification reaction using primers which are able to amplify a region
CC of DNA comprising part of the C. reticulata 1120 bp sequence given in the
CC specification, but not the corresponding part of the C. sinensis 1140 bp
CC sequence also given in the specification, and detecting the presence of
CC amplified product. This method can be used for detecting or identifying
CC plants or plant derived material within food products. It can be used to
CC detect certain fruit species in particular citrus fruits such as
CC mandarin, e.g. within fruit containing food products or juice products,
CC or particular oil components such as olive oil, to determine the
CC authenticity of the products. The analysis by PCR amplification and
CC restriction fragment length polymorphism (RFLP) analysis of chloroplast
CC DNA can be used to distinguish between closely related plant species,
CC including species which are closely related
XX
SQ Sequence 22 BP; 14 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTT 2176
|||||| ||||| ||||
Db 22 TTTCTCCATTTTTGTTTT 5

RESULT 3672
AAV82676
ID AAV82676 standard; DNA; 22 BP.
XX
AC AAV82676;
XX
DT 16-FEB-1999 (first entry)
XX
DE 5' PCR primer F2 used to amplify a cDNA fragment encoding ST38.2.
XX
KW Rat; chemokine; ST38.2; chemotaxis; leucocyte-activating; inflammation;
KW immune response; brain injury; trauma; ischaemia;
KW autoimmune inflammation; multiple sclerosis; stroke;
KW rheumatoid arthritis; meningitis; encephalitis; PCR primer; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN WO9849309-A1.
XX
PD 05-NOV-1998.
XX
PF 23-APR-1998; 98WO-EP002405.
XX
PR 30-APR-1997; 97EP-00107135.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Lesslauer W, Utansschneitz U;
XX
DR WPI; 1999-009430/01.
XX
PT New chemokine ST38.2 with chemotactic and leucocyte-activating properties
PT - used to treat inflammation and immune responses and to identify
PT specific modulators.
XX
PS Example 5; Page 30; 64pp; English.
XX
CC PCR primers AAV82676-77 were used to amplify a ST38.2 cDNA fragment in a
CC RT-PCR assay, in the course of the invention. ST38.2 is a novel rat
CC chemokine designated ST38.2. The protein has chemotactic and leucocyte-
CC activating properties. ST38.2 is involved in inflammation and immune
CC responses, particularly inflammatory response to brain injury (trauma,

```
CC   ischaemia or autoimmune inflammation) but also in multiple sclerosis,
CC   stroke, rheumatoid arthritis and infections (particularly meningitis and
CC   encephalitis)
XX
SQ   Sequence 22 BP; 4 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        611 CTGCTGCCCCACGCACAC 628
              |||||||| |||| ||||
Db          5 CTGCTGCCTCACGTACAC 22


RESULT 3673
ABZ10343/c
ID   ABZ10343 standard; DNA; 22 BP.
XX
AC   ABZ10343;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Haematopoietic cell proliferation disorder related primer SEQ ID NO:483.
XX
KW   Human; haematopoietic cell proliferation disorder; cytostatic;
KW   gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW   cytosine methylation state; probe; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200277272-A2.
XX
PD   03-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-EP003401.
XX
PR   26-MAR-2001; 2001US-0278333P.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Berlin K,  Braun A,  Distler J,  Guetig D,  Howe A,  Mueller J;
PI   Olek A,  Piepenbrock C,  Adorjan P,  Grabs G,  Lesche R,  Leu E;
PI   Lewin A,  Lipscher E,  Maier S,  Model F,  Mueller V,  Otto T,  Pelet C;
PI   Schwope I,  Ziebarth H;
XX
DR   WPI; 2003-018942/01.
XX
PT   Detecting and differentiating between hematopoietic cell proliferative
PT   disorders, comprises contacting a target nucleic acid with a reagent that
PT   distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS   Claim 11; Page 37; 117pp; English.
XX
CC   The present invention describes a method for detecting and
CC   differentiating between haematopoietic cell proliferative disorders
CC   associated with at least 1 gene and/or their regulatory regions in a
CC   subject. The method comprises contacting a target nucleic acid in a
CC   biological sample obtained from the subject with at least 1 reagent,
CC   which distinguishes between methylated and non-methylated CpG
CC   dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC   represent specifically claimed nucleotide sequences from the present
CC   invention. Oligonucleotides from the present invention can be used: for
CC   differentiating between healthy haematopoietic cells and proliferative
CC   disorder haematopoietic cells; for differentiating between acute
CC   lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC   determining the cytosine methylation state and/or single nucleotide
CC   polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC   related sequences and their complements; and as primers for the
CC   amplification of haematopoietic cell proliferation disorder related DNA
CC   sequences. The nucleotide sequences from the present invention can also
CC   be used for detecting a predisposition to, differentiation between
CC   subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC   haematopoietic cell proliferative disorders. The present method enables a
CC   highly specific classification of haematopoietic cell proliferative
CC   disorders allowing for improved and informed treatment of patients
XX
SQ   Sequence 22 BP; 9 A; 0 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        340 CTACTTTCCCCCTCCCTA 357
              ||||||| ||| ||||||
Db         21 CTACTTTTCCCATCCCTA 4


RESULT 3674
ACC80022/c
ID   ACC80022 standard; DNA; 22 BP.
XX
AC   ACC80022;
XX
DT   25-JUL-2003  (first entry)
XX
DE   Human HDAC9 exon 21 5' splice donor consensus sequence.
XX
KW   Human; HDAC9; histone deacetylase 9; enzyme; cytostatic; cancer;
KW   leukaemia; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003029451-A2.
XX
PD   10-APR-2003.
XX
PF   02-OCT-2002; 2002WO-GB004455.
XX
PR   02-OCT-2001; 2001GB-00023664.
XX
PA   (CANC-) CANCER RES INST.
PA   (ZELE/) ZELENT A.
PA   (PETR/) PETRIE K.
PA   (GUID/) GUIDEZ F.
XX
PI   Zelent A,  Petrie K,  Guidez F;
XX
DR   WPI; 2003-381634/36.
XX
PT   New histone deacetylase 9 polypeptide, useful for screening for candidate
PT   compounds that share a, bind to, or inhibits the histone deacetylase 9
PT   biological activity, and for diagnosing or prognosing cancer, e.g.
PT   leukemia.
XX
PS   Disclosure; Page 44; 71pp; English.
XX
CC   The invention relates to an isolated polypeptide having histone
CC   deacetylase (HDAC) activity. Polypeptides and nucleic acids of the
CC   invention are useful for screening for candidate compounds that share,
CC   bind to, or inhibit histone deacetylase 9 (HDAC9) biological activity,
CC   and for diagnosing or prognosing cancer, e.g. leukaemia such as TEL-AML1
CC   positive and negative pre-B cell acute lymphoblastic leukemia or B cell
CC   lymphoma. The current sequence the human HDAC9 exon 21 alternative 5'
CC   splice donor consensus sequence
XX
SQ   Sequence 22 BP; 5 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        919 GTCCCCACCTGAATGCTT 936
              || || ||||||||||||
Db         18 GTACCAACCTGAATGCTT 1
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RESULT 3675
ADE84289/c
ID   ADE84289 standard; DNA; 22 BP.
XX
AC   ADE84289;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human lymphoid cell proliferative disorder pre-treated DNA primer #73.
XX
KW   lymphoid cell proliferative disorder; methylation;
KW   methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW   diffuse large B-cell lymphoma; mantle cell lymphoma;
KW   chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW   follicular lymphoma; diagnosis; prognosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003044226-A2.
XX
PD   30-MAY-2003.
XX
PF   25-NOV-2002; 2002WO-EP013265.
XX
PR   23-NOV-2001; 2001DE-01057491.
PR   28-DEC-2001; 2001DE-01064501.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Burger M,  Caldwell C,  Genc B,  Becker E,  Maier S,  Nimmrich I;
XX
DR   WPI; 2003-457621/43.
XX
PT   Detecting and differentiating between lymphoid cell proliferative
PT   disorders comprises contacting a target nucleic acid with at least one
PT   reagent that distinguishes between methylated and non-methylated CpG
PT   dinucleotides.
XX
PS   Claim 11; SEQ ID NO 285; 448pp; English.
XX
CC   The invention relates to a method of detecting and differentiating
CC   between lymphoid cell proliferative disorders associated with at least
CC   one gene and/or their regulatory regions in a subject by contacting a
CC   target nucleic acid in a biological sample obtained from the subject with
CC   at least one reagent or series of reagents that distinguish between
CC   methylated and non-methylated CpG dinucleotides within the target nucleic
CC   acid. The genes and/or their regulatory regions are preferably selected
CC   from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3,
CC   MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
CC   GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC,
CC   GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC   acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC   of the genes are useful for detecting the methylation state of all the
CC   CpG dinucleotides within one or more the sequences, or their complements,
CC   for determining the cytosine methylation state and or single nucleotide
CC   polymorphisms (SNPs), and for differentiating at least two of the medical
CC   conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC   chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC   lymphoma. They are also useful for detecting of a predisposition to,
CC   differentiation between subclasses, diagnosis, prognosis, treating and/or
CC   monitoring of lymphoid cell proliferative disorder. This sequence
CC   represents a PCR primer used to amplify the nucleic acid of a pretreated
CC   genomic DNA derived from the above mentioned genes.
XX
SQ   Sequence 22 BP; 9 A; 0 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 22;
  Best Local Similarity   88.9%;  Pred. No. 3.7e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        340 CTACTTTCCCCCTCCCTA 357
              ||||||| ||| ||||||
Db         21 CTACTTTTCCCATCCCTA 4


RESULT 3676
AAH91823/c
ID   AAH91823 standard; DNA; 23 BP.
XX
AC   AAH91823;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human inflammatory bowel disease associated polymorphic site #898.
XX
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW   chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    11
FT                   /*tag=  a
FT                   /note= "SNP, optionally T or A at this position"
XX
PN   WO200142511-A2.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US033632.
XX
PR   10-DEC-1999;   99US-0170257P.
PR   10-APR-2000; 2000US-0196046P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI   Daly M,  Hudson TJ,  Lander ES,  Rioux J,  Siminovitch K;
XX
DR   WPI; 2001-367874/38.
XX
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay.
XX
PS   Claim 1; Page 76; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention
XX
SQ   Sequence 23 BP; 0 A; 4 C; 0 G; 18 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 23;
  Best Local Similarity   84.2%;  Pred. No. 3.9e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||   || ||
Db         23 AAAAAAAAAAAANGAAGAA 5


RESULT 3677
AAC96428/c
ID   AAC96428 standard; DNA; 24 BP.
XX
AC   AAC96428;
XX
DT   26-FEB-2001  (first entry)
```

```
XX
DE   HLA DQA1 gene PCR primer #30.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 24 BP; 3 A; 5 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAA 2796
              ||| || ||||||||||
Db         18 AGAGTTAAAAAAAAAAAA 1


RESULT 3678
AAZ07017
ID   AAZ07017 standard; DNA; 24 BP.
XX
AC   AAZ07017;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Murine alpha-L-iduronidase genomic DNA oligonucleotide #3.
XX
KW   Murine; mouse; alpha-L-iduronidase; IDUA; hepatic sulphate transporter;
KW   SAT-1; mucopolysaccharidosis type I; MPS I; transgenic mouse;
KW   cell-specific targeting system; tissue-specific targeting system;
KW   lysosomal disorder; ss.
XX
OS   Mus sp.
XX
PN   CA2205710-A.
XX
PD   20-NOV-1997.
XX
PF   20-MAY-1997;   97CA-02205710.
XX
PR   20-MAY-1996;   96US-0017156P.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Jirik F,  Clarke LA;
XX
DR   WPI; 1999-494691/42.
XX
PT   New transgenic mouse, useful for modeling lysosomal disorders and testing
PT   cell- or tissue-specific targeting systems.
XX
PS   Example 3; Page 12; 20pp; English.
XX
CC   The present invention describes a mouse (I), homozygous for a disruption
CC   in the alpha-L-iduronidase (IDUA) gene but with normal expression of the
CC   hepatic sulphate transporter SAT-1 gene. (I) is used to evaluate
CC   therapeutic agents for use in treating mucopolysaccharidosis Type I (MPS
CC   I) by administering the agent to (I) and evaluating the mouse for
CC   pathology associated with iduronidase deficiency. (I) may also be used to
CC   evaluate the ability of a targeting system to deliver a therapeutic agent
CC   to a specific tissue or organ in the mouse using the same techniques.
CC   Targeting systems which may be tested using this regime include a target-
CC   specific label, a viral expression vector or a liposome coupled to
CC   iduronidase. (I) may also be used as a general model for studying the
CC   pathology of MPS I. The SAT-1 gene overlaps with the IDUA gene but in (I)
CC   the expression of the SAT-1 gene is unaffected. Therefore any
CC   pathological effects observed in (I) are due solely to the disruption of
CC   the IDUA gene. The present sequence represents a IDUA genomic DNA
CC   oligonucleotide used in the exemplification of the present invention
XX
SQ   Sequence 24 BP; 20 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||| |||||| ||||
Db          5 AAAAAACAAAAAACAAAA 22


RESULT 3679
AAS19218
ID   AAS19218 standard; DNA; 24 BP.
XX
AC   AAS19218;
XX
DT   09-APR-2002  (first entry)
XX
DE   Kringle protein 14, RT-PCR primer #2.
XX
KW   Kringle protein 14; cytostatic; haemostatic; virucide; immunomodulatory;
KW   antiinflammatory; malignant tumour; haemopathy; inflammation; primer;
KW   human immunodeficiency virus; HIV; immunological disease; RT-PCR; ss;
KW   reverse transcriptase PCR.
XX
OS   Unidentified.
XX
PN   WO200192318-A1.
XX
PD   06-DEC-2001.
XX
PF   21-MAY-2001; 2001WO-CN000845.
XX
PR   24-MAY-2000; 2000CN-00115849.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-090030/12.
XX
PT   Kringle protein 14 and encoding polynucleotide, used in diagnosis and
```

```
PT   treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT   infection, immunological diseases and inflammation.
XX
PS   Example 2; Page 17; 37pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide (I) of Kringle protein
CC   14 and the polynucleotide (II) encoding (I). (I) and (II) are used in
CC   diagnosis and treatment of malignant tumour, haemopathy, human
CC   immunodeficiency virus (HIV) infection, immunological diseases and
CC   various inflammations. The present sequence represents a reverse
CC   transcriptase (RT)-PCR primer used to isolate the coding sequence of
CC   kringle protein 14 as described in the invention
XX
SQ   Sequence 24 BP; 20 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 24;
  Best Local Similarity   88.9%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              |||||  |||||  ||||||
Db          2 AAAAACAAAAACAAAAAA 19


RESULT 3680
AAC96784/c
ID   AAC96784 standard; DNA; 25 BP.
XX
AC   AAC96784;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #161.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 57; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAA 2796
              ||||  | ||||||||||
Db         18 AGAAGTAAAAAAAAAAAA 1


RESULT 3681
AAC96182/c
ID   AAC96182 standard; DNA; 25 BP.
XX
AC   AAC96182;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #149.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 46; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 6 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||  ||||||||||||||||
Db         18 TGTTAAAAAAAAAAAAAA 1


RESULT 3682
AAC96089
ID   AAC96089 standard; DNA; 25 BP.
XX
AC   AAC96089;
XX
DT   26-FEB-2001  (first entry)
XX
DE   16s rRNA gene PCR primer #56.
XX
```

KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 45; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 5 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTAAC 2189
||||||||||||| |||
Db 1 TTTTTTTTTTTTTACAAC 18

RESULT 3683
AAH28308/c
ID AAH28308 standard; RNA; 25 BP.
XX
AC AAH28308;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from CTCF gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 25 BP; 2 A; 4 C; 0 G; 0 T; 19 U; 0 Other;

Query Match 0.5%; Score 14.8; DB 1; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2802
|||||||| | ||||||
Db 24 GAAAAAAAAGAGAAAAAA 7

RESULT 3684
AAC96511/c
ID AAC96511 standard; DNA; 25 BP.
XX
AC AAC96511;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #63.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of

```
PT   specific length.
XX
PS   Claim 14; Page 52; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 2 C; 5 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAA 2800
              || || ||||||||||||
Db         18 TTAAACAAAAAAAAAAAA 1


RESULT 3685
AAC96618/c
ID   AAC96618 standard; DNA; 25 BP.
XX
AC   AAC96618;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB345 gene PCR primer #89.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 54; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.8;  DB 1;  Length 25;
  Best Local Similarity   88.9%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              || || ||||||||||||
Db         18 GAGTTCAAAAAAAAAAAA 1


RESULT 3686
ABN87920
ID   ABN87920 standard; DNA; 15 BP.
XX
AC   ABN87920;
XX
DT   12-AUG-2002  (first entry)
XX
DE   Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
XX
KW   Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;
KW   gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    14
FT                   /*tag=  a
FT                   /note= "polymorphic base"
XX
PN   WO200242320-A2.
XX
PD   30-MAY-2002.
XX
PF   13-NOV-2001; 2001WO-US046473.
XX
PR   10-NOV-2000; 2000US-0247202P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Sanchis A,  Sausker EA,  Sun X;
XX
DR   WPI; 2002-471719/50.
XX
PT   New genetic variants of Glutathione reductase isogenes, useful for
PT   improving efficiency and reliability in drug development for treating
PT   hemolytic anemia.
XX
PS   Claim 14; Page 14; 137pp; English.
XX
CC   The present invention describes genetic variants of the human glutathione
CC   reductase (GSR) gene (I). (I) has antianaemic activity and can be used in
CC   gene therapy. (I) can be used in screening for drugs targeting (I) that
CC   are useful for treating haemolytic anaemia. Methods from the present
CC   invention can be used: for improving the efficiency and reliability of
CC   several steps in the discovery and development of drugs for treating
CC   diseases associated with GSR activity; for haplotyping, which is also
CC   used by the pharmaceutical research scientist to validate GSR as a
CC   candidate target for treating a specific condition or disease predicted
CC   to be associated with GSR activity, e.g. haemolytic anaemia, and in the
CC   design of clinical trials for treating a specific condition of disease
CC   associated with GSR activity; and for screening compounds targeting GSR.
CC   (I) is useful in studying the expression and function of GSR, and in
CC   expressing GSR protein for use in screening for candidate drugs to treat
CC   diseases related to GSR activity. (I) is also useful in studying the
CC   effect of the variation on the biological activity of GSR as well as on
CC   the binding affinity of candidate drugs targeting GSR for the treatment
CC   of haemolytic anaemia. The present sequence represents an allele specific
CC   oligonucleotide (ASO) primer for the human GSR gene, which is given in
CC   the exemplification of the present invention. N.B. The polymorphic base
CC   (showing a single nucleotide polymorphism) in the ASO primer is shown
CC   using an IUPAC ambiguity code (as given in the present invention)
XX
SQ   Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 15;
```

```
  Best Local Similarity   93.3%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
                ||||||||||||||:|
Db          1 TTTTTTTTTTTTTTWA 15


RESULT 3687
ADB88602
ID   ADB88602 standard; DNA; 21 BP.
XX
AC   ADB88602;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Frizzled-4 (FZD4) modulating agent related oligo, SEQ ID No 49.
XX
KW   Frizzled-4; FZD4; immunodulatory compound; ophthalmological; vasotropic;
KW   antiinflammatory; vulnerary; osteopathic; antimicrobial; antipsoriatic;
KW   antidiabetic; modulator; neovascularisation; myocardial ischaemia;
KW   coronary artery disease; wound healing; fracture; tendon repair;
KW   cancer tumour growth; metastatis; ocular neovascularisation; bone;
KW   cartilage destruction; inflammatory; infectious disease; psoriasis;
KW   pre-eclampsia; respiratory distress; peritoneal sclerosis; diabetes;
KW   FzD4; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003005034-A2.
XX
PD   16-JAN-2003.
XX
PF   04-JUL-2002; 2002WO-CA001004.
XX
PR   05-JUL-2001; 2001US-0303285P.
PR   29-OCT-2001; 2001US-0340409P.
XX
PA   (XENO-) XENON GENETICS INC.
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Macdonald ML,  Zeisler JM,  Samuels M,  Goldberg YP,  Robataille JM;
PI   Hayden MR;
XX
DR   WPI; 2003-221619/21.
XX
PT   Identifying Frizzled-4 (FZD4) gene modulators for treating e.g. familial
PT   exudative vitreoretinopathy or Coat's disease, comprises contacting a
PT   compound with an FZD4 polypeptide or with a cell expressing FZD4
PT   polypeptide.
XX
PS   Disclosure; Page 103; 116pp; English.
XX
CC   The invention relates to a novel method for identifying a Frizzled-4
CC   (FZD4) modulating agent. The method comprises contacting a compound with
CC   an FZD4 polypeptide or with a cell expressing an FZD4 polypeptide, and
CC   determining the difference in the biological activity or expression of
CC   the FZD4 polypeptide compared with when the compound is not present. The
CC   immunodulatory compounds of the invention can have the follwing
CC   activities of ophthalmological, vasotropic, antiinflammatory, vulnerary,
CC   osteopathic, antimicrobial, antipsoriatic, and antidiabetic. The method
CC   is useful for identifying modulators of FZD4, and such modulators are
CC   useful in treating diseases related to Fzd-4 expression or activity. The
CC   modulators are particularly useful in treating e.g. familial exudative
CC   vitreoretinopathy, retinopathy of prematurity, Coat's disease, Norrie
CC   disease, retinal angiomatosis, ocular toxocariasis, retinoblastoma,
CC   retinal dysplasia, neovascular inflammatory vitreoretinopathy or
CC   retinitis pigmentosa. The modulators are also useful for treating other
CC   diseases involving the physiological and pathological processes of
CC   neovascularisation, such as indications that may require stimulation of
CC   neovascularisation (e.g. myocardial ischaemia, coronary artery disease,
CC   wound healing, or fracture and tendon repair), indications that may
CC   require inhibition of neovascularisation (e.g. cancer tumour growth and
CC   metastatis, ocular neovascularisation, bone and cartilage destruction,
CC   inflammatory and infectious diseases), indications that require vascular
CC   remodeling (e.g. psoriasis or pre-eclampsia), and indications that
CC   require inhibition of neovascularisation (e.g. respiratory distress,
CC   peritoneal sclerosis, or diabetes). This polynucleotide sequence
CC   represents an oligo relating to the FzD4 gene of the invention.
XX
SQ   Sequence 21 BP; 4 A; 4 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATT 1791
              ||||||||||| || | || |
Db          1 TTTTTTTTTTTCAATCACACT 21


RESULT 3688
AAZ26632
ID   AAZ26632 standard; DNA; 21 BP.
XX
AC   AAZ26632;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 821.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
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CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 15 A; 2 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAA 2800
              | ||| |  ||||||||||||
Db          1 GCATTAACTAAAAAAAAAAAA 21


RESULT 3689
AAQ61989
ID   AAQ61989 standard; DNA; 21 BP.
XX
AC   AAQ61989;
XX
DT   25-MAR-2003  (revised)
DT   04-NOV-1994  (first entry)
XX
DE   HIV replication inhibiting oligomer, T13G4T4.
XX
KW   Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
KW   human cytomegalovirus; influenza virus; inflammation; telomere length;
KW   neurological disorders; phospholipase A2 activity; hyperproliferation;
KW   malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /note= "Labeled with 32P"
XX
PN   WO9408053-A1.
XX
PD   14-APR-1994.
XX
PF   29-SEP-1993;   93WO-US009297.
XX
PR   29-SEP-1992;   92US-00954185.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Hanecak RC,  Anderson KP,  Bennett CF,  Chiang M,  Brown-Driver VL;
PI   Ecker DJ,  Vickers TA,  Wyatt JR,  Imbach JL;
XX
DR   WPI; 1994-135613/16.
XX
PT   New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT   of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT   of chromosomes.
XX
PS   Example 21; Page 60; 144pp; English.
XX
CC   This sequence may be used for inhibiting replication of human immuno-
CC   deficiency virus (HIV). Oligonucleotides such as this may also be used
CC   for inhibiting activity of HSV, human cytomegalovirus or influenza virus,
CC   or for treating inflammatory and neurological disorders caused by
CC   phospholipase A2 activity in cases of hyper- proliferation, malignancy,
CC   cardiovascular disease and snake bite. They may also be used for
CC   inhibiting division of malignant cells by modualting telomere length,
CC   which may also retard aging. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||    ||||
Db          1 TTTTTTTTTTTTGGGGTTTT 21


RESULT 3690
AAQ99590
ID   AAQ99590 standard; cDNA; 21 BP.
XX
AC   AAQ99590;
XX
DT   25-MAR-2003  (revised)
DT   30-APR-1996  (first entry)
XX
DE   Human TPO anti-sense primer hTPO-F.
XX
KW   Thrombopoietin; TPO; humoral factor; platelet; antibody; therapy; AIDS;
KW   thrombocytopenia; hypoplastic anaemia; thrombotic thombocytopenia;
KW   disseminated intravascular coagulation syndrome; PCR; primer; amplify;
KW   polymerase chain reaction; rat; human; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .21
FT                   /*tag=  a
FT                   /note= "corresponds to bases 127 to 147 of AAQ99553"
XX
PN   WO9521919-A2.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-JP000208.
XX
PR   14-FEB-1994;   94JP-00039090.
PR   14-MAR-1994;   94US-00212164.
PR   25-MAR-1994;   94JP-00079842.
PR   01-APR-1994;   94US-00221020.
PR   01-JUN-1994;   94JP-00155126.
PR   15-JUN-1994;   94JP-00167328.
PR   20-JUL-1994;   94US-00278083.
PR   17-AUG-1994;   94JP-00193169.
PR   17-AUG-1994;   94JP-00227159.
PR   18-AUG-1994;   94JP-00193916.
PR   11-OCT-1994;   94US-00320300.
PR   01-NOV-1994;   94JP-00304167.
PR   01-DEC-1994;   94JP-00298669.
PR   22-DEC-1994;   94US-00361811.
PR   28-DEC-1994;   94JP-00341200.
PR   31-JAN-1995;   95US-00318478.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
PI   Miyazaki H,  Kato T,  Ohgami K,  Iwamatsu A,  Akahori H,  Kuroki R;
PI   Shimizu T,  Muto T;
XX
DR   WPI; 1995-293120/38.
XX
PT   Thrombopoietin polypeptide which specifically stimulates or increases
PT   platelet production - useful in treatment of thrombocytopenia, also
PT   related DNA and vectors.
XX
PS   Example 24; Page 139; 383pp; English.
XX
CC   AAQ99589-Q99592 represent amplification primers based on regions of a
CC   thrombopoietin (TPO) cDNA (see AAQ99553). These primers were used to test
CC   for the presence of TPO DNA in a phage comprising a human cDNA library.
CC   TPO is a humoral factor capable of promoting platelet production. The
CC   protein encoded by the full length sequence can be purified by using a
CC   gel affinity column where Mpl has been coupled to a resin. AAQ99551 and
CC   AAQ99552 also encode TPO proteins. The full length DNA sequences are
CC   inserted into vectors which are used to transform prokaryotic and
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CC   eukaryotic host cells. Using the proteins encoded by the full length
CC   sequences, and derivatives of them, antibodies specifically
CC   immunoreactive with a TPO protein can be created. The antibodies, DNA
CC   sequences and vectors are used to isolate the protein sequences. The TPO
CC   proteins can then be used in the treatment of platelet disorders. These
CC   include thrombocytopenia, hypoplastic anaemia, AIDS, disseminated
CC   intravascular coagulation syndrome and thrombotic thrombocytopenia.
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2298 AGGGTAGGCACGAAGCAATTT 2318
              | || || ||||||||| |||
Db          1 ATGGGAGTCACGAAGCAGTTT 21


RESULT 3691
AAT35001
ID   AAT35001 standard; DNA; 21 BP.
XX
AC   AAT35001;
XX
DT   25-MAR-2003  (revised)
DT   03-DEC-1996  (first entry)
XX
DE   HIV inhibitor #4.
XX
KW   HIV; infection inhibitor; triplex forming; purine rich promoter; V3 loop;
KW   transcription inhibitor; gp120 protein; viral growth; enzyme inhibitor;
KW   PLA2; telomere length; glove coating; condom; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .21
FT                   /*tag=  a
FT                   /note= "phosphorothioate nucleotides"
XX
PN   US5523389-A.
XX
PD   04-JUN-1996.
XX
PF   28-SEP-1993;   93US-00128011.
XX
PR   29-SEP-1992;   92US-00954185.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Imbach JL,  Ecker DJ,  Wyatt JR;
XX
DR   WPI; 1996-285782/29.
XX
PT   New octa:nucleotide with guanosine quartet and phosphoro:thioate links -
PT   is inhibitor of HIV infection by binding to the V3 loop.
XX
PS   Example 3; Col 8; 14pp; English.
XX
CC   AAT34998-T35001 represent HIV inhibitors. Sequences containing only G and
CC   T residues (such as these sequences) are triplex forming
CC   oligonucleotides, and form purine rich promoter elements used to inhibit
CC   transcription. These sequences bind to the HIV gp120 protein at the V3
CC   loop via the internal guanosine quartet. This binding prevents cell-to-
CC   cell and virus-to-cell infection. The sequences may also be used for
CC   inhibiting viral growth, and other viral genes, for inhibiting the enzyme
CC   PLA2, and to modulate telomere length. In some cases these sequences need
CC   to be chemically modified. The chemically modified oligonucleotides
CC   preferably include at least one phosphorothioate linkage. Other modified
CC   intersugar links, or 2'-modified sugar residues can also be used. These
CC   oligonucleotides can be used for coating gloves, condoms, etc, or for
CC   topical application. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||    ||||
Db          1 TTTTTTTTTTTTGGGGTTTT 21


RESULT 3692
AAT10482
ID   AAT10482 standard; DNA; 21 BP.
XX
AC   AAT10482;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Anti-HIV TAR region 'Aptastruc' family IV oligonucleotide #6.
XX
KW   Aptastruc oligonucleotide; non-linear; target; self-annealing; hairpin;
KW   stem; TAR; HIV; tat protein; viral development; regulatory element;
KW   mini-exon; trypanosome; iron response element; ribozyme; ss.
XX
OS   Synthetic.
XX
PN   WO9604374-A1.
XX
PD   15-FEB-1996.
XX
PF   01-AUG-1995;.  95WO-FR001036.
XX
PR   02-AUG-1994;   94FR-00009578.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Toulme J,  Mishra R;
XX
DR   WPI; 1996-129391/13.
XX
PT   New oligo:nucleotide with affinity for non-linear target - includes a
PT   sequence preventing canonical interaction but able to form a complex,
PT   used to prevent development of viruses, bacteria and parasites.
XX
PS   Example 2; Page 22; 48pp; French.
XX
CC   The oligonucleotides AAT10455-82 represent examples of novel
CC   oligonucleotides designated 'Aptastruc'. The oligonucleotides have
CC   affinity for non-linear target sequences e.g a self-annealed hairpin
CC   structure. They have a complementary sequence to part of the linear
CC   (stem) of the target whereas the remainder (i.e. either end) of the
CC   oligonucleotide does not interact with the target sequence. The
CC   oligonucleotides presented here are targeted to the TAR region of HIV,
CC   which binds to the tat protein during viral development. The novel
CC   oligonucleotides are generally targeted to regulatory elements such as a
CC   mini-exon from trypanosomes, the HIV TAR or an iron response element.
CC   They may either bind to the target sequence to interfere with its
CC   regulatory role or may contain a functional group e.g. a ribozyme to
CC   cleave the target sequence
XX
SQ   Sequence 21 BP; 3 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2099 TCAAACGGGGGCCTTCTGGTT 2119
              || |||||| |||| || |||
Db          1 TCTAACGGGTGCCTACTCGTT 21
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RESULT 3693
AAZ26823
ID   AAZ26823 standard; DNA; 21 BP.
XX
AC   AAZ26823;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 1012.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 9 A; 0 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTGAAA 2196
              ||||||||||||    ||||
Db          1 TTTTTTTTTTTAAAAAAGAAA 21


RESULT 3694
AAZ26499
ID   AAZ26499 standard; DNA; 21 BP.
XX
AC   AAZ26499;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 688.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 13 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1970 TTTACCTTGAAAAAAAGAAAA 1990
              | ||| || ||||||| ||||
Db          1 TCTACTTTCAAAAAAAAAAAA 21


RESULT 3695
AAZ26499/c
ID   AAZ26499 standard; DNA; 21 BP.
XX
AC   AAZ26499;
XX
DT   30-NOV-1999  (first entry)
```

```
XX
DE   Human polymorphic region 688.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 13 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGA 2194
             ||||||||||||  ||  | ||
Db         21 TTTTTTTTTTTTGAAAGTAGA 1


RESULT 3696
AAZ26114
ID   AAZ26114 standard; DNA; 21 BP.
XX
AC   AAZ26114;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 303.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1639 ATTTAAAGAGCCTTCACTGGT 1659
              | | || |||||| |||||||
Db          1 ACTGAATGAGCCTCCACTGGT 21


RESULT 3697
AAV99170/c
ID   AAV99170 standard; DNA; 21 BP.
XX
AC   AAV99170;
XX
DT   09-MAR-1999  (first entry)
XX
DE   Antisense primer for intron boundary mapping of DNA MeTase exons 7-8.
XX
KW   DNA methyltransferase; DNA MeTase; antisense oligonucleotide; human;
KW   cellular growth; tumour growth inhibition; silenced gene activation;
KW   beta thalassemia; sickle cell anemia; PCR primer; ss.
XX
OS   Synthetic.
```

```
OS   Homo sapiens.
XX
PN   WO9854313-A2.
XX
PD   03-DEC-1998.
XX
PF   29-MAY-1998;   98WO-IB001107.
XX
PR   30-MAY-1997;   97US-00866340.
PR   17-DEC-1997;   97US-0069865P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Szyf M,  Bigey P,  Ramchandani S;
XX
DR   WPI; 1999-059833/05.
XX
PT   New DNA methyltransferase nucleotide sequences - used particularly to
PT   develop antisense oligonucleotides for diagnostic and therapeutic
PT   purposes, particularly for inhibiting tumour growth.
XX
PS   Example 8; Page 31; 108pp; English.
XX
CC   PCR primers AAV99163-220 were used to map the intron boundaries of the
CC   exons of DNA methyltransferase (DNA MeTase) genomic sequence. Antisense
CC   oligonucleotides which inhibit inhibit DNA MeTase expression can be
CC   derived from the genomic DNA MeTase sequence. The antisense
CC   oligonucleotides can be used in investigating the role of DNA MeTase in
CC   cellular growth. They can be administered at different points in the cell
CC   cycle, or in conjugation with promoters or inhibitors of cell growth to
CC   determine the role of DNA MeTase in the growth of the cell type of
CC   interest. The antisense oligonucleotides can also be used for inhibiting
CC   tumour growth in a mammal, or to activate silenced genes to provide a
CC   missing gene function. This ameliorates disease symptoms, e.g. in beta
CC   thalassemia and sickle cell anemia. The antisense oligonucleotides can
CC   also be used an analytical and diagnostic tools and a potentiators of
CC   transgenic plant and animal studies
XX
SQ   Sequence 21 BP; 1 A; 6 C; 4 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1402 GCAGAACTACATCAAAGAAGC 1422
              ||||||  || | ||||||||
Db         21 GCAGAAGAACCTGAAAGAAGC 1


RESULT 3698
AAX33038
ID   AAX33038 standard; DNA; 21 BP.
XX
AC   AAX33038;
XX
DT   21-JUN-1999  (first entry)
XX
DE   Human BRCA2 gene PCR primer SEQ ID NO:51.
XX
KW   Human; BRCA2; genetic testing; protein therapy; haplotype; detection;
KW   gene therapy; breast cancer; ovarian cancer; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9909164-A1.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1998;   98WO-US016905.
XX
PR   15-AUG-1997;   97US-0055784P.
PR   07-NOV-1997;   97US-0064926P.
PR   12-NOV-1997;   97US-0065367P.
PR   01-MAY-1998;   98US-00071715.
PR   22-MAY-1998;   98US-00084471.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD,  White MB,  Rabin MB,  Olson SJ,  Yoshikawa M,  Jackson GM;
PI   Eskandari T,  Schryer B,  Park M;
XX
DR   WPI; 1999-190163/16.
XX
PT   New coding sequence haplotypes of the human BRCA2 gene - used to develop
PT   products for determining susceptibility to, detection and treatment of
PT   breast or ovarian cancer.
XX
PS   Example 1; Page 32; 226pp; English.
XX
CC   The present invention describes genomic DNA which contains a BRCA2 gene
CC   where the first 12 nucleotides beginning exon 5 are 5'-TCCTGTTGTTCT-3' as
CC   in sequence (I) (see AAX03249), where nucleotides numbers 5782-5790 are
CC   GTTTGTGTT as in sequence (IV) (see AAX30255), and where the last 20
CC   nucleotides encoding exon 15 are 5'-CTGCGTGTTCTCATAAACAG-3' as in
CC   sequence (II) (see AAX30251) and the first 20 nucleotides beginning exon
CC   16 are 5'-CTGTATACGTATGGCGTTTC-3' as in sequence (III) (see AAX30253).
CC   Products and methods from the present invention can be used for
CC   identifying mutations in the BRCA2 gene leading to predisposition or
CC   higher susceptibility to breast or ovarian cancer. They can also be used
CC   for detection and gene therapy for breast and ovarian cancers. They can
CC   be used in methods for monitoring disease progression, for determining
CC   patients suited for gene and protein replacement progression, or for
CC   detecting the presence or quantifying the amount of a tumour growth
CC   inhibitor following such therapy. The BRCA2 protein, polypeptides, their
CC   functional equivalents, antibodies, and PNs may also be useful in the
CC   study of the characteristics of BRCA2 proteins, such as structure and
CC   function of BRCA2 in oncogenesis or subcellular localisation of BRCA2
CC   protein in normal and cancerous cells. AAX33001 to AAX33097 represent PCR
CC   primers used in the amplification of the human BRCA2 gene
XX
SQ   Sequence 21 BP; 8 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1401 TGCAGAACTACATCAAAGAAG 1421
              ||||||  |||||| || |||
Db          1 TGCAGAGGTACATCCAATAAG 21


RESULT 3699
AAZ59327
ID   AAZ59327 standard; DNA; 21 BP.
XX
AC   AAZ59327;
XX
DT   05-APR-2000  (first entry)
XX
DE   Human STP2 exon 7 polymorphism sequence 85.
XX
KW   Single nucleotide polymorphism; SNP; STP2; phenol sulphotransferase;
KW   probe; genotyping; human; drug metabolism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       11
FT                   /*tag=  a
FT                   /note= "Site of polymorphism"
XX
PN   WO9964630-A1.
XX
PD   16-DEC-1999.
XX
```

```
PF   09-JUN-1999;   99WO-US013094.
XX
PR   10-JUN-1998;   98US-0088710P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Guida M,  Kurth J;
XX
DR   WPI; 2000-105892/09.
XX
PT   Novel nucleic acid used for genotyping, e.g. to predict rate of drug
PT   metabolism.
XX
PS   Claim 2; Page 16; 46pp; English.
XX
CC   Sequences AAZ59305-Z59352 are fragments of the human STP2 gene. The
CC   fragments are from the 8 exons, the promoter region, 3' and 5'
CC   untranslated regions of the STP2 gene. Each sequence contains a newly
CC   identified STP2 gene single nucleotide polymorphism (SNP). STP2 is a
CC   phenol sulphotransferase. Substrates for STP2 include minoxidil,
CC   acetaminophen, and paranitrophenol. Several of the nucleotide changes
CC   identified at the polymorphism sites, give rise to an amino acid change.
CC   Amino acid changes may result in altered enzyme activity. The sequences
CC   can be used as probes for detecting STP2 polymorphisms. The polymorphic
CC   probes are used in screening and genotyping, i.e. to predict the rate of
CC   metabolism of STP2 substrates, potential drug-drug interactions and
CC   adverse side effects. They can also be used to detect diseases resulting
CC   from accidental or occupational exposure to toxins and to establish
CC   animal, cell or in vitro models for drug metabolism
XX
SQ   Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        764 ATGACCAAGAACCCTCTGAAC 784
              ||||  ||||||||| ||| |
Db          1 ATGAAGAAGAACCCTATGACC 21


RESULT 3700
AAZ58833/c
ID   AAZ58833 standard; DNA; 21 BP.
XX
AC   AAZ58833;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human beta2-microglobulin gene specific primer beta-21F.
XX
KW   Mucin; MUC11; MUC12; human; chromosome 7q22; epithelial inflammation;
KW   Crohn's disease; ulcerative colitis; asthma; chronic bronchitis;
KW   colorectal cancer; cystic fibrosis; inflammatory bowel disease;
KW   breast cancer; beta2-microglobulin; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004142-A1.
XX
PD   27-JAN-2000.
XX
PF   16-JUL-1999;   99WO-AU000579.
XX
PR   16-JUL-1998;   98AU-00004708.
XX
PA   (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA   (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX
PI   Williams SJ,  Antalis TM,  Mcguckin MA,  Gotley DC;
XX
DR   WPI; 2000-182416/16.
XX
PT   Novel MUC nucleic acid corresponding to mucin gene, useful for treating
PT   associated disease conditions e.g. colorectal, breast cancer, cystic
PT   fibrosis and inflammatory bowel disease.
XX
PS   Example 7; Page 40; 103pp; English.
XX
CC   The invention provides mucin genes (MUC11 and MUC12) located on human
CC   chromosome 7q22. The mucin genes or its portion is used in detecting
CC   polymorphism, mutation, deletion, truncation and expansion in the gene or
CC   its gene transcript. Pharmaceutical compositions and gene therapy
CC   constructs comprising the mucin genes are used for treating disease
CC   conditions associated with aberrant Mucin expression, altered properties
CC   of mucus or epithelial inflammatory processes involving Mucins like
CC   Crohn's disease, ulcerative colitis, asthma, chronic bronchitis and
CC   colorectal cancer, cystic fibrosis, inflammatory bowel disease and breast
CC   cancer. The mucin genes and the polypeptides are used for determining
CC   these diseases or their predisposition. The MUC11 and MUC12 polypeptides
CC   are used for preparing antagonist and antibodies. Sequences AAZ58833-34
CC   represent beta2-microglobulin gene specific primers
XX
SQ   Sequence 21 BP; 3 A; 2 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1858 ACCCACACACTTAGCCATTGA 1878
              ||||| |||| |||| ||| |
Db         21 ACCCAGACACATAGCAATTCA 1


RESULT 3701
AAZ99642
ID   AAZ99642 standard; DNA; 21 BP.
XX
AC   AAZ99642;
XX
DT   12-JUL-2000  (first entry)
XX
DE   Nucleotide sequence of G-motif oligonucleotide PZ332.
XX
KW   G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW   antigen presenting cell activation; natural killer cell; septic shock;
KW   cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW   rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW   Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW   helper T cell response 1-mediated disease; Lyme arthritis;
KW   Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW   psoriasis vulgaris; experimental allergic encephalomyelitis;
KW   insulin-dependent diabetes mellitus; bacterial infection;
KW   parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX
OS   Synthetic.
XX
PN   WO200014217-A2.
XX
PD   16-MAR-2000.
XX
PF   03-SEP-1999;   99WO-EP006502.
XX
PR   03-SEP-1998;   98EP-00116652.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX
PI   Wagner H,  Lipford GB,  Heeg K;
XX
DR   WPI; 2000-256970/22.
XX
PT   Compositions comprising G-motif oligonucleotides useful for treating e.g.
PT   septic shock, rheumatoid arthritis, diabetes and human immunodeficiency
PT   virus infections.
XX
PS   Disclosure; Page 34; 75pp; English.
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```
XX
CC   The present sequence represents a G-motif oligonucleotide of the
CC   invention. The specification describes compositions comprising G-motif
CC   oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC   antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC   stimulating natural killer cells, or by co-stimulating cytotoxic T-
CC   lymphocytes. The G-motif oligonucleotides may be used for the productions
CC   of vaccines for treating septic shock, inflammation, autoimmune diseases
CC   (e.g. rheumatoid arthritis, Crohn's disease, sarcoidosis, multiple
CC   sclerosis, Kawasaki syndrome, graft-versus-host disease and transplant
CC   rejection), helper T cell response 1-mediated diseases (e.g.
CC   Streptococcal induced arthritis, Lyme arthritis, chronic inflammatory
CC   bowel disease, psoriasis vulgaris, experimental allergic
CC   encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
CC   infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
CC   viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
CC   (HIV)-infections), spontaneous abortions and tumours. They may also be
CC   used to induce proliferation of bone marrow cells, especially macrophage
CC   precursor cells
XX
SQ   Sequence 21 BP; 2 A; 5 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTT 2182
              ||||| ||||||||||  | |
Db          1 CTCCTATTTTTTTTTCCTAT 21


RESULT 3702
AAZ74861/c
ID   AAZ74861 standard; DNA; 21 BP.
XX
AC   AAZ74861;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:9217.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 2195; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 21 BP; 7 A; 9 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2674 GTGTGTGTGGGTGAAATGGAG 2694
              |||| ||||| ||| ||| ||
Db         21 GTGTATGTGGTTGAGATGAAG 1


RESULT 3703
AAF97598
ID   AAF97598 standard; DNA; 21 BP.
XX
AC   AAF97598;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #2359.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 209; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
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```
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        758 ATTTCCATGACCAAGAACCCT 778
              |||   |||||||||| ||||
Db          1 ATTGGAATGACCAAGATCCCT 21


RESULT 3704
AAF96163
ID   AAF96163 standard; DNA; 21 BP.
XX
AC   AAF96163;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #924.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 113; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        189 ATGTCAAGTACGAAGAGGACT 209
              ||| || | |||| |||||||
Db          1 ATGACATGGACGAGGAGGACT 21


RESULT 3705
AAF95716/c
ID   AAF95716 standard; DNA; 21 BP.
XX
AC   AAF95716;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #477.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 81; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
```

```
SQ   Sequence 21 BP; 1 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        432 CCCTGCACCAGCCGGCGCCCA 452
              ||| | | ||||||| |||||
Db         21 CCCCGAAGCAGCCGGTGCCCA 1


RESULT 3706
AAF30891/c
ID   AAF30891 standard; DNA; 21 BP.
XX
AC   AAF30891;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Mismatched target of ODN-MGB-LF conjugate.
XX
KW   ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
KW   hybridisation; detection; fluorescence; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200131063-A1.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029786.
XX
PR   26-OCT-1999;   99US-00428236.
XX
PA   (EPOC-) EPOCH BIOSCIENCES INC.
XX
PI   Dempcy RO,  Afonina IA,  Vermeulen NMJ;
XX
DR   WPI; 2001-328656/34.
XX
PT   Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT   useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT   mismatch discrimination.
XX
PS   Example 9; Page 78; 105pp; English.
XX
CC   The present sequence is that of a mismatched target sequence for an
CC   oligonucleotide (ODN)-minor groove binder (MGB)-latent fluorophore (LF)
CC   conjugate of the invention. It contains a single nucleotide mismatch to
CC   the ODN moiety of the conjugate, and was used to demonstrate the use of
CC   ODN-MGB-LF conjugates as primers in real-time PCR. The template was the
CC   4518 bp pBK-CMV phagemid. The template contained a LacZ gene insert in
CC   which the region between nucleotides 1060 and 1083 was substituted with
CC   either the present mismatched target sequence, or with the matched target
CC   sequence given in AAF30890. Primers (see AAF30892-94) were chosen to
CC   produce a 42 bp amplicon. A strong fluorescence output was observed for
CC   the template with the perfectly-matched sequence, but only background
CC   fluorescence was observed for the template with the single-base mismatch
XX
SQ   Sequence 21 BP; 2 A; 5 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              ||||||| |||| || ||| |
Db         21 ATTGAAAGAAAAGAAGAAAGA 1


RESULT 3707
AAH62490/c
ID   AAH62490 standard; DNA; 21 BP.
XX
AC   AAH62490;
XX
DT   12-SEP-2001  (first entry)
XX
DE   PTK2 polymorphism containing DNA fragment #391.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 60; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        718 CCTGTTGCTGCACGATCAGAC 738
              ||||||||||   ||| ||||
Db         21 CCTGTTGCTGTCGGATTAGAC 1


RESULT 3708
AAH62659/c
ID   AAH62659 standard; DNA; 21 BP.
XX
AC   AAH62659;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Glucosidase alpha acid polymorphism containing DNA fragment #560.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
```

```
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 74; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 4 A; 12 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        139 GCGACTGTTTTGGGGGACGCC 159
              ||| |||||  |||||||| |
Db         21 GCGGCTGTTGGGGGGGACGTC 1


RESULT 3709
ABA04384
ID   ABA04384 standard; DNA; 21 BP.
XX
AC   ABA04384;
XX
DT   06-MAR-2002  (first entry)
XX
DE   AtERF4 PCR primer 1 SEQ ID NO:3.
XX
KW   Arabidopsis thaliana; ethylene responsive element binding factor 4;
KW   AtERF4; transcription inhibition; antiallergic; gene therapy; plant;
KW   allergen; PCR primer; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   JP2001269178-A.
XX
PD   02-OCT-2001.
XX
PF   27-MAR-2000; 2000JP-00087556.
XX
PR   27-MAR-2000; 2000JP-00087556.
XX
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-078280/11.
XX
PT   New peptides having inhibitory function to gene transcription for
PT   preparation of plants with reduced allergen.
XX
PS   Example; Page 3; 13pp; Japanese.
XX
CC   The present invention describes gene transcription inhibitory peptides.
CC   The peptides having a gene transcription inhibitory function are encoded
CC   by the Arabidopsis thaliana ethylene responsive element binding factor 4
CC   (AtERF4) 795 base sequence, or comprises a sequence of 40 amino acids or
CC   a derivative with deleted, replaced or added amino acid(s) of AtERF4. The
CC   peptides have antiallergic activity and can be used in gene therapy. The
CC   peptides can be used in the preparation of plants with reduced allergen.
CC   The present sequence represents a PCR primer for AtERF4, which is used in
CC   an example from the present invention
XX
SQ   Sequence 21 BP; 6 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1009 GTTGGACAAGATCGGGTTGAA 1029
              | ||| |||||| || |||||
Db          1 GATGGCCAAGATGGGCTTGAA 21


RESULT 3710
ABK70498
ID   ABK70498 standard; DNA; 21 BP.
XX
AC   ABK70498;
XX
DT   15-JUL-2002  (first entry)
XX
DE   In-situ analysis synthetic probe #63.
XX
KW   Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KW   Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;
KW   kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KW   Epstein-Barr early RNA; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200222874-A2.
XX
PD   21-MAR-2002.
XX
PF   06-SEP-2001; 2001WO-US028014.
XX
PR   15-SEP-2000; 2000US-0233177P.
XX
PA   (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX
PI   Utermohlen JG,  Connaughton J;
XX
DR   WPI; 2002-371972/40.
XX
PT   Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT   probes useful for detecting or localizing nucleic acid target genes
PT   within a cell or tissue sample.
XX
PS   Example 4; Page 19; 71pp; English.
XX
CC   The present invention relates to a new oligonucleotide label-domain
CC   comprising the sequence (CTATTTT)_n and its complement (AAAATAG)_n, where
CC   n is 1. The probe sets of the invention are useful for detecting kappa or
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CC   lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC   RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC   early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC   sequences. The invention is a useful generic sequence for incorporation
CC   into oligonucleotide probes for detecting gene-specific sequences within
CC   cells or tissue samples in in situ hybridisation analysis and for
CC   attaching a label to immunoglobulins or other proteins for detecting
CC   haptens and antigens in immunohistochemical analyses. The present nucleic
CC   acid sequence represents one of a collection (ABK70376-ABK70501) of
CC   oligonucleotide probes that were used in the invention for detecting or
CC   localising a plurality nucleic acid target gene or antigen within a cell
CC   or tissue sample
XX
SQ   Sequence 21 BP; 2 A; 3 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              || ||||| | ||||| ||||
Db          1 CTATTTTTCTATTTTCTTTT 21


RESULT 3711
ABA03336/c
ID   ABA03336 standard; DNA; 21 BP.
XX
AC   ABA03336;
XX
DT   12-FEB-2002  (first entry)
XX
DE   S chrysomallus actinomycin biosynthase gene acmC fragment #4.
XX
KW   Modular enzyme system; cyclic gene synthesis; repetitive coding sequence;
KW   antibiotic; non-ribosomal peptide synthetase; NRPS; PKS;
KW   polyketide synthase; actinomycin biosynthase; ds.
XX
OS   Streptomyces chrysomallus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .21
FT                   /*tag=  a
FT                   /product= "antinomycin biosynthesis protein fragment"
FT                   /partial
FT                   /note= "no start or stop codon"
XX
PN   WO200181564-A2.
XX
PD   01-NOV-2001.
XX
PF   25-APR-2001; 2001WO-DE001578.
XX
PR   26-APR-2000; 2000DE-01021267.
XX
PA   (ACTI-) ACTINODRUG PHARM GMBH.
XX
PI   Schauwecker F;
XX
DR   WPI; 2002-049276/06.
DR   P-PSDB; AAM47146.
XX
PT   Preparing DNA encoding modular protein for e.g. producing new enzymes for
PT   synthesis of polyketide antibiotics, comprises cyclic integration of
PT   fragments into a vector.
XX
PS   Example 3; Page 53; 83pp; German.
XX
CC   The present invention relates to the preparation of DNA, in a circular
CC   vector, that encodes one or more segments of a modular polypeptide. DNA
CC   or DNA libraries produced this way are used to produce modular
CC   polypeptides, particularly enzymes, which can be used to act on
CC   substrates to produce compounds for therapeutic testing. Enzymes of
CC   particular interest are those involved in non-ribosomal peptide synthesis
CC   or polyketide synthesis, and compounds for testing are particularly
CC   macrolide antibiotics, including penicillins, vancomycins or
CC   erythromycins, but may also be modular receptors. The present sequence is
CC   a fragment of a Streptomyces chrysomallus actinomycin biosynthesis gene
CC   which was used in the exemplification of the invention
XX
SQ   Sequence 21 BP; 1 A; 11 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGGCGGCGGC 67
              | ||||||||  |||||| ||
Db         21 GTGCGCGGCGACGGCGGCCGC 1


RESULT 3712
ABS97903
ID   ABS97903 standard; DNA; 21 BP.
XX
AC   ABS97903;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human UDP-glucuronosyl transferase 24B polymorphic sequence #21.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 18; Page 134; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
```

CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention
XX
SQ Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAAA 2804
| ||||||||||||| |||
Db 1 TCAAAAAAAAAAAAATCCAAA 21

RESULT 3713
ABS97903/c
ID ABS97903 standard; DNA; 21 BP.
XX
AC ABS97903;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human UDP-glucuronosyl transferase 24B polymorphic sequence #21.
XX
KW Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 18; Page 134; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention
XX
SQ Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2167 TTTTTTTTTTTTTTTTTTTA 2187
||| ||||||||||||| |
Db 21 TTTGGATTTTTTTTTTTTGA 1

RESULT 3714
ABS98297/c
ID ABS98297 standard; DNA; 21 BP.

XX
AC ABS98297;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human lactoferrin (LTF) gene polymorphic sequence #60.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 23; Page 149; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 21 BP; 9 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2624 ACTTTGTCTCGTTCCTGTTGG 2644
| | | ||||||| |||||||
Db 21 AGTATCTCTCGTTGCTGTTGG 1

RESULT 3715
ABS66996
ID ABS66996 standard; DNA; 21 BP.
XX
AC ABS66996;
XX
DT 29-NOV-2002 (first entry)
XX
DE Human MRP-1 polymorphic DNA region #258.
XX
KW Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200259142-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-EP000796.
XX
PR 26-JAN-2001; 2001EP-00101651.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI Brinkmann U, Hoffmeyer S, Mornhinweg E;
XX
DR WPI; 2002-657475/70.
XX
PT Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT diagnosis and treatment of cancer and multidrug resistance related
PT diseases, and for identifying single nucleotide polymorphisms.
XX
PS Claim 1; Page 84; 198pp; English.
XX
CC The invention relates to a multidrug resistance-associated protein 1 (MRP
CC -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC for identifying a single nucleotide polymorphism and for identifying and
CC obtaining a pro-drug or drug capable of modulating the activity of a
CC molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC of the activity of a molecular variant of MRP-1. The sequences are useful
CC for diagnosing a disorder related to the presence of a molecular variant
CC of MRP-1 or susceptibility to such a disorder, where the disorder is
CC cancer (particularly renal cancer) or a disease related to multidrug
CC resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ Sequence 21 BP; 3 A; 15 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 21;

```
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCCA 309
              ||||||||||| |||   ||||
Db          1 CCCCGCGCCATCCCCACCCCA 21


RESULT 3716
ABS66995/c
ID   ABS66995 standard; DNA; 21 BP.
XX
AC   ABS66995;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human MRP-1 polymorphic DNA region #257.
XX
KW   Human; multidrug resistance-associated protein 1; MRP-1; ss; cancer;
KW   renal cancer; cytostatic; single nucleotide polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO200259142-A2.
XX
PD   01-AUG-2002.
XX
PF   25-JAN-2002; 2002WO-EP000796.
XX
PR   26-JAN-2001; 2001EP-00101651.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIES AG.
XX
PI   Brinkmann U,  Hoffmeyer S,  Mornhinweg E;
XX
DR   WPI; 2002-657475/70.
XX
PT   Novel multidrug resistance-associated protein 1 polynucleotide useful for
PT   diagnosis and treatment of cancer and multidrug resistance related
PT   diseases, and for identifying single nucleotide polymorphisms.
XX
PS   Claim 1; Page 84; 198pp; English.
XX
CC   The invention relates to a multidrug resistance-associated protein 1 (MRP
CC   -1) polynucleotide. The polynucleotide is useful in an in vitro method
CC   for identifying a single nucleotide polymorphism and for identifying and
CC   obtaining a pro-drug or drug capable of modulating the activity of a
CC   molecular variant of MRP-1 or for identifying and obtaining an inhibitor
CC   of the activity of a molecular variant of MRP-1. The sequences are useful
CC   for diagnosing a disorder related to the presence of a molecular variant
CC   of MRP-1 or susceptibility to such a disorder, where the disorder is
CC   cancer (particularly renal cancer) or a disease related to multidrug
CC   resistance. This sequence represents a human MRP-1 polymorphic DNA region
XX
SQ   Sequence 21 BP; 1 A; 2 C; 15 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        289 CCCCGCGCCACCCCTCTCCCA 309
              ||||||||||| |||   ||||
Db         21 CCCCGCGCCATCCCCACCCCA 1


RESULT 3717
ABV73012
ID   ABV73012 standard; DNA; 21 BP.
XX
AC   ABV73012;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Murine cPLA2/B mutagenising oligonucleotide.
XX
KW   Calcium independent phospholipase A2/B; cPLA2/B; phospholipase;
KW   antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
KW   antiasthmatic; mutagenesis; ss.
XX
OS   Mus sp.
XX
PN   US2002106364-A1.
XX
PD   08-AUG-2002.
XX
PF   09-AUG-2001; 2001US-00927180.
XX
PR   27-JUL-1994;   94US-00281193.
PR   14-APR-1995;   95US-00422106.
PR   14-APR-1995;   95US-00422420.
PR   26-JUN-1995;   95WO-US008069.
PR   08-NOV-1995;   95US-00555568.
PR   09-SEP-1998;   98US-00149988.
PR   06-MAR-2000; 2000US-00519223.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jones S,  Tang J;
XX
DR   WPI; 2002-739923/80.
XX
PT   Novel composition comprising purified mammalian calcium independent
PT   phospholipase enzyme, useful for the screening of inhibitors of
PT   phospholipase activity, is active in the absence of calcium.
XX
PS   Example 6; Page 9; 41pp; English.
XX
CC   The invention relates to a purified mammalian calcium independent
CC   cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC   characterized by activity in the absence of calcium and has a molecular
CC   weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC   calcium independent phospholipase enzyme is useful for identifying an
CC   inhibitor of phospholipase activity which involves combining (I),
CC   phospholipid and candidate inhibitor compound, and observing whether the
CC   enzyme cleaves the phospholipid and releases fatty acid from it. A
CC   pharmaceutical composition (PC) comprising a therapeutically effective
CC   amount of the inhibitor is useful for reducing inflammation and for
CC   treating inflammatory conditions including rheumatoid arthritis,
CC   psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC   by increased levels of prostaglandins, leukotriene or platelet activating
CC   factor. A composition comprising an antibody which binds to (I) is useful
CC   as research and diagnostic tool, and is also useful in the study of
CC   phospholipase A2 activity and inflammatory conditions. The present
CC   sequence represents a cPLA2/B enzyme mutagenising oligonucleotide
XX
SQ   Sequence 21 BP; 2 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1283 CATGGGACCAGCAGGCTCGCC 1303
              ||||||||| || ||||  ||
Db          1 CATGGGACCCGCTGGCTTTCC 21


RESULT 3718
ABX70767/c
ID   ABX70767 standard; DNA; 21 BP.
XX
AC   ABX70767;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human RTQ-PCR primer #1 for NOV27.
XX
```

KW Human; ss; NOVX; metabolic disorder; diabetes; cardiomyopathy; obesity;
KW infectious disease; anorexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic disturbance;
KW metabolic syndrome X; wasting disorder; cancer; RTQ-PCR; primer;
KW real-time quantitative PCR.
XX
OS Homo sapiens.
XX
PN WO200281518-A2.
XX
PD 17-OCT-2002.
XX
PF 21-FEB-2002; 2002WO-US005374.
XX
PR 21-FEB-2001; 2001US-0270220P.
PR 21-FEB-2001; 2001US-0270523P.
PR 23-FEB-2001; 2001US-0270797P.
PR 23-FEB-2001; 2001US-0270810P.
PR 08-MAR-2001; 2001US-0274295P.
PR 16-MAR-2001; 2001US-0276400P.
PR 16-MAR-2001; 2001US-0276677P.
PR 26-MAR-2001; 2001US-0278796P.
PR 04-APR-2001; 2001US-0281521P.
PR 25-APR-2001; 2001US-0286548P.
PR 17-MAY-2001; 2001US-0291765P.
PR 10-AUG-2001; 2001US-0311595P.
PR 13-AUG-2001; 2001US-0311980P.
PR 10-SEP-2001; 2001US-0318526P.
PR 17-SEP-2001; 2001US-0322712P.
PR 18-OCT-2001; 2001US-0330307P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Pena CEA, Shimkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA;
PI Vernet CAM, Malyankar UL, Guo X, Gusev VY, Casman SJ, Boldog FL;
PI Furtak K, Tchernev VT, Patturajan M, Gangolli EA, Padigaru M, Liu X;
PI Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD;
XX
DR WPI; 2003-046859/04.
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Example 3; Page 462; 479pp; English.
XX
CC The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a,
CC 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15,
CC 16a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABU52578-ABU52624), a
CC variant of NOVX, a mature form of NOVX, and a variant of the mature form
CC of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding
CC NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX
CC NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining
CC the presence or amount of NOVX or NOVX NA in a sample, and identifying an
CC agent that binds or modulates the expression or activity of NOVX. NOVX,
CC NOVX NA or ab is useful for treating or preventing a NOVX-associated
CC disorder in a subject, preferably human. Ab is useful for determining the
CC presence or amount of NOVX in a sample. NOVX is useful for identifying an
CC agent that binds to NOVX . NOVX, NOVX NA or ab is useful for treating
CC metabolic disorders, diabetes, cardiomyopathy, obesity, infectious
CC disease, anorexia, neurodegenerative disorders, Alzheimer's disease,
CC Parkinson's disease, immune disorders, haematopoietic disorders, and
CC various dyslipidaemias, metabolic disturbances associated with obesity,
CC the metabolic syndrome X and wasting disorders associated with chronic
CC diseases, various cancers, endocrine, connective tissue, blood, vascular,
CC skin, renal, bone, brain, muscle disorders, or bacterial, fungal,
CC protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening
CC assays, detection assays, predictive medicine, and in methods of
CC treatment. NOVX is useful as immunogen, to screen for potential
CC ant/agonist compounds, and as bait protein in a two-hybrid or three-
CC hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to
CC detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX
CC activity. The cell is useful for producing non-human transgenic animals.
CC Ab is useful for isolating, and purifying NOVX and to monitor protein
CC levels in tissue as part of a clinical testing procedure. The present
CC sequence is a real-time quantitative (RTQ)-PCR primer used to assay
CC tissue specific expression of mRNA encoding a NOVX protein
XX
SQ Sequence 21 BP; 7 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         827 ACTGAGGTCTTCTGCTCAGTC 847
               |||| |||  ||| |||||||
Db          21 ACTGTGGTGCTCTCCTCAGTC 1
```

RESULT 3719
ABQ83354/c
ID ABQ83354 standard; DNA; 21 BP.
XX
AC ABQ83354;
XX
DT 20-JAN-2003 (first entry)
XX
DE Beta-2-microglobulin PCR primer #1.
XX
KW Human; KLK4; cancer; benign tumour; cytostatic; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277243-A1.
XX
PD 03-OCT-2002.
XX
PF 27-MAR-2002; 2002WO-AU000378.
XX
PR 27-MAR-2001; 2001AU-00004022.
XX
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
PI Dong Y, Clements JA;
XX
DR WPI; 2003-029939/02.
XX
PT Detecting the presence or diagnosing the risk of cancer or benign tumor,
PT e.g. an ovarian, endometrial or prostate cancer, by determining the
PT presence of or detecting aberrant expression of KLK4 in a biological
PT sample from the patient.
XX
PS Example 2; Page 67; 126pp; English.
XX
CC The present invention describes a method (M1) for detecting the presence
CC or diagnosing the risk of cancer or benign tumour in a patient. M1
CC comprises determining the presence of or detecting aberrant expression of
CC KLK4 in a biological sample obtained from the patient. KLK4 has
CC cytostatic activity. The method is useful for detecting the presence or
CC diagnosing the risk of a cancer or a benign tumour in a patient,
CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
CC benign tumour associated with an organ or tissue from the ovaries,
CC endometrium or prostate. An agent which can be used for restoring or
CC modulating KLK4 expression can be used for treating or preventing cancer
CC or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
CC molecules from the present invention can be used for detecting aberrant
CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
CC cancer or a benign tumour. The present sequence represents a PCR primer
CC for beta-2-microglobulin, which is used in an example from the present
CC invention
XX
SQ Sequence 21 BP; 3 A; 2 C; 7 G; 9 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1858 ACCCACACACTTAGCCATTGA 1878
              ||||| |||| |||| ||| |
Db         21 ACCCAGACACATAGCAATTCA 1


RESULT 3720
ABQ83360/c
ID   ABQ83360 standard; DNA; 21 BP.
XX
AC   ABQ83360;
XX
DT   20-JAN-2003  (first entry)
XX
DE   Beta-2-microglobulin PCR primer #3.
XX
KW   Human; KLK4; cancer; benign tumour; cytostatic; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200277243-A1.
XX
PD   03-OCT-2002.
XX
PF   27-MAR-2002; 2002WO-AU000378.
XX
PR   27-MAR-2001; 2001AU-00004022.
XX
PA   (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
PI   Dong Y,  Clements JA;
XX
DR   WPI; 2003-029939/02.
XX
PT   Detecting the presence or diagnosing the risk of cancer or benign tumor,
PT   e.g. an ovarian, endometrial or prostate cancer, by determining the
PT   presence of or detecting aberrant expression of KLK4 in a biological
PT   sample from the patient.
XX
PS   Example 4; Page 68; 126pp; English.
XX
CC   The present invention describes a method (M1) for detecting the presence
CC   or diagnosing the risk of cancer or benign tumour in a patient. M1
CC   comprises determining the presence of or detecting aberrant expression of
CC   KLK4 in a biological sample obtained from the patient. KLK4 has
CC   cytostatic activity. The method is useful for detecting the presence or
CC   diagnosing the risk of a cancer or a benign tumour in a patient,
CC   particularly an ovarian, endometrial or prostate cancer, or a cancer or
CC   benign tumour associated with an organ or tissue from the ovaries,
CC   endometrium or prostate. An agent which can be used for restoring or
CC   modulating KLK4 expression can be used for treating or preventing cancer
CC   or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
CC   molecules from the present invention can be used for detecting aberrant
CC   KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
CC   cancer or a benign tumour. The present sequence represents a PCR primer
CC   for beta-2-microglobulin, which is used in an example from the present
CC   invention
XX
SQ   Sequence 21 BP; 3 A; 2 C; 7 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1858 ACCCACACACTTAGCCATTGA 1878
              ||||| |||| |||| ||| |
Db         21 ACCCAGACACATAGCAATTCA 1


RESULT 3721
ACF04379/c
ID   ACF04379 standard; RNA; 21 BP.
XX
AC   ACF04379;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Respiratory syncytial virus activator-antisense RNA #5.
XX
KW   RSV; RNase L; viral infection; virucide; antisense; antisense therapy;
KW   phosphorothioate linkage; ss.
XX
OS   Respiratory syncytial virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .4
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "5' phosphorothioate linkages"
FT   modified_base    4. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "linked by S9"
FT   modified_base    5. .7
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    19. .21
FT                    /*tag=  d
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate linkages"
FT   modified_base    21
FT                    /*tag=  e
FT                    /mod_base= OTHER
FT                    /note= "2'-O-methyl nucleotide"
XX
PN   WO2003062258-A1.
XX
PD   31-JUL-2003.
XX
PF   22-JAN-2003; 2003WO-US002143.
XX
PR   22-JAN-2002; 2002US-0350532P.
XX
PA   (CLEV-) CLEVELAND CLINIC FOUND.
XX
PI   Silverman R,  Leaman D,  Torrence P,  Cramer H;
XX
DR   WPI; 2003-636726/60.
XX
PT   New composition having RNase L activator-antisense complexes, useful for
PT   inhibiting infection by RNA viruses with complexes of an activator of
PT   RNase L, such as respiratory syncytial virus.
XX
PS   Example; Page 27; 36pp; English.
XX
CC   The present invention relates to a composition comprising an
CC   oligonucleotide having at least one 2'-O-methyl nucleotide, in which the
CC   oligonucleotide is complementary to nucleotides of a genomic RNA strand,
CC   a terminus of the oligonucleotide being attached to a linker, and an
CC   activator of RNase L attached to the linker. Also described is a method
CC   of identifying respiratory syncytial virus (RSV) infection in a mammalian
CC   cell. The methods and compositions are useful for inhibiting infection by
CC   RNA viruses with complexes of an activator of RNase L, such as
CC   respiratory syncytial virus. The present sequence is an RSV antisense RNA
CC   used in the exemplification of the invention
XX
SQ   Sequence 21 BP; 14 A; 1 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy       2155 TTTTTTTCTCCTTTTTTTTT 2175
              || ||| | || |||||||||
Db         21 TTATTTGCCCCATTTTTTTT 1


RESULT 3722
ACF04375/c
ID   ACF04375 standard; RNA; 21 BP.
XX
AC   ACF04375;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Respiratory syncytial virus activator-antisense RNA #1.
XX
KW   RSV; RNase L; viral infection; virucide; antisense; antisense therapy;
KW   phosphorothioate linkage; ss.
XX
OS   Respiratory syncytial virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .7
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-5' linkages"
FT   modified_base   4. .5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "linked by p(CH2CH2O)3"
FT   modified_base   19. .21
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   21
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyl nucleotide"
XX
PN   WO2003062258-A1.
XX
PD   31-JUL-2003.
XX
PF   22-JAN-2003; 2003WO-US002143.
XX
PR   22-JAN-2002; 2002US-0350532P.
XX
PA   (CLEV-) CLEVELAND CLINIC FOUND.
XX
PI   Silverman R,  Leaman D,  Torrence P,  Cramer H;
XX
DR   WPI; 2003-636726/60.
XX
PT   New composition having RNase L activator-antisense complexes, useful for
PT   inhibiting infection by RNA viruses with complexes of an activator of
PT   RNase L, such as respiratory syncytial virus.
XX
PS   Disclosure; Page 16; 36pp; English.
XX
CC   The present invention relates to a composition comprising an
CC   oligonucleotide having at least one 2'-O-methyl nucleotide, in which the
CC   oligonucleotide is complementary to nucleotides of a genomic RNA strand,
CC   a terminus of the oligonucleotide being attached to a linker, and an
CC   activator of RNase L attached to the linker. Also described is a method
CC   of identifying respiratory syncytial virus (RSV) infection in a mammalian
CC   cell. The methods and compositions are useful for inhibiting infection by
CC   RNA viruses with complexes of an activator of RNase L, such as
CC   respiratory syncytial virus. The present sequence is an RSV antisense RNA
CC   used in the exemplification of the invention
XX
SQ   Sequence 21 BP; 14 A; 1 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2175
              || ||| | || |||||||||
Db         21 TTATTTGCCCCATTTTTTTT 1


RESULT 3723
ACF04377/c
ID   ACF04377 standard; RNA; 21 BP.
XX
AC   ACF04377;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Respiratory syncytial virus activator-antisense RNA #3.
XX
KW   RSV; RNase L; viral infection; virucide; antisense; antisense therapy;
KW   phosphorothioate linkage; ss.
XX
OS   Respiratory syncytial virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .4
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' phosphorothioate linkages"
FT   modified_base   4. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "linked by Bu2"
FT   modified_base   5. .7
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   19. .21
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate linkages"
FT   modified_base   21
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methyl nucleotide"
XX
PN   WO2003062258-A1.
XX
PD   31-JUL-2003.
XX
PF   22-JAN-2003; 2003WO-US002143.
XX
PR   22-JAN-2002; 2002US-0350532P.
XX
PA   (CLEV-) CLEVELAND CLINIC FOUND.
XX
PI   Silverman R,  Leaman D,  Torrence P,  Cramer H;
XX
DR   WPI; 2003-636726/60.
XX
PT   New composition having RNase L activator-antisense complexes, useful for
PT   inhibiting infection by RNA viruses with complexes of an activator of
PT   RNase L, such as respiratory syncytial virus.
XX
PS   Claim 3; Page 27; 36pp; English.
XX
CC   The present invention relates to a composition comprising an
CC   oligonucleotide having at least one 2'-O-methyl nucleotide, in which the
CC   oligonucleotide is complementary to nucleotides of a genomic RNA strand,
CC   a terminus of the oligonucleotide being attached to a linker, and an
```

CC activator of RNase L attached to the linker. Also described is a method
CC of identifying respiratory syncytial virus (RSV) infection in a mammalian
CC cell. The methods and compositions are useful for inhibiting infection by
CC RNA viruses with complexes of an activator of RNase L, such as
CC respiratory syncytial virus. The present sequence is an RSV antisense RNA
CC used in the exemplification of the invention
XX
SQ Sequence 21 BP; 14 A; 1 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTT 2175
|| ||| | || |||||||||
Db 21 TTATTTGCCCCATTTTTTTT 1

RESULT 3724
AAL56640
ID AAL56640 standard; DNA; 21 BP.
XX
AC AAL56640;
XX
DT 09-OCT-2003 (first entry)
XX
DE S36 primer to amplify contig 13 of the Escherichia coli genome.
XX
KW Genomics; DNA sequencing; random fragmentation; primer linked fragment;
KW S36; positional amplification; PCR; primer; ss.
XX
OS Escherichia coli.
XX
PN WO2003050242-A2.
XX
PD 19-JUN-2003.
XX
PF 13-NOV-2002; 2002WO-US037322.
XX
PR 13-NOV-2001; 2001US-0338224P.
XX
PA (RUBI-) RUBICON GENOMICS INC.
XX
PI Makarov VL, Sleptsova I, Kamberov E, Bruening E;
XX
DR WPI; 2003-532900/50.
XX
PT Preparing a DNA molecule, useful in genomics, molecular biology and
PT sequencing, comprises attaching a primer having substantially known
PT sequence to at least one end of DNA fragments.
XX
PS Example 2; Page 42; 120pp; English.
XX
CC This invention relates to a novel method for preparing DNA molecules that
CC are useful in genomics, molecular biology and particularly for sequencing
CC purposes. Specifically, the invention describes preparing DNA fragments
CC from the random fragmentation of a parent DNA molecule, attaching a
CC primer to at least one end of each fragment to produce primer linked
CC fragments such that this plurality can be amplified as a whole.
CC Accordingly, this method prepares DNA templates that provide more
CC efficient sequencing for difficult DNA molecules, higher sequence quality
CC and longer reads. Furthermore, applications of this method include
CC conditioning the 3' end or providing 3' exonuclease activity to the end
CC of a DNA molecule, detecting a damaged DNA molecule and repairing the 3'
CC end, and preparing a DNA probe. This oligonucleotide sequence is the S36
CC primer used for positional amplification and sequencing of an Escherichia
CC coli (E. coli) genomic region. Specifically, the S36 primer is used in
CC the primary amplification of contig 13 of the E. coli genome, a method of
CC the invention
XX
SQ Sequence 21 BP; 6 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1469 CCAGCTGATTCTAACAAAACC 1489
||||| ||||| || |||||
Db 1 CCAGCGCATTCTGACTAAACC 21

RESULT 3725
ADC16469
ID ADC16469 standard; RNA; 21 BP.
XX
AC ADC16469;
XX
DT 18-DEC-2003 (first entry)
XX
DE Short interfering double-stranded RNA oligonucleotide SEQ ID NO:194.
XX
KW expression interference; expression inhibition; target gene;
KW short interfering double stranded RNA; cytostatic; gene therapy;
KW proliferative disease; cancer; ds.
XX
OS Synthetic.
XX
PN WO2003012052-A2.
XX
PD 13-FEB-2003.
XX
PF 30-JUL-2002; 2002WO-US024226.
XX
PR 30-JUL-2001; 2001US-0308640P.
PR 08-APR-2002; 2002US-0370970P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CARN-) CARNEGIE INST WASHINGTON.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S;
PI Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;
XX
DR WPI; 2003-248169/24.
XX
PT New RNA comprising double stranded RNA and a 3' or 5' overhang having a
PT length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse
PT genetic and/or therapeutic tools for interfering or inhibiting expression
PT of a target gene.
XX
PS Claim 71; SEQ ID NO 194; 176pp; English.
XX
CC The present invention describes an RNA (I) used for the interference or
CC inhibition of expression of a target gene, where (I) comprises double
CC stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang
CC having a length of 0-nucleotide to 5-nucleotides on each strand, where
CC the sequence of the double stranded RNA is substantially identical to a
CC portion of a mRNA or transcript of the target gene. Also described: (1)
CC interfering with or inhibiting the expression of a target gene in a cell
CC by exposing the cell to an amount of (I); (2) a gene silencing array
CC comprising a substantially flat substrate, and addressably arrayed
CC different double-stranded RNAs; (3) an array-based method of assessing a
CC phenotypic effect of a double-stranded RNA on a target gene; (4)
CC validating a gene as a potential drug target for a disease or condition;
CC (5) selecting an optimised sequence of a double-stranded RNA for
CC interference with or inhibition of expression of a target gene in a cell;
CC and (6) a short double-stranded RNA effective for interfering with or
CC inhibiting expression of a target gene comprising any of 311 20-78
CC nucleotide sequences (see ADC16276 to ADC16586). (I) has cytostatic
CC activity, and can be used in gene therapy. The RNAs are useful as reverse
CC genetic and/or therapeutic tools for interfering or inhibiting expression
CC of a target gene. They are useful for treating proliferative diseases,
CC e.g. cancer.
XX
SQ Sequence 21 BP; 3 A; 7 C; 6 G; 0 T; 5 U; 0 Other;

```
  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   61.9%;  Pred. No. 3.6e+03;
  Matches   13;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        915 GACTGTCCCCACCTGAATGCT 935
              ||  |:| |||||:| |:||:
Db          1 GAUCGUCGCCACCUGGAUGCU 21
```

RESULT 3726
ADC16522/c
ID ADC16522 standard; RNA; 21 BP.
XX
AC ADC16522;
XX
DT 18-DEC-2003 (first entry)
XX
DE Short interfering double-stranded RNA oligonucleotide SEQ ID NO:247.
XX
KW expression interference; expression inhibition; target gene;
KW short interfering double stranded RNA; cytostatic; gene therapy;
KW proliferative disease; cancer; ds.
XX
OS Synthetic.
XX
PN WO2003012052-A2.
XX
PD 13-FEB-2003.
XX
PF 30-JUL-2002; 2002WO-US024226.
XX
PR 30-JUL-2001; 2001US-0308640P.
PR 08-APR-2002; 2002US-0370970P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CARN-) CARNEGIE INST WASHINGTON.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Caplen NJ, Morgan RA, Fire A, Parrish S, Mousses S;
PI Kallioniemi O, Cornelison JR, Alton EW, Griesenbach U;
XX
DR WPI; 2003-248169/24.
XX
PT New RNA comprising double stranded RNA and a 3' or 5' overhang having a
PT length of 0-nucleotide to 5-nucleotides on each strand, useful as reverse
PT genetic and/or therapeutic tools for interfering or inhibiting expression
PT of a target gene.
XX
PS Claim 71; SEQ ID NO 247; 176pp; English.
XX
CC The present invention describes an RNA (I) used for the interference or
CC inhibition of expression of a target gene, where (I) comprises double
CC stranded RNA of 15-40 nucleotides in length and a 3' or 5' overhang
CC having a length of 0-nucleotide to 5-nucleotides on each strand, where
CC the sequence of the double stranded RNA is substantially identical to a
CC portion of a mRNA or transcript of the target gene. Also described: (1)
CC interfering with or inhibiting the expression of a target gene in a cell
CC by exposing the cell to an amount of (I); (2) a gene silencing array
CC comprising a substantially flat substrate, and addressably arrayed
CC different double-stranded RNAs; (3) an array-based method of assessing a
CC phenotypic effect of a double-stranded RNA on a target gene; (4)
CC validating a gene as a potential drug target for a disease or condition;
CC (5) selecting an optimised sequence of a double-stranded RNA for
CC interference with or inhibition of expression of a target gene in a cell;
CC and (6) a short double-stranded RNA effective for interfering with or
CC inhibiting expression of a target gene comprising any of 311 20-78
CC nucleotide sequences (see ADC16276 to ADC16586). (I) has cytostatic
CC activity, and can be used in gene therapy. The RNAs are useful as reverse
CC genetic and/or therapeutic tools for interfering or inhibiting expression
CC of a target gene. They are useful for treating proliferative diseases,
CC e.g. cancer.
XX
SQ Sequence 21 BP; 3 A; 4 C; 6 G; 0 T; 8 U; 0 Other;

```
  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1174 ACCTCATCTTGGAGGACGAAA 1194
              | |||||| | |||||||| |
Db         21 AACTCATCATCGAGGACGACA 1
```

RESULT 3727
ADD56745
ID ADD56745 standard; DNA; 21 BP.
XX
AC ADD56745;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human gene expression analysis multiplex StaRT-PCR primer #265.
XX
KW Gene expression; multiplex standardised reverse transcriptase-PCR;
KW StaRT-PCR; high density oligonucleotide array; cDNA array;
KW small biological sample; fine needle aspirate biopsy;
KW laser captured microdissected material; human; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003186246-A1.
XX
PD 02-OCT-2003.
XX
PF 28-MAR-2002; 2002US-00109349.
XX
PR 28-MAR-2002; 2002US-00109349.
XX
PA (WILL/) WILLEY J C.
PA (CRAW/) CRAWFORD E L.
XX
PI Willey JC, Crawford EL;
XX
DR WPI; 2003-811730/76.
XX
PT Direct comparison of numerical gene expression values between samples of
PT genes comprises using multiplex standardized reverse transcription-
PT polymerase chain reaction.
XX
PS Example 1; SEQ ID NO 265; 59pp; English.
XX
CC The present invention relates to a method for the direct comparison of
CC numerical gene expression values between samples of genes. The method
CC comprises amplifying cDNA in the presence of a competitive template
CC mixture and primer pairs for several genes and then amplifying aliquots
CC of the PCR products using a primer pair specific for each gene. The
CC method of amplification is by multiplex standardised reverse
CC transcriptase-polymerase chain reaction (StaRT-PCR). High density
CC oligonucleotide or cDNA arrays are used to measure PCR products following
CC quantitative StaRT-PCR. The method is useful for the assessment of gene
CC expression in small biological samples such as fine needle aspirate
CC biopsies, and laser captured microdissected materials. The method allows
CC for the standardised measurement of hundreds of genes from the same
CC sample, which in prior art, could only be assessed for one gene. The
CC present sequence represents a multiplex StaRT-PCR primer which can be
CC used in the method of the present invention.
XX
SQ Sequence 21 BP; 5 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.6;  DB 1;  Length 21;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        712 CCAGCACCTGTTGCTGCACGA 732
              |||||  ||||||| ||| ||
Db          1 CCAGCCACTGTTGCAGCATGA 21
```

```
RESULT 3728
AAQ42237/c
ID   AAQ42237 standard; cDNA; 22 BP.
XX
AC   AAQ42237;
XX
DT   25-MAR-2003  (revised)
DT   13-SEP-1993  (first entry)
XX
DE   PCR primer Gelo-19 used to mutagenise gelonin coding sequences.
XX
KW   Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate;
KW   autoimmune disease; cell killing; toxin;
KW   Mutagenic polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9309130-A1.
XX
PD   13-MAY-1993.
XX
PF   04-NOV-1992;   92WO-US009487.
XX
PR   04-NOV-1991;   91US-00787567.
PR   19-JUN-1992;   92US-00901707.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Berhard SL,  Better MD,  Carroll SF,  Lane JA,  Lei SP;
XX
DR   WPI; 1993-167617/20.
XX
PT   Analogues of type I ribosome inactivating protein - useful as cytotoxic
PT   agents, immuno toxins for treating auto immune diseases, cancer, graft
PT   versus host disease and selective cell killing in=vivo.
XX
PS   Example 3; Page 33; 163pp; English.
XX
CC   Fifteen analogues of gelonin were constructed. Ten non-cysteine residues
CC   in surface positions and available for conjugation to a second protein
CC   were targeted for substn. In the other analogues, one or both of the
CC   native Cys residues present in gelonin were substd. Overlap extension PCR
CC   was used to construct the various analogues. Primer gelo-19 was one of
CC   the synthetic oligonucleotides used in the mutagenic reactions. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        232 CAGCAATGGGAATCCGCGGGT 252
              ||||||||||| |||  || |
Db         22 CAGCAATGGGATTCCATGGCT 2


RESULT 3729
AAQ87318
ID   AAQ87318 standard; DNA; 22 BP.
XX
AC   AAQ87318;
XX
DT   25-MAR-2003  (revised)
DT   03-OCT-1995  (first entry)
XX
DE   PCR primer of microsatellite marker D13S299 (0.79) for Wilson's. disease
DE   region loci.
XX
KW   Wilson's disease; chromosome 13; D13S31; D13S59; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9506714-A1.
XX
PD   09-MAR-1995.
XX
PF   01-SEP-1994;   94WO-US009851.
XX
PR   01-SEP-1993;   93US-00118441.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Gilliam TC,  Tanzi RE;
XX
DR   WPI; 1995-115430/15.
XX
PT   Isolated Wilson's disease nucleic acid mol. - also probes, vectors, etc.,
PT   useful for diagnosis and gene therapy of Wilson's disease.
XX
PS   Example; Page 7; 175pp; English.
XX
CC   D13S31 is the centromeric flanking marker and D13S59 is the telomeric
CC   flanking marker for the Wilson's disease (WD) region loci. There are a
CC   number of microsatellite markers for this region. Primer pairs and
CC   hetrozygosity values for the microsatellite markers are given in AAQ87305
CC   -Q87320. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 22 BP; 2 A; 12 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        346 TCCCCCTCCCTACCAGCAGCT 366
              ||||||||| | || ||| ||
Db          2 TCCCCCTCCTTGCCTGCAACT 22


RESULT 3730
AAT37086/c
ID   AAT37086 standard; DNA; 22 BP.
XX
AC   AAT37086;
XX
DT   15-OCT-1996  (first entry)
XX
DE   DNA primer to amplify E. coli chromosomal DNA.
XX
KW   thrABC operon; ilvGMEDA operon; thrA gene; ilvA gene; amino acid;
KW   aspartokinase-I; homoserine-dehydrogenase-I; threonine-deaminase; enzyme;
KW   metabolic engineering; L-isoleucine; feedback-inhibition; DNA primer;
KW   PCR; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   EP685555-A1.
XX
PD   06-DEC-1995.
XX
PF   30-MAY-1995;   95EP-00108315.
XX
PR   30-MAY-1994;   94JP-00116340.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Hashiguchi K,  Kishino H,  Tsujimoto N,  Matsui H;
XX
DR   WPI; 1996-012380/02.
XX
PT   New Escherichia transformant producing L-isoleucine - carrying thr ABC
PT   operon, ilv GMEDA operon and opt. Lys C gene, all of which are released
PT   from feedback inhibition.
```

```
XX
PS   Disclosure; Page 19; 48pp; English.
XX
CC   This DNA primer is used to amplify chromosomal DNA of E. coli using the
CC   chromosomal DNA of strain MI162 as a template. It is used during the
CC   contruction of plasmid pMWD5 which carries the ilvGMEDA operon. The DNA
CC   fragment amplified by the PCR method is the DNA fragment having a base
CC   sequence extending from 1161- 2421 of sequence AAT07115
XX
SQ   Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2


RESULT 3731
AAT12804/c
ID   AAT12804 standard; DNA; 22 BP.
XX
AC   AAT12804;
XX
DT   08-OCT-1996  (first entry)
XX
DE   E. coli ilvGMEDA operon PCR primer for nucleotides 1161-2421.
XX
KW   ilvGMEDA operon; modification; ilvG; ilvM; ilvE; ilvD; ilvA;
KW   threonine deaminase; L-Valine; L-isoleucine; L-leucine; repression;
KW   transformation; bacterial host; lipoic acid; H+-ATPase deficient;
KW   production; high yield; PCR; primer; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9606926-A1.
XX
PD   07-MAR-1996.
XX
PF   30-AUG-1995;   95WO-JP001719.
XX
PR   30-AUG-1994;   94JP-00204856.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Tomita F,  Yokota A,  Hashiguchi K,  Ishigooka M,  Kurahashi O;
XX
DR   WPI; 1996-160357/16.
XX
PT   Efficient microbial prodn. of L-valine and L-leucine - by culturing
PT   Escherichia strain which requires lipoic acid for growth and/or is
PT   deficient in H+-ATPase.
XX
PS   Example 1; Page 40; 53pp; Japanese.
XX
CC   The primer pair AAT12804/05 was used for the PCR amplification of
CC   nucleotides 1161-2421 of the E. coli ilvGMEDA operon, which can be
CC   modified by the removal of nucleotides 953-1160 to express only the ilvG,
CC   ilvM, ilvE and ilvD genes, but not the ilvA (threonine deaminase) gene,
CC   which is required for L-Valine, L-isoleucine and/or L-leucine repression.
CC   The modified operon can be used to transform a bacterial host, esp. E.
CC   coli, which requires lipoic acid for growth and/or is deficient in H+-
CC   ATPase, for the efficient prodn. of L-Valine and L-leucine in high yield.
CC   A specific example is the transformed H+-ATPase deficient E. coli strain
CC   W1485atpA401/pMWdAR6, which when cultured in 1 microg/L lipoic acid at 37
CC   degrees C for 24 hrs. gave 8.0 g/L L-Valine in the medium, compared to
CC   0.1 g/L for the untransformed strain
XX
SQ   Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2


RESULT 3732
AAT62748/c
ID   AAT62748 standard; DNA; 22 BP.
XX
AC   AAT62748;
XX
DT   24-NOV-1997  (first entry)
XX
DE   Primer for Escherichia coli ilvG gene.
XX
KW   ilvG; L-isoleucine; production; primer; amplification; PCR;
KW   polymerase chain reaction; Escherichia coli; ss.
XX
OS   Synthetic.
XX
PN   WO9708333-A1.
XX
PD   06-MAR-1997.
XX
PF   27-AUG-1996;   96WO-JP002399.
XX
PR   30-AUG-1995;   95JP-00221561.
PR   30-JUL-1996;   96JP-00200860.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Kishino H,  Izui M,  Ono Y,  Ito H,  Kurahashi O;
XX
DR   WPI; 1997-179289/16.
XX
PT   Production of L-amino acids (phenylalanine etc) by microbial culture -
PT   using microorganisms such as Escherichia or Corynebacterium having an
PT   enhanced ability to produce phospho:enol:pyruvic acid.
XX
PS   Example 5; Page 32; 41pp; Japanese.
XX
CC   The present sequence is a primer for the PCR amplification of the
CC   Escherichia coli ilvG gene, which is involved in the production of L-
CC   isoleucine
XX
SQ   Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2


RESULT 3733
AAT93818
ID   AAT93818 standard; DNA; 22 BP.
XX
AC   AAT93818;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 8 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
```

```
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP005388.
XX
PR   04-DEC-1995;   95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 5; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 79%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 22 BP; 0 A; 0 C; 4 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              || || ||||| |||| ||||
Db          2 TTGTTGTTTTTGTTTTGTTTT 22


RESULT 3734
AAV47448
ID   AAV47448 standard; DNA; 22 BP.
XX
AC   AAV47448;
XX
DT   10-NOV-1998  (first entry)
XX
DE   Antisense oligonucleotide 2, targeting adenosine A2b receptor.
XX
KW   Secondary structure; mRNA; phosphorothioate backbone; G-protein;
KW   bronchoconstriction; lung inflammation; asthma; pulmonary disease;
KW   allergy; emphysema; cystic fibrosis; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .22
FT                   /*tag=  a
FT                   /note= "contains phosphorothioate internucleotide
FT                   linkages"
XX
PN   WO9823294-A1.
XX
PD   04-JUN-1998.
XX
PF   26-NOV-1997;   97WO-US022017.
XX
PR   26-NOV-1996;   96US-00757024.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1998-322464/28.
XX
PT   Treating respiratory disease with antisense sequences directed against
PT   adenosine or bradykinin receptors - with localised delivery to the
PT   respiratory system, suitable for long term treatment of asthma, adult
PT   respiratory distress syndrome etc.
XX
PS   Claim 13; Page 24; 47pp; English.
XX
CC   Sequences AAV47447-V47451 are anti-sense oligonucleotides that target the
CC   human adenosine A2b receptor, the design of which required the secondary
CC   structure of this targets mRNA. The adenosine receptor mRNA secondary
CC   structure was both analysed and used to construct antisense
CC   oligonucleotides containing a phosphorothioate backbone. Once the
CC   antisense molecules are created they can be used to target their
CC   predetermined target, thus causing the gene product to decrease. The
CC   antisense oligonucleotides were targeted to specific mRNA regions
CC   containing either a junction between the intron and exon, or where they
CC   may overlap the initiation codon. The receptor is a member of the G-
CC   protein coupled family of cell surface receptors that have 7-
CC   transmembrane segments. These oligonucleotides can be used to treat or
CC   prevent conditions associated with bronchoconstriction and/or lung
CC   inflammation in humans or other animals e.g. asthma, pulmonary disease,
CC   allergy, emphysema and cystic fibrosis
XX
SQ   Sequence 22 BP; 1 A; 9 C; 11 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1371 GCCAGGCCATCTGTGCCGCGG 1391
              ||| ||||| ||| ||| |||
Db          2 GCCGGGCCAGCTGGGCCCCGG 22


RESULT 3735
AAX14678
ID   AAX14678 standard; DNA; 22 BP.
XX
AC   AAX14678;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 9-30 of gamma-crystallin gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
```

PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 15-16; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ Sequence 22 BP; 1 A; 5 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2158 TTTTCTCCTTTTTTTTTTTTT 2178
              |||||| || ||||| ||| |
Db          2 TTTTCTTCTCTTTTTATTTCT 22
```

RESULT 3736
AAV74151
ID AAV74151 standard; DNA; 22 BP.
XX
AC AAV74151;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human thyroid gene NIS PCR primer DNA #1.
XX
KW Thyroid; NIS gene; detection; epithelial cell; thyroid-specific gene;
KW blood cell; cancer; recurrence; cell sorting; thyroidectomy; diagnosis;
KW hormone replacement therapy; thyroglobulin; immunoassay; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9856953-A1.
XX
PD 17-DEC-1998.
XX
PF 09-JUN-1998; 98WO-US011934.
XX
PR 10-JUN-1997; 97US-0049144P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Levine MA, Ringel MD;
XX
DR WPI; 1999-070335/06.
XX
PT Detecting thyroid epithelial cells in blood - by detecting cDNA from
PT thyroid-specific RNA, particularly for monitoring treatment and recovery
PT from thyroid cancer following thyroidectomy.
XX
PS Claim 29; Page 63; 80pp; English.
XX
CC AAV74143-V74155 are PCR primers and probes used to detect thyroid
CC epithelial cells (TEC) in a patient. The detection method comprises
CC detecting a transcript of a thyroid-specific gene in a sample of reverse-
CC transcribed total RNA of blood cells. The specification also describes a
CC method for detecting TEC by polymerase chain reaction (PCR) of reverse-
CC transcribed RNA (not necessarily total RNA) from blood cells, using
CC primers that produce an amplicon that spans at least one intron, then
CC detecting the PCR product and also a method for monitoring recurrence of
CC thyroid cancer in a recovering patient by detecting, in a sample of
CC reverse-transcribed total RNA of blood cells, a transcript of a thyroid-
CC specific gene as an indicator of recurrence. The specification also
CC describes a method for detecting TEC by cell-sorting to isolate a TEC-
CC containing fraction from blood, then detecting TEC in this fraction. The
CC methods are used to monitor treatment of, and recovery from, thyroid
CC cancer, in patients who have had a total thyroidectomy. The method does
CC not require the patient to stop thyroid hormone replacement therapy and
CC is not subject to interference from antibodies against thyroglobulin
CC which may falsify the conventional immunoassay. Peripheral blood is an
CC easily obtained source of sample and the process is more sensitive than
CC immunoassay. By amplifying fragments from several thyroid specific genes,
CC even rare forms of thyroid cancer may be diagnosed
XX
SQ Sequence 22 BP; 4 A; 10 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1585 CACAGACTGGGAACCCCTCCT 1605
              ||| ||||| || || |||||
Db          2 CACTGACTGCGACCCTCTCCT 22
```

RESULT 3737
AAA35437/c
ID AAA35437 standard; DNA; 22 BP.
XX
AC AAA35437;
XX
DT 06-AUG-2003 (revised)
DT 25-JUL-2000 (first entry)
XX
DE Myrtaceae microsatellite scu072TT detection PCR primer.
XX
KW Myrtaceae; microsatellite; isolation; genotyping; plant; tea tree;
KW breeding; Melaleuca alternifolia; broad-spectrum germicidal oil;
KW pharmaceutical; cosmetic; identification; detection; PCR primer; ss.
XX
OS Myrtaceae.
XX
PN WO200017341-A1.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-AU000820.
XX
PR 23-SEP-1998; 98AU-00006099.
PR 16-FEB-1999; 99AU-00008718.
XX
PA (BUSI-) BUSINESS & RES MANAGEMENT PTY LTD.
XX
PI Rossetto M, Mclauchlan A, Harriss FCL, Henry RJ, Baverstock PR;
PI Lee LS, Maguire TL, Edwards KJ;
XX
DR WPI; 2000-292840/25.
XX
PT Isolating microsatellites from Myrtaceae, useful for genotyping,
PT particularly in breeding programs for tea tree, by reacting plant nucleic

```
PT   acid with immobilized oligonucleotides.
XX
PS   Claim 10; Page 37; 100pp; English.
XX
CC   A method has been developed of isolating a microsatellite (MS) from
CC   nucleic acid extract of a plant of Myrtaceae family. The method
CC   comprises: (i) treating the extract with one or more immobilised, single-
CC   stranded oligonucleotides (ON) having a consensus MS repeat sequence
CC   (MSRS) or its complement; (ii) washing under specified stringency
CC   conditions; (iii) eluting nucleic acid bound to ON; and (iv) sequencing
CC   the eluted nucleic acids to identify those containing an MSRS.
CC   Microsatellites (MS) isolated by the method, specifically from Melaleuca
CC   alternifolia (the tea tree, a source of a broad-spectrum germicidal oil,
CC   useful in pharmaceuticals and cosmetics), are useful as genotyping
CC   markers, particularly for breeding plants that produce the oil in higher
CC   yield or of better quality. Primers based on MS are useful for both inter
CC   - and intra-species genotyping. The selected washing conditions improve
CC   efficiency of recovery of microsatellites (MS) and reduce the number of
CC   washing stages required. Particularly about 86% of recovered sequence
CC   contain an MS repeat sequence, compared with 50-70% when the conventional
CC   washing procedure is followed. AAA35313 to AAA35357, and AAA35562 to
CC   AAA35575 represent nucleotide sequences from the present invention which
CC   contain microsatellite sequences. AAA35358 to AAA35561 represent
CC   oligonucleotide PCR primers used for identifying Myrtaceae microsatellite
CC   sequences. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 22 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1433 ATAGACAAATCCTACATGAAC 1453
                ||||  ||| |||||||||  |
Db         22 ATAGCGAAACCCTACATGACC 2


RESULT 3738
AAA12754/c
ID   AAA12754 standard; DNA; 22 BP.
XX
AC   AAA12754;
XX
DT   25-JUL-2000  (first entry)
XX
DE   5' PCR primer for exon 7 of DNA encoding human TREX protein.
XX
KW   Tumour necrosis factor receptor-associated Factor; TRAF;
KW   TRF-protein-interacting hereditary multiple extoses protein; TREX;
KW   signal modulator; tumour necrosis factor receptor;
KW   CD40 mediated signal transduction; TRAF protein; cancer;
KW   hereditary multiple extosis; autoimmune disease; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200018959-A1.
XX
PD   06-APR-2000.
XX
PF   17-SEP-1999;   99WO-US021654.
XX
PR   17-SEP-1998;   98US-00156191.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Sato T;
XX
DR   WPI; 2000-293180/25.
XX
PT   New nucleic acid encoding Tumor necrosis factor Receptor-Associated
PT   Factor (TRAF) protein-interacting hereditary multiple extoses (TREX)
PT   protein, useful in the diagnosing cancer.
XX
PS   Disclosure; Page 52; 161pp; English.
XX
CC   PCR primers AAA12754-55 were used to amplify exon 7 of DNA encoding human
CC   tumour necrosis factor receptor-associated Factor (TRAF) protein-
CC   interacting hereditary multiple extoses (TREX) protein. TREX is a signal
CC   modulator which bridges between the tumour necrosis factor (TNF) receptor
CC   and CD40 mediated signal transduction. Anti-TREX antibodies are useful
CC   for treating an abnormality in a patient by inhibiting binding of a TREX
CC   protein and a TRAF protein (that is, TRAF 2, TRAF 3 or TRAF 5). The
CC   abnormality is cancer, a hereditary multiple extosis or an autoimmune
CC   disease. The cancer is colon cancer, gastric cancer, human head and neck
CC   squamous cell carcinoma, prostate carcinoma, breast cancer, thyroid
CC   cancer, oesophageal cancer, lung cancer, colorectal cancer, ovarian
CC   cancer, papillary bladder cancer, osteosarcoma, chondrosarcoma,
CC   liposarcoma, giant cell tumour, Ewing sarcoma, or other malignant tumours
XX
SQ   Sequence 22 BP; 3 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1469 CCAGCTGATTCTAACAAAACC 1489
                ||||||  ||  ||  |||  ||||
Db         21 CCAGCTAATACTGACAGAACC 1


RESULT 3739
AAD00662
ID   AAD00662 standard; DNA; 22 BP.
XX
AC   AAD00662;
XX
DT   21-SEP-2000  (first entry)
XX
DE   Synthetic oligonucleotide linker fragment, MV06JA.
XX
KW   Llama; HC-V; heavy chain variable domain; antigen binding protein;
KW   linker; conformational flexibility; multivalent binding protein; bi-head;
KW   human chorionic gonadotropin; hCG; immunoassay; agglutination assay;
KW   purification; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /label= Sticky_end
FT                   /note= "The 3' end of the complementary strand overhangs
FT                   the 5' end of this sequence by the sequence 5'-CAG-3'"
FT   misc_feature    22
FT                   /*tag=  b
FT                   /label= Sticky_end
FT                   /note= "The 5' end of the complementary strand overhangs
FT                   the 3' end of this sequence by the sequence 5'-CTAG-3'"
XX
PN   WO200024884-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-EP008323.
XX
PR   27-OCT-1998;   98WO-EP006991.
PR   22-APR-1999;   99EP-00303118.
XX
PA   (UNIL ) UNILEVER PLC.
PA   (UNIL ) UNILEVER NV.
PA   (HIND-) HINDUSTAN LEVER LTD.
XX
PI   Frenken LGJ,  Howell S,  Van Der Vaart JM;
XX
DR   WPI; 2000-350728/30.
XX
```

PT Use of a linker whose amino acid sequence confers restricted
PT conformational flexibility to generate multivalent and multispecific
PT antigen binding proteins.
XX
PS Example 1.1d; Page 20; 50pp; English.
XX
CC The present DNA sequence is the synthetic oligonucleotide linker
CC fragment, MV06JA. It is used for the construction of Saccharomyces
CC cerevisiae episomal expression plasmid, pUR5332, encoding anti-hCG- anti-
CC RR6 bispecific biheads, containing the linker peptide. The peptide linker
CC confers restricted conformational flexibility for linking binding units
CC in a multivalent binding protein. The linker is used to generate
CC multivalent or multispecific antigen binding proteins for immunoassays,
CC agglutination assays or for purification
XX
SQ Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1489 CCTGGAGAAAATGGAGAAACA 1509
||||| ||| ||||||| ||
Db 2 CCTGGTGAACCTGGAGAACCA 22

RESULT 3740
AAA06866/c
ID AAA06866 standard; DNA; 22 BP.
XX
AC AAA06866;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human IgG4 PCR primer 1.
XX
KW IgG4; gamma-4; immunoglobulin G; FcRn receptor; FcRb; constant region;
KW serum half life; antibody; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200009560-A2.
XX
PD 24-FEB-2000.
XX
PF 17-AUG-1999; 99WO-US018777.
XX
PR 17-AUG-1998; 98US-0096868P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gallo M, Junghans R, Foord O;
XX
DR WPI; 2000-224282/19.
XX
PT Modifying antibody half life by linking the antibody to an FcRn binding
PT domain.
XX
PS Example 3; Fig 2; 79pp; English.
XX
CC The invention relates to modification of the half-life of an antibody.
CC The method of the invention comprises physically linking an antibody
CC which contains an FcRn receptor binding moiety (hinge, CH2 and CH3
CC domains) to a second FcRn binding moiety. IgG (immunoglobulin G)
CC molecules are protected from degradation by the endosomal FcRb/FcRn
CC receptors, which gives them a relatively extended serum half-life
CC relative to other serum proteins. The presence of a second FcRn binding
CC moiety further extends the serum half-life of an antibody. By increasing
CC the serum half life of an antibody, the amount of antibody needed in
CC clinical treatments is lowered. This could significantly lower costs for
CC treatment, and lead to less frequent hospital visits as fewer doses are
CC required, thereby increasing the quality of life for patients, and
CC potentially reducing the likelihood of toxicity. The technology can also
CC be adapted to extend the serum half life of other proteins, in addition
CC to antibodies. Sequences AAA06866-A06867 represent PCR primers used to
CC introduce a a Bsu36I restriction site into DNA encoding the last 4 amino
CC acids of the human IgG4 constant region. This restriction site was then
CC used for the insertion of DNA encoding human IgG1 hinge, CH2 and CH3
CC domains, generating a construct encoding a human IgG4 fused via the CH3
CC domain to a human IgG1 FcRn receptor binding moiety
XX
SQ Sequence 22 BP; 3 A; 6 C; 12 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 508 GCCCTCGCACCACGGGCGCCC 528
||||||||||| || | | ||
Db 22 GCCCTCGCACCCCGTGGGTCC 2

RESULT 3741
AAA53024
ID AAA53024 standard; DNA; 22 BP.
XX
AC AAA53024;
XX
DT 03-JAN-2001 (first entry)
XX
DE Human beta-1,3-galactosyltransferase znssp2 PCR primer ZC18227.
XX
KW Human; beta-1,3-galactosyltransferase; znssp2; cell-cell interaction;
KW cancer; autoimmune disease; digestive disorder; gene therapy;
KW inflammation; chromosome 19q13.2; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200034485-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029477.
XX
PR 10-DEC-1998; 98US-00208970.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC, Yamamoto G, Jaspers SR, Gao Z;
XX
DR WPI; 2000-423428/36.
XX
PT Novel Znssp2 polypeptides belonging to galactosyltransferase family
PT useful for treating disorders associated with glycoprotein synthesis.
XX
PS Example 1; Page 99; 107pp; English.
XX
CC The present sequence is a PCR primer for the human Znssp2 coding
CC sequence. This protein is a beta-1,3-galactosyltransferase, and is a type
CC II membrane protein involved in cell-cell interactions. The gene is found
CC on human chromosome 19q13.2. The gene and protein can be used in the
CC treatment of cancer, particularly metastases, inflammation, autoimmune
CC diseases such as diabetes, digestive disorders including Crohn's disease
CC and ulcerative colitis, and disorders associated with cell migration,
CC contact inhibition, tissue interactions, neuronal specificity,
CC fertilisation, embryonic cell adhesion, limb bud morphogenesis,
CC mesenchyme development, immune recognition, growth control, and
CC glycoprotein and glycolipid biosynthesis. One possible method of
CC treatment is the use of gene therapy
XX
SQ Sequence 22 BP; 6 A; 3 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy        793 TCAGAAGGAGCTGGTGGGGGC 813
              ||||| |||||||  || |||
Db          2 TCAGAGGGAGCTGAGGGAGGC 22
```

RESULT 3742
AAC83021/c
ID AAC83021 standard; DNA; 22 BP.
XX
AC AAC83021;
XX
DT 22-FEB-2001 (first entry)
XX
DE alpha V integrin primer #2.
XX
KW Primer; cancer; psoriasis; diabetic retinopathy; atherosclerosis;
KW menorrhagia; arthritis; macular degeneration; Paget's disease;
KW alpha5-integrin; ss.
XX
OS Homo sapiens.
XX
PN WO200064480-A1.
XX
PD 02-NOV-2000.
XX
PF 13-APR-2000; 2000WO-GB001446.
XX
PR 24-APR-1999; 99GB-00009392.
XX
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX
PI Bicknell R, Zhang H;
XX
DR WPI; 2000-687268/67.
XX
PT Compound comprising a group that selectively binds alpha 5-integrin and
PT another group, used to treat cancer, psoriasis, diabetic retinopathy, and
PT atherosclerosis, in which angiogenesis contributes to pathology.
XX
PS Example 1; Page 47; 69pp; English.
XX
CC The present invention relates to a compound comprising a group which
CC selectively binds alpha5-integrin and another group. The compound may be
CC useful for treating a patient who has cancer, psoriasis, diabetic
CC retinopathy, atherosclerosis, or menorrhagia, in which angiogenesis
CC contributes to pathology and also arthritis (both inflammatory and
CC rheumatoid), macular degeneration, Paget's disease, benign vascular
CC proliferations and fibroses. The compound is also useful as a
CC contraceptive
XX
SQ Sequence 22 BP; 4 A; 9 C; 2 G; 7 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 3.9e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2546 AGAATTAAGAGGATGCTGGGC 2566
              ||| | |||| |||| |||||
Db         21 AGACTGAAGAAGATGTTGGGC 1
```

RESULT 3743
AAA66933
ID AAA66933 standard; DNA; 22 BP.
XX
AC AAA66933;
XX
DT 09-OCT-2000 (first entry)
XX
DE Dog genomic marker oligonucleotide sequence SEQ ID NO:795.
XX
KW Dog; genome; genomic marker; radiation hybrid map; identification;
KW chromosome location; gene marker; polymorphic microsatellite marker;
KW phenotype; behaviour; pedigree; ss.
XX
OS Canis familiaris.
XX
PN WO200029615-A2.
XX
PD 25-MAY-2000.
XX
PF 15-NOV-1999; 99WO-IB001907.
XX
PR 13-NOV-1998; 98US-0108193P.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Galibert F, Andre C;
XX
DR WPI; 2000-387821/33.
XX
PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral traits
PT or in genetic diseases and for studying dog pedigrees.
XX
PS Claim 1; Page 87; 87pp; English.
XX
CC The present invention describes a radiation hybrid map of the dog (Canine
CC familiaris) genome comprising the genome location of a marker selected
CC from AAA66139 to AAA66942. The radiation hybrid map is useful for
CC identifying and localising dog genes, since it covers approximately 80 %
CC of the dog genome and provides a dense map integrating different types
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC (or complementary sequences) are especially useful to identify genes
CC responsible for phenotypic and behavioural traits in dogs, to identify
CC morbid genes, to analyse diseases and identify implicated genes in such
CC diseases and their alleles, and to study dog pedigrees. They may also be
CC useful for isolating corresponding human gene sequences e.g. genes
CC involved in genetic diseases
XX
SQ Sequence 22 BP; 2 A; 8 C; 3 G; 9 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 3.9e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy        829 TGAGGTCTTCTGCTCAGTCCC 849
              | || ||||||| || |||||
Db          1 TTAGCTCTTCTGATCTGTCCC 21
```

RESULT 3744
AAH22316
ID AAH22316 standard; DNA; 22 BP.
XX
AC AAH22316;
XX
DT 21-AUG-2001 (first entry)
XX
DE Brain ankyrin-2 hybridisation probe SEQ ID NO:62.
XX
KW Human; differentially expressed gene; angiogenesis; diagnosis;
KW angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KW vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KW rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KW neovascularisation; restenosis; hypertension; aneurysm; angina;
KW myocardial infarction; chronic heart condition; osteoporosis; PCR primer;
KW hybridisation; probe; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200132926-A2.
XX
PD 10-MAY-2001.

XX
PF 01-NOV-2000; 2000WO-US030051.
XX
PR 01-NOV-1999; 99US-0162699P.
PR 13-APR-2000; 2000US-0196802P.
PR 31-OCT-2000; 2000US-00703350.
XX
PA (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
XX
PI Mehraban F, Gerritsen M, Rastelli L;
XX
DR WPI; 2001-291056/30.
XX
PT Differentially expressed genes involved in angiogenesis, useful for
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis
PT subsequent to balloon angioplasty.
XX
PS Example 19; Page 148; 182pp; English.
XX
CC The present invention describes differentially expressed genes involved
CC in angiogenesis (I), and the polypeptides that encode them. (I) have
CC cardiovascular activity, and can be used in the modulation of
CC angiogenesis. The nucleic acids and polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate angiogenesis. The polypeptides may also be used as antigens
CC in the production of antibodies against them and in assays to identify
CC modulators of their expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity and
CC modulate angiogenesis. The antibodies may also be used as diagnostic
CC agents for detecting the presence of the polypeptides in samples.
CC Disorders that may be prevented, diagnosed and/or treated by the above
CC methods include, for example vascular tumours, proliferative tumours,
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC associated with neovascularisation, restenosis subsequent to balloon
CC angioplasty, scar tissue over production. peripheral vascular disease,
CC hypertension, inflammatory vasculitides, Reynaud's disease and Reynaud's
CC phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC reperfusion injury, angina, myocardial infarctions, chronic heart
CC conditions, heart failure such as congestive heart failure, age-related
CC macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322
CC to AAB98325 represent sequence used in the exemplification of the present
CC invention
XX
SQ Sequence 22 BP; 8 A; 9 C; 4 G; 1 T; 0 U; 0 Other;

```
  Query Match              0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1261 TCTCAGCCAAGACCGGACACC 1281
              || |||||||| | | ||||
Db          1 TCGCAGCCAAGAACAGCCACC 21
```

RESULT 3745
AAH28299
ID AAH28299 standard; RNA; 22 BP.
XX
AC AAH28299;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from neuronal cadherin gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 22 BP; 2 A; 1 C; 1 G; 0 T; 18 U; 0 Other;

```
  Query Match              0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   0.0%;  Pred. No. 3.9e+03;
  Matches    0;  Conservative   17;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              :::::: :::: : : :::::
Db          1 UUUUUUAUUUUCUGUAUUUUU 21
```

RESULT 3746
AAH28297
ID AAH28297 standard; RNA; 22 BP.
XX
AC AAH28297;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from neuronal cadherin gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.

XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 22 BP; 2 A; 1 C; 1 G; 0 T; 18 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 0.0%; Pred. No. 3.9e+03;
Matches 0; Conservative 17; Mismatches 4; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
: : : : : : : : : : : : : : : : : : : :
Db 1 UUUUUUAUUUUCUGUAUUUUU 21

RESULT 3747
AAC85377/c
ID AAC85377 standard; DNA; 22 BP.
XX
AC AAC85377;
XX
DT 29-MAR-2001 (first entry)
XX
DE Mutagenic primer #2 to amplify murine SOCS-3 promoter.
XX
KW Suppressor of cytokine signalling; SOCS-3; promoter; inflammation;
KW STAT binding element; human; CIS gene; growth retardation; stress;
KW growth acceleration; autoimmune disease; multiple sclerosis; PCR;
KW Crohn's disease; ulcerative colitis; systemic lupus erythematosus;
KW rheumatoid arthritis; Grave's disease; polymerase chain reaction;
KW amplify; primer; mutagenesis; ss.
XX
OS Synthetic.
XX
PN WO200075326-A1.
XX
PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000WO-US040151.
XX
PR 07-JUN-1999; 99US-00327138.
XX
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
XX
PI Auernhammer CJ, Shlomo M;
XX
DR WPI; 2001-091211/10.
XX
PT New nucleic acid construct comprising suppressor of cytokine signaling-3
PT promoter useful in gene therapy for treating growth retardation or
PT acceleration disorder, (auto)immune diseases, or inflammatory conditions.
XX
PS Example 1; Page 22; 64pp; English.
XX
CC The sequences given in AAC85376-77 and AAC85379-80 are primers which were
CC used to mutate the murine suppressor of cytokine signalling (SOCS)-3
CC promoter around the STAT binding elements. The murine SOCS-3 gene
CC promoter contains a pair of STAT binding elements TTNNNNNAA, separated by
CC 14 nucleotides, making it structurally similar to the human CIS gene
CC promoter. However only the STAT-binding element at -74 to -66 is
CC essential for optimal operability. The SOCS-3 promoter or the operative
CC fragments of it, are useful for treating growth retardation or
CC acceleration disorder, autoimmune diseases, immune diseases and
CC inflammatory conditions, including Crohn's disease, ulcerative colitis,
CC multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis,
CC Grave's disease, allergic or anaphylactic reaction, or
CC neuroendocrinological response to stress. The promoter sequence can be
CC used to correct clinical disorders derived from defective negative
CC regulation of cytokine signal transduction in GH-responsive or gp-
CC responsive cells
XX
SQ Sequence 22 BP; 5 A; 8 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2100 CAAACGGGGGCCTTCTGGTTT 2120
|| || |||||| || |||||
Db 22 CAGACTGGGGCCCTCGGGTTT 2

RESULT 3748
ABQ79748
ID ABQ79748 standard; DNA; 22 BP.
XX
AC ABQ79748;
XX
DT 05-DEC-2002 (first entry)
XX
DE Human znssp2 cDNA amplifying primer ZC18227.
XX
KW Human; znssp2; galactosyltransferase; cytostatic; antidiabetic; PCR;
KW antiinflammatory; gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
PN US6416988-B1.
XX
PD 09-JUL-2002.
XX
PF 10-DEC-1999; 99US-00459133.
XX
PR 10-DEC-1998; 98US-0111697P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Conklin DC, Yamamoto G, Jaspers SR, Gao Z;
XX
DR WPI; 2002-634736/68.
XX
PT Novel polynucleotide encoding mature znssp2 polypeptide which is a member
PT of galactosyltransferase family, useful for diagnosing, treating
PT disorders associated with pancreas, digestive system and glycoprotein
PT synthesis.
XX

```
PS   Example 1; Col 63-64; 38pp; English.
XX
CC   The invention relates to a znssp2 polypeptide, a novel member of the
CC   galactosyltransferase family. The znssp2 is a homologue of beta-1,3-
CC   galactosyltransferase and can be expressed by standard recombinant
CC   methodology. The znssp2 polypeptide is useful to study pancreatic cell
CC   proliferation or differentiation. The znssp2 polynucleotide is useful for
CC   regulating the maturation of UDP-glycosyltransferase substrate-bearing
CC   cells, such as fibroblasts, lymphocytes and haematopoietic cells, for
CC   treating disorder associated with cell migration, contact inhibition,
CC   tissue interaction, neuronal specificity, fertilization, embryonic cell
CC   adhesions, limp bud morphogenesis, mesenchyme development, immune
CC   recognition, inflammation, tumourigenesis, growth control, tumour
CC   metastasis and intracellular and extracellular glycoprotein and
CC   glycolipid biosynthesis. It is also useful in diagnostic applications,
CC   chromosomal identification and/or mapping. Znssp2 gene is useful as probe
CC   to identify humans having a defective pancreatic or colonic specific
CC   beta,1,3, galactosyltransferase gene and as indicators of pancreatic and
CC   colonic cancer and disease. Znssp2 polypeptide and polynucleotide are
CC   useful in the treatment of disorders associated with pancreas, diabetes,
CC   hypoglycemia, digestive systems including pancreas, colon and small
CC   intestine, neuronal tissues, bone marrow and peripheral leukocytes, and
CC   in disorders associated with glycoprotein synthesis. The present sequence
CC   represents a human znssp2 cDNA amplifying primer
XX
SQ   Sequence 22 BP; 6 A; 3 C; 11 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        793 TCAGAAGGAGCTGGTGGGGGC 813
              ||||| |||||||  || |||
Db          2 TCAGAGGGAGCTGAGGGAGGC 22


RESULT 3749
ABT06326/c
ID   ABT06326 standard; DNA; 22 BP.
XX
AC   ABT06326;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Human NOVX coding sequence PCR primer SEQ ID NO: 150.
XX
KW   Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;
KW   storage disorder; muscle disorder; neurodegenerative disorder; nootropic;
KW   developmental defect; neuroprotective; antiparkinsonian; hypotensive;
KW   hypertensive; haemostatic; cardiant; antianginal; dermatological;
KW   immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;
KW   antiparasitic; antiallergic; antiasthmatic; antirheumatic; antiarthritic;
KW   vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic;
KW   nephrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant;
KW   antiinfertility; antimanic; antidepressant; metabolic; cytostatic;
KW   tranquilizer; analgesic; probe; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200257450-A2.
XX
PD   25-JUL-2002.
XX
PF   29-NOV-2001; 2001WO-US048922.
XX
PR   29-NOV-2000; 2000US-0253834P.
PR   30-NOV-2000; 2000US-0250926P.
PR   25-JAN-2001; 2001US-0264180P.
PR   20-AUG-2001; 2001US-0313656P.
PR   05-OCT-2001; 2001US-0327456P.
PR   28-NOV-2001; 2001US-00327456.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Edinger S,  Macdougall JR,  Millet I,  Ellerman K,  Stone DJ;
PI   Gerlach V,  Grosse WM,  Alsobrook JP,  Lepley DM,  Rieger D,  Burgess CE;
PI   Casman SJ,  Spytek KA,  Boldog FL,  Li L,  Padigaru M,  Mishra V;
PI   Patturajan M,  Shenoy S,  Rastelli L,  Tchernev VT,  Vernet CAM;
PI   Zerhusen BD,  Malyankar UM,  Guo X,  Miller CE,  Gangolli EA;
XX
DR   WPI; 2002-590741/63.
XX
PT   Novel isolated polypeptide, designated NOVX, useful for treating or
PT   preventing in NOVX-associated disorders e.g. cardiomyopathy,
PT   atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.
XX
PS   Example 2; Page 246; 353pp; English.
XX
CC   The present invention provides the protein and coding sequences of
CC   several novel human proteins, designated NOVX. These can be used in the
CC   treatment of, amongst others, cancers, autoimmune diseases, infections,
CC   inflammatory diseases, storage disorders, muscle disorders,
CC   neurodegenerative diseases and developmental defects. The present
CC   sequence is a PCR primer or probe used to isolate the sequences of the
CC   invention. All of the probes are modified at the 5' end by TET and at the
CC   3' end by TAMRA
XX
SQ   Sequence 22 BP; 7 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGAAATGGA 2693
              | | ||| ||| |||||||||
Db         21 ACTTTGTATGGCTGAAATGGA 1


RESULT 3750
ABZ31358
ID   ABZ31358 standard; DNA; 22 BP.
XX
AC   ABZ31358;
XX
DT   30-JAN-2003  (first entry)
XX
DE   Candida albicans GRACE strain PCR primer SEQ ID NO 5577.
XX
KW   Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW   signal transduction; DNA replication; cell division; growth;
KW   proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS   Candida albicans.
XX
PN   WO200253728-A2.
XX
PD   11-JUL-2002.
XX
PF   26-DEC-2001; 2001WO-US049486.
XX
PR   29-DEC-2000; 2000US-0259128P.
PR   20-FEB-2001; 2001US-00792024.
PR   22-AUG-2001; 2001US-0314050P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Roemer T,  Jiang B,  Boone C,  Bussey H,  Ohlsen KL;
XX
DR   WPI; 2002-566694/60.
XX
PT   Constructing strains for identifying gene products as effective targets
PT   for therapeutic intervention, by inactivating in the strain one allele of
PT   a gene and placing other allele of the gene under conditional expression.
XX
PS   Claim 36; SEQ ID NO 5577; 167pp + Sequence Listing; English.
XX
```

CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 22 BP; 6 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2479 CTTTTAATGGTGATGGGGTAA 2499
              | | ||||| ||| |||||||
Db          2 CGTATAATGCTGACGGGGTAA 22
```

RESULT 3751
AAL47282
ID AAL47282 standard; DNA; 22 BP.
XX
AC AAL47282;
XX
DT 30-AUG-2002 (first entry)
XX
DE Hepatitis C virus NS5B region PCR primer #1.
XX
KW Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
KW virucide; hepatotropic; gene therapy; anti-viral; PCR; primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200238793-A2.
XX
PD 16-MAY-2002.
XX
PF 02-NOV-2001; 2001WO-US046350.
XX
PR 07-NOV-2000; 2000US-0245866P.
XX
PA (ANAD-) ANADYS PHARM INC.
XX
PI Bichko V;
XX
DR WPI; 2002-490082/52.
XX
PT Novel nucleic acid encoding replication competent recombinant hepatitis C
PT virus genome useful for screening anti-hepatitis C virus therapeutics and
PT for vaccine development.
XX
PS Example 1; Page 75; 85pp; English.
XX
CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement non-
CC infectious, replication-defective infection-component, and replication-
CC defective non-infectious HCV, in gene therapy or gene vaccination
CC targeted to hepatic tissue for treating an animal infected or susceptible
CC to HCV infection and for studying HCV infection and propagation. The
CC present sequence is a PCR primer used to amplify the HCV NS5B region in
CC the exemplification of the invention
XX
SQ Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1895 GCCCTAGATCAACAGATCAAC 1915
              |||||||||   |||||| ||
Db          1 GCCCTAGATTGTCAGATCTAC 21
```

RESULT 3752
AAD32695/c
ID AAD32695 standard; DNA; 22 BP.
XX
AC AAD32695;
XX
DT 29-AUG-2003 (revised)
DT 01-JUL-2002 (first entry)
XX
DE Escherichia coli M1162 chromosomal DNA amplifying PCR primer #3.
XX
KW Bacterium; L-threonine; L-isoleucine; phosphoenolpyruvate carboxylase;
KW transhydrogenase activity; PCR primer; ss.
XX
OS Escherichia coli; M1162.
XX
PN EP1179597-A1.
XX
PD 13-FEB-2002.
XX
PF 31-JUL-2001; 2001EP-00118456.
XX
PR 11-AUG-2000; 2000JP-00244921.
XX
PA (AJIN) AJINOMOTO KK.
XX
PI Miyata Y, Nakai Y, Nakanishi K, Ito H, Kojima H, Kurahashi O;
XX
DR WPI; 2002-229928/29.
XX
PT New bacterium belonging to genus Escherichia, useful for producing L-
PT threonine or L-isoleucine, in which intracellular phosphoenolpyruvate
PT carboxylase activity and transhydrogenase activity are enhanced.
XX
PS Example 1; Page 11; 24pp; English.
XX
CC The invention relates to a bacterium belonging to the genus Escherichia,
CC having an ability to produce L-threonine or L-isoleucine, and in which
CC intracellular phosphoenolpyruvate carboxylase activity and
CC transhydrogenase activity are enhanced. The bacterium is useful for
CC producing L-threonine or L-isoleucine, by culturing the bacterium in a
CC medium. The present sequence is a PCR primer used to amplify Escherichia
CC coli M1162 chromosomal DNA. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 22 BP; 5 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;

```
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2352 GTTCTGTATTTTAAGAAACAG 2372
              || ||| || || ||||||||
Db         22 GTCCTGAATCTTGAGAAACAG 2

RESULT 3753
ABT21552/c
ID   ABT21552 standard; DNA; 22 BP.
XX
AC   ABT21552;
XX
DT   16-APR-2003  (first entry)
XX
DE   Multiplex group PCR primer #299.
XX
KW   Racing potential; horse; grandpaternal DNA; over-represented; breeding;
KW   grandmother; performance; progeny horse; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200292851-A2.
XX
PD   21-NOV-2002.
XX
PF   15-MAY-2002; 2002WO-GB002273.
XX
PR   15-MAY-2001; 2001GB-00011886.
XX
PA   (ANIM-) ANIMAL HEALTH TRUST.
PA   (BRHO-) BRITISH HORSERACING BOARD.
XX
PI   Binns MM,  Swinburne JE;
XX
DR   WPI; 2003-129314/12.
XX
PT   Determining the racing potential of a horse comprises measuring whether
PT   grandpaternal or grandmaternal DNA from the selected grandmother DNA is
PT   over-represented in the genome of the horse.
XX
PS   Example 2; Page 25; 49pp; English.
XX
CC   The invention relates to a novel method for determining racing potential
CC   of a horse. The method comprises measuring: whether grandpaternal DNA is
CC   over-represented in the genome of the horse; or in the case where one of
CC   the grandmothers was selected for breeding on the basis of racing
CC   performance, whether grandmaternal DNA from the selected grandmother is
CC   over-represented in the genome of the horse which indicates that the
CC   horse has good racing potential. The method of the invention is useful
CC   for determining the racing potential of a horse or for obtaining a
CC   progeny horse with good racing potential. This polynucleotide sequence
CC   represents a PCR primer used in the detection method of over-
CC   representation of DNA from male grandparents of the invention
XX
SQ   Sequence 22 BP; 6 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2412 GGGGTCTGTAAATACTGGTGC 2432
              || |||| |||| | ||||||
Db         21 GGAGTCTATAAACATTGGTGC 1

RESULT 3754
ACC78700/c
ID   ACC78700 standard; DNA; 22 BP.
XX
AC   ACC78700;
XX
DT   02-SEP-2003  (first entry)
XX
DE   Nucleotide sequence of a PCR primer ZASP_R.
XX
KW   Cardiopathy; nucleic acid marker; therapy; human; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003040407-A2.
XX
PD   15-MAY-2003.
XX
PF   08-NOV-2002; 2002WO-EP012522.
XX
PR   09-NOV-2001; 2001EP-00126800.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Ruiz P,  Grzweskowiak R,  Drungowski M,  Witt H,  Osterziel KJ;
PI   Perrot A,  Saleh A;
XX
DR   WPI; 2003-430678/40.
XX
PT   New diagnostic composition comprising at least one nucleic acid molecule
PT   that is capable of specifically hybridizing to the mRNA of the gene,
PT   useful for diagnosing cardiopathy, e.g. cardiomyopathy or dilated
PT   cardiomyopathy.
XX
PS   Example 1; Page 22; 82pp; English.
XX
CC   The invention relates to a diagnostic composition comprising at least one
CC   nucleic acid molecule listed in the specification that is capable of
CC   specifically hybridizing to the mRNA of at least one of the genes given
CC   in the specification. The diagnostic composition and nucleic acid
CC   molecules are useful for diagnosing cardiopathy or a disposition to
CC   cardiopathy, e.g. cardiomyopathy or dilated cardiomyopathy. The method
CC   involves contacting a target sample with the nucleic acid molecule cited
CC   above, and comparing the concentration of the individual mRNA(s) with the
CC   concentration of the corresponding mRNAs from at least one of the healthy
CC   donor. The nucleic acids are also useful for the isolation and
CC   development of a compound useful for therapy or prevention of a
CC   cardiopathy. Sequences ACC78653-700 represent primers used in real-time
CC   quantitative PCR for amplifying human genes, during the course of the
CC   invention
XX
SQ   Sequence 22 BP; 5 A; 2 C; 11 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        753 GTCCCATTTCCATGACCAAGA 773
              |||||||| ||||  ||| ||
Db         21 GTCCCATTCCCATCTCCACGA 1

RESULT 3755
ACC90648
ID   ACC90648 standard; DNA; 22 BP.
XX
AC   ACC90648;
XX
DT   13-AUG-2003  (first entry)
XX
DE   Human CYP1A2 PCR primer SEQ ID NO:14.
XX
KW   CYP1A2; cytochrome P450; cytostatic; hepatotropic; dermatological;
KW   cerebroprotective; gene therapy; cancer; congenital jaundice;
KW   porphyria cutanea tarda; tardive dyskinesia; schizophrenia; human; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003014387-A2.
```

XX
PD 20-FEB-2003.
XX
PF 08-AUG-2002; 2002WO-EP008893.
XX
PR 08-AUG-2001; 2001EP-00118770.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Presecan-Siedel E;
XX
DR WPI; 2003-256599/25.
XX
PT New CYP1A2 polynucleotide and polypeptide, useful for the preparation of
PT a diagnostic or therapeutic composition for cancer, congenital jaundice,
PT porphyria cutanea tarda or tardive dyskinesia in schizophrenia.
XX
PS Example 1; Page 38; 117pp; English.
XX
CC The invention relates to a novel polynucleotide comprising any of 37 11-
CC 761 base pair sequences, given in the specification, encoding a
CC polypeptide with any of 4 28-31 residue amino acid sequences, in the
CC specification, hybridising to a CYP1A2 gene, or encoding a CYP1A2
CC polypeptide or fragment comprising an amino acid substitution at position
CC 61, 298, 401 or 438. A polypeptide of the invention has cytostatic,
CC hepatotropic, dermatological, and cerebroprotective activity. A
CC polynucleotide of the invention may act as a CYP1A2-antagonist or CPY1A2-
CC agonist, and may have a use in gene therapy. The methods and compositions
CC of the present invention are useful for the preparation of a diagnostic
CC or therapeutic composition for a disease, in particular cancer,
CC congenital jaundice, porphyria cutanea tarda or tardive dyskinesia in
CC schizophrenia. The sequences shown in ACC90635-ACC90686 represent PCR
CC primer used in the invention to screen for polymorphisms within CYP1A2
XX
SQ Sequence 22 BP; 3 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1675 CCTGGACTTCTTAGTTGTTTC 1695
||||| | || |||||| |||
Db 2 CCTGGCCATCCTAGTTGATTC 22

RESULT 3756
ACD06310/c
ID ACD06310 standard; DNA; 22 BP.
XX
AC ACD06310;
XX
DT 06-AUG-2003 (first entry)
XX
DE Reverse RT-PCR primer for human NOV7a.
XX
KW Human; ss; PCR; NOVX; cardiomyopathy; atherosclerosis; hypertension;
KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;
KW neoplasm; graft versus host disease; AIDS; bronchial asthma; primer;
KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;
KW cancer-associated cachexia; neurodegenerative disorder; RT-PCR;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy;
KW reverse transcriptase PCR.
XX
OS Homo sapiens.
XX
PN WO2003023008-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028596.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318130P.
PR 10-SEP-2001; 2001US-0318430P.
PR 12-SEP-2001; 2001US-0318765P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 15-FEB-2002; 2002US-0357303P.
PR 28-FEB-2002; 2002US-0360973P.
PR 20-MAR-2002; 2002US-0366131P.
PR 25-MAR-2002; 2002US-0367753P.
PR 02-APR-2002; 2002US-0369479P.
PR 10-MAY-2002; 2002US-0379532P.
PR 17-MAY-2002; 2002US-0381664P.
PR 17-MAY-2002; 2002US-0381672P.
PR 28-MAY-2002; 2002US-0383651P.
PR 29-MAY-2002; 2002US-0384012P.
PR 19-JUN-2002; 2002US-0390155P.
PR 06-SEP-2002; 2002US-00390155.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
PI Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
PI Patturajan M, Pena CEA, Tchernev VT, Padigaru M, Gusev VY;
PI Malyankar UM, Burgess CE, Gerlach VL, Casman SJ, Rieger DK;
PI Grosse WM, Smithson G, Peyman JA, Starling G, Rothenberg ME;
PI Larochelle WJ, Shimkets RA, Crabtree J, Rastelli L, Voss EZ;
PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
PI Chapoval A;
XX
DR WPI; 2003-313246/30.
XX
PT New polypeptides and polynucleotides having properties related to
PT stimulation of biochemical or physiological responses in a cell or
PT tissue, useful for diagnosing or preventing e.g. atherosclerosis,
PT hypertension, prostate cancer.
XX
PS Example C; Page 332; 849pp; English.
XX
CC The invention relates to an isolated polypeptide comprising one of 127
CC sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature
CC form of NOVX, an amino acid sequence which is at least 95% identical to
CC NOVX or an amino acid sequence comprising one or more conservative
CC substitutions in NOVX. Also included are nucleic acids encoding NOVX
CC proteins, determining the presence or amount of NOVX or NOVX DNA in a
CC sample (by introducing the sample to an antibody that binds
CC immunospecifically to the polypeptide, and determining the presence or
CC amount of antibody bound to the polypeptide), determining the presence of
CC or predisposition to a disease associated with altered levels of
CC expression of NOVX or NOVX DNA in a first mammalian subject, identifying
CC an agent that binds to NOVX, identifying a potential therapeutic agent
CC for treatment of a pathology related to aberrant expression or aberrant
CC physiological interactions of NOVX, screening for a modulator of activity
CC of or of latency or predisposition to a pathology associated with NOVX, a
CC vector comprising NOVX DNA, a cell comprising the vector (used to produce
CC NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides
CC are useful as a marker for cell or tissue type, and in diagnosing and
CC treating pathologies, diseases, conditions or disorders associated with
CC NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, prostate cancer, diabetes, metabolic disorders,
CC neoplasm, graft versus host disease, AIDS, bronchial asthma, Crohn's
CC disease, multiple sclerosis, infectious diseases, anorexia, cancer-
CC associated cachexia, neurodegenerative disorders (e.g. Alzheimer's
CC disease or Parkinson's disease), immune disorders, haematopoietic
CC disorders, dyslipidaemias, and wasting disorders associated with chronic
CC diseases. These may also be used to screen for molecules which inhibit or
CC enhance NOVX activity or function, and for detecting specific cell types.
CC These may also be used in chromosome mapping, gene therapy, tissue

```
CC   typing, and in forensic biology. The present sequence is a reverse
CC   transcriptase (RT)-PCR primer used to assess the tissue specific
CC   expression of mRNA encoding a NOVX protein
XX
SQ   Sequence 22 BP; 9 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1829 TCTTTTAAATACATTCCCTGG 1849
              |||||| |  ||||||| |||
Db         21 TCTTTTGATGACATTCCATGG 1

RESULT 3757
ACC84173
ID   ACC84173 standard; DNA; 22 BP.
XX
AC   ACC84173;
XX
DT   03-OCT-2003  (first entry)
XX
DE   Human butyrylcholinesterase sense PCR primer Acb710.
XX
KW   Human; butyrylcholinesterase; transgenic; poisoning; antidote; enzyme;
KW   PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003054182-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-IB005526.
XX
PR   21-DEC-2001; 2001US-0344295P.
XX
PA   (NEXI-) NEXIA BIOTECHNOLOGIES INC.
XX
PI   Karatzas C,  Huang Y,  Lazaris A;
XX
DR   WPI; 2003-559148/52.
XX
PT   New transgenic mammal (e.g. goat) expressing a butyrylcholinesterase
PT   (BChE) enzyme in its milk or urine, useful for large-scale production of
PT   recombinant BChE to prevent or treat organophosphate poisoning or cocaine
PT   intoxication.
XX
PS   Example 1; Page 41; 112pp; English.
XX
CC   The present sequence is that of sense primer Acb710, which was used in
CC   the PCR amplification of human butyrylcholinesterase (BChE) cDNA (see
CC   ACC84169) from pCMV/BChE. The PCR product was used in the construction of
CC   pCMV/BChE/hSA, used to prepare a BChE-hSA fusion protein in mammalian
CC   cells. The primer was also used to generate a probe for detection of a
CC   BChE transgene. The invention provides methods for large-scale production
CC   of recombinant BChE in cell culture, and in the milk and/or urine of
CC   transgenic mammals. The recombinant BChE can be used in preventing and/or
CC   treating organophosphate pesticide poisoning, nerve gas poisoning,
CC   cocaine intoxication or succinylcholine-induced apnoea
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2598 TGAAACTCTCTGTTCAGAAAG 2618
              || |||||||| |  ||||||
Db          2 TGTAACTCTCTTTGGAGAAAG 22

RESULT 3758
ADD21875/c
ID   ADD21875 standard; DNA; 22 BP.
XX
AC   ADD21875;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Protein translation efficiency-related DNA sequence #59.
XX
KW   nucleotide production; translation efficiency; protein synthesis; ds.
XX
OS   Unidentified.
XX
PN   WO2003056009-A1.
XX
PD   10-JUL-2003.
XX
PF   27-DEC-2002; 2002WO-JP013756.
XX
PR   27-DEC-2001; 2001JP-00396941.
XX
PA   (ENDO/) ENDO Y.
XX
PI   Endo Y,  Sawasaki T;
XX
DR   WPI; 2003-618079/58.
XX
PT   Preparing translation controlling nucleotides used for increased
PT   efficiency during protein synthesis.
XX
PS   Claim 11; Page 55; 87pp; Japanese.
XX
CC   The invention comprises a method for preparing nucleotides that control
CC   translation efficiency of proteins. The nucleotides of the invention are
CC   useful for increasing efficiency during protein synthesis. The present
CC   DNA sequence is used in the exemplification of the invnetion.
XX
SQ   Sequence 22 BP; 4 A; 4 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 22;
  Best Local Similarity   81.0%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAA 2800
              |||| |||||  || ||||||
Db         22 GAATGGAAAATTAAGAAAAAA 2

RESULT 3759
ABQ78896/c
ID   ABQ78896 standard; DNA; 24 BP.
XX
AC   ABQ78896;
XX
DT   17-OCT-2002  (first entry)
XX
DE   Human zinc finger protein 27.50 PCR primer 2.
XX
KW   Human; zinc finger protein 27.50; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1341649-A.
XX
PD   27-MAR-2002.
XX
PF   07-SEP-2000; 2000CN-00125059.
XX
PR   07-SEP-2000; 2000CN-00125059.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
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PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-520724/56.
XX
PT   Novel human zinc finger protein 27.50.
XX
PS   Example 3; Page 17 (Disclosure); 31pp; Chinese.
XX
CC   The invention relates to a novel human zinc finger protein 27.50, and the
CC   polynucleotide encoding it. The polypeptide is useful for treating
CC   several diseases, such as solid tumour, nervous system disease, malignant
CC   disease of blood, development disturbance and HIV infection. The sequence
CC   represents a PCR primer used in example 3 of the invention
XX
SQ   Sequence 24 BP; 5 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 24;
  Best Local Similarity   81.0%;  Pred. No. 4.3e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||| |||| |||| |||
Db         24 TAAAAAATAAAATAAAATAAA 4


RESULT 3760
ADD19369/c
ID   ADD19369 standard; DNA; 24 BP.
XX
AC   ADD19369;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Salmo salar SNP OLA primer SEQ ID NO:4.
XX
KW   single nucleotide polymorphism; SNP; fish; Salmo salar;
KW   Orechromis niloticus; Atlantic halibut; microsatellite; cod;
KW   polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW   detection; primer; ss.
XX
OS   Synthetic.
OS   Salmo salar.
XX
PN   WO2003060160-A2.
XX
PD   24-JUL-2003.
XX
PF   17-JAN-2003; 2003WO-IB000112.
XX
PR   18-JAN-2002; 2002US-0349950P.
PR   16-AUG-2002; 2002US-0404200P.
XX
PA   (GENO-) GENOMAR ASA.
XX
PI   Lie O,  Slettan A,  Hoyum M,  Lingaas F;
XX
DR   WPI; 2003-627388/59.
XX
PT   Novel isolated nucleic acid molecule comprising single nucleotide
PT   polymorphism associated with fish, useful for forming PCR primers which
PT   are used for detecting single nucleotide polymorphisms in fish nucleic
PT   acids.
XX
PS   Claim 1; SEQ ID NO 4; 233pp; English.
XX
CC   The present invention describes an isolated nucleic acid (I) comprising a
CC   single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC   Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC   and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC   (i), or its complement under highly stringent hybridisation conditions.
CC   Also described: (1) an isolated oligonucleotide (II) comprising at least
CC   17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites, or their complement; (2)
CC   a primer pair (III) suitable for use in PCR, comprising two (II) capable
CC   of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC   origin of fish sample comprising providing a parentage genotype database
CC   comprising a collection of candidate parent genotypes, where each of the
CC   candidate parent genotype represents a distinct origin, and comparing a
CC   sample genotype to the parentage genotype database, where a match between
CC   the sample genotype and one of the candidate parent genotype identifies
CC   to the origin of the sample. (M1) is useful for determining the origin of
CC   a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC   rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC   detecting nucleic acid molecule comprising SNP in a sample, which
CC   involves contacting the sample containing nucleic acids with one or more
CC   (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC   SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC   useful for detecting nucleic acid molecule comprising a polymorphic
CC   sequence in a sample, comprising contacting the sample containing nucleic
CC   acids with one or more (II) which is derived from O. niloticus
CC   microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC   sites or seabass polymorphic sites, and identifying a nucleic acid that
CC   hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC   comprising a microsatellite sequence in sample. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 24 BP; 16 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 24;
  Best Local Similarity   81.0%;  Pred. No. 4.3e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTT 2191
              ||||||| ||||||  || ||
Db         21 TTTTTTTGTTTTTTCCAATTT 1


RESULT 3761
AAK99651/c
ID   AAK99651 standard; DNA; 24 BP.
XX
AC   AAK99651;
XX
DT   08-JUL-2002  (first entry)
XX
DE   Human alpha 2, 3-sialyltransferase (ST3 GalVI) 9-13 cDNA PCR primer 1.
XX
KW   Human alpha 2, 3-sialyltransferase; ST3 GalVI 9-13; DNA recombination;
KW   immunological deficiency; inflammation; tumour; human; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1329158-A.
XX
PD   02-JAN-2002.
XX
PF   21-JUN-2000; 2000CN-00116664.
XX
PR   21-JUN-2000; 2000CN-00116664.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-292825/34.
XX
PT   New polypeptide-human alpha 2,3-sialytransferase (ST3 GalVI) 9.13 for
PT   treating several diseases, such as immunological deficiency, various
PT   inflammations and tumors.
XX
PS   Example 2; Page 20 Disclosure; 36pp; Chinese.
XX
CC   The present invention relates to a novel polypeptide-human alpha 2, 3-
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CC   sialyltransferase (ST3 GalVI) 9.13, the polynucleotide encoding the
CC   polypeptide and producing the polypeptide by using a DNA recombination
CC   technique. The invention also discloses the method for curing several
CC   diseases, such as immunological deficiency, various inflammations and
CC   tumours by using the polypeptide. The invention also discloses an
CC   antagonist for resisting the polypeptide and its therapeutic action, and
CC   also discloses the application of the polynucleotide encoding the novel
CC   human alpha 2.3-sialyltransferase (ST3 GalVI) 9.13. This polynucleotide
CC   sequence represents a PCR primer of the cDNA encoding the human alpha 2.3
CC   -sialyltransferase (ST3 GalVI) 9.13 protein of the invention
XX
SQ   Sequence 24 BP; 4 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 24;
  Best Local Similarity   81.0%;  Pred. No. 4.3e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | || ||| ||||| ||||||
Db         23 TAAATAAATAAAAATAAAAAA 3


RESULT 3762
AAC96700/c
ID   AAC96700 standard; DNA; 25 BP.
XX
AC   AAC96700;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-A gene PCR primer #77.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 55; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 4.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAA 2797
              ||| ||   ||||||||||||
Db         21 TTACAAGCTAAAAAAAAAAAA 1


RESULT 3763
AAC95708
ID   AAC95708 standard; DNA; 25 BP.
XX
AC   AAC95708;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #5.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 2 A; 6 C; 2 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 4.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||  || | |
Db          1 TTTTTTTTTTTTTCCAAGTCT 21


RESULT 3764
AAC95789/c
ID   AAC95789 standard; DNA; 25 BP.
XX
AC   AAC95789;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DRB1 gene PCR primer #33.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
```

KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 40; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 25;
Best Local Similarity 81.0%; Pred. No. 4.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2777 TTAGAATTGAAAAAAAAAAAA 2797
| ||| | ||||||||||||
Db 21 TCAGACGTAAAAAAAAAAAAA 1

RESULT 3765
AAC96432
ID AAC96432 standard; DNA; 25 BP.
XX
AC AAC96432;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #34.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 1 A; 5 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.6; DB 1; Length 25;
Best Local Similarity 81.0%; Pred. No. 4.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
|||||||||||||| || ||
Db 1 TTTTTTTTTTTTTCATTCCTT 21

RESULT 3766
AAC96396
ID AAC96396 standard; DNA; 25 BP.
XX
AC AAC96396;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #128.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 50; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.6;  DB 1;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 4.5e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||| ||  | |
Db          1 TTTTTTTTTTTTTGTTCCAGT 21


RESULT 3767
AAV07974/c
ID   AAV07974 standard; DNA; 26 BP.
XX
AC   AAV07974;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1999  (first entry)
XX
DE   Helicobacter pylori polypeptide GHPO 711 5' DNA primer.
XX
KW   GHPO 711; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR;
KW   primer; ss.
XX
OS   Synthetic.
OS   Helicobacter pylori.
XX
PN   WO9843479-A1.
XX
PD   08-OCT-1998.
XX
PF   31-MAR-1998;   98WO-US006421.
XX
PR   01-APR-1997;   97US-00831310.
PR   01-APR-1997;   97US-00834666.
XX
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Kleanthous H,  Lissolo L,  Tomb J,  Miller C,  Algarawi A;
XX
DR   WPI; 1998-568251/48.
XX
PT   New isolated Helicobacter polynucleotides - used to develop products for
PT   the diagnosis, prevention and treatment of Helicobacter infections and
PT   gastroduodenal diseases.
XX
PS   Example 3.B; Page 64; 184pp; English.
XX
CC   This 5' primer was used with a 3' primer (see AAV07975) in the PCR
CC   amplification of Helicobacter pylori strain ORV2001 genomic DNA in order
CC   to obtain DNA (see AAV07917) encoding a 76 kDa polypeptide (see AAW73028)
CC   designated GHPO 711. The primer pair includes a 5' clamp and BamHI and
CC   XhoI restriction enzyme reocgnition sequences for cloning purposes. The
CC   PCR product was ligated into vector pET28a, and recombinant polypeptide
CC   was expressed as a histidine-tagged fusion protein in E. coli host cells.
CC   The polypeptide can be used to develop vaccines for the treatment and
CC   prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct
CC   PI field.)
XX
SQ   Sequence 26 BP; 16 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.6;  DB 1;  Length 26;
  Best Local Similarity   81.0%;  Pred. No. 4.6e+03;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||  ||||||| || |
Db         24 TTTTTTTCGTTTTTTTGAATT 4


RESULT 3768
AAX18362
ID   AAX18362 standard; DNA; 16 BP.
XX
AC   AAX18362;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 3.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||  |
Db          1 TTTTTTTTTTTTTTCA 16


RESULT 3769
AAX18369/c
ID   AAX18369 standard; DNA; 16 BP.
XX
AC   AAX18369;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 10.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
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PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              | ||||||||||||||
Db         16 GTAAAAAAAAAAAAAA 1


RESULT 3770
AAX18363
ID   AAX18363 standard; DNA; 16 BP.
XX
AC   AAX18363;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 4.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              ||||||||||||||| |
Db          1 TTTTTTTTTTTTTTCT 16


RESULT 3771
AAX18365/c
ID   AAX18365 standard; DNA; 16 BP.
XX
AC   AAX18365;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 6.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              | ||||||||||||||
Db         16 GCAAAAAAAAAAAAAA 1


RESULT 3772
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```
AAX18366
ID   AAX18366 standard; DNA; 16 BP.
XX
AC   AAX18366;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 7.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||||
Db          1 TTTTTTTTTTTTTTGA 16


RESULT 3773
AAX18366/c
ID   AAX18366 standard; DNA; 16 BP.
XX
AC   AAX18366;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 7.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db         16 TCAAAAAAAAAAAAAA 1


RESULT 3774
AAX18367
ID   AAX18367 standard; DNA; 16 BP.
XX
AC   AAX18367;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 8.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
```

```
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              ||||||||||||||  |
Db          1 TTTTTTTTTTTTTGT 16


RESULT 3775
AAX18367/c
ID   AAX18367 standard; DNA; 16 BP.
XX
AC   AAX18367;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 8.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              | |||||||||||||||
Db         16 ACAAAAAAAAAAAAA 1
```

```
RESULT 3776
AAC91050/c
ID   AAC91050 standard; DNA; 16 BP.
XX
AC   AAC91050;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Selection target #2.
XX
KW   Gene switch; DNA binding ligand; transcription; gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO200073434-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-GB002071.
XX
PR   28-MAY-1999;   99GB-00012635.
PR   24-JAN-2000; 2000GB-00001578.
XX
PA   (GEND-) GENDAQ LTD.
XX
PI   Choo Y,  Ullman CG;
XX
DR   WPI; 2001-061525/07.
XX
PT   Selecting gene switches useful for regulating transcription of a DNA
PT   sequence comprises complexing target DNA with DNA binding molecule in the
PT   presence and absence of DNA binding ligand, and comparing the binding.
XX
PS   Example 1; Page 70; 106pp; English.
XX
CC   The present invention relates to selecting a gene switch with a target
CC   DNA molecule, a DNA binding molecule which binds to the target such that
CC   it may be modulated by a DNA binding ligand. The invention is useful for
CC   regulating transcription from a DNA sequence. The ligand is useful for
CC   modulating the expression of one or more nucleotide sequences of interest
CC   in a host cell, preferably a plant cell
XX
SQ   Sequence 16 BP; 12 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 3777
AAS11434/c
ID   AAS11434 standard; DNA; 16 BP.
XX
AC   AAS11434;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Selection target #2 used to screen Zif268 zinc finger phage library.
XX
KW   Zif268; sub-cellular trafficking; signal transduction; diagnostic;
KW   gene therapy; agricultural technology; zinc finger; ss; oligonucleotide.
XX
OS   Synthetic.
XX
PN   WO200153479-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-GB000187.
```

```
XX
PR   24-JAN-2000; 2000GB-00001578.
PR   24-JAN-2000; 2000GB-00001582.
PR   30-MAY-2000; 2000WO-GB002071.
PR   30-MAY-2000; 2000WO-GB002080.
PR   07-DEC-2000; 2000GB-00029901.
XX
PA   (GEND-) GENDAQ LTD.
XX
PI   Choo Y,  Ullman CG,  Moore M;
XX
DR   WPI; 2001-457607/49.
XX
PT   Selecting switching system components comprising first molecule, second
PT   molecule and ligand, involves determining degree of binding between the
PT   molecules in the presence and absence of the ligand.
XX
PS   Example 1.1; Page 138; 193pp; English.
XX
CC   The invention relates to a method of selecting components of a switching
CC   system comprising first molecule (M1), selecting (I) a ligand (L2) which
CC   is capable of modulating the interaction between a nucleic acid binding
CC   molecule (NBM) and a target nucleic acid (TN). NBM, TN and the ligands
CC   are useful for regulating a biological process selected from sub-cellular
CC   trafficking and signal transduction, and for regulating transcription or
CC   translation from a nucleic acid sequence comprising TN to which NBM binds
CC   in a manner modulatable by the ligand. They are also useful for
CC   modulating a biological process affecting one or more genes, such as in
CC   transcription, translation, phosphorylation, replication, transport,
CC   splicing, integration and recombination, in a host cell. The polypeptides
CC   or ligands selected from (S) are useful for regulating a biological
CC   process involving binding of first polypeptide with second polypeptide,
CC   selected from sub-cellular trafficking and signal transduction. (I) is
CC   also useful for screening any or all the components of the gene switch
CC   system or protein switch system, and for modulating the interaction
CC   between the components of the switching system. The binding molecules are
CC   useful as diagnostic and research tools, and for switching or modulating
CC   gene expression, especially in gene therapy applications and agricultural
CC   technology applications. The ligands are also useful in the treatment of
CC   diseases. Multiple target nucleic acids or polypeptides could be used in
CC   a single selective step, thus enabling multiple nucleic acid or
CC   polypeptide binding molecules to be isolated simultaneously, even in the
CC   same physical vessel. The present sequence represents the selection
CC   target #2 used to screen a phage library comprising variants of the
CC   middle finger from the DNA binding domain of Zif268, used in the method
CC   of the invention
XX
SQ   Sequence 16 BP; 12 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 3778
AAS11444/c
ID   AAS11444 standard; DNA; 16 BP.
XX
AC   AAS11444;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Oligonucleotide #2 used to mutate zinc finger DNA binding domain.
XX
KW   sub-cellular trafficking; signal transduction; oligonucleotide;
KW   diagnostic; gene therapy; agricultural technology; zinc finger; ss;
KW   mutagenic.
XX
OS   Synthetic.
XX
PN   WO200153479-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-GB000187.
XX
PR   24-JAN-2000; 2000GB-00001578.
PR   24-JAN-2000; 2000GB-00001582.
PR   30-MAY-2000; 2000WO-GB002071.
PR   30-MAY-2000; 2000WO-GB002080.
PR   07-DEC-2000; 2000GB-00029901.
XX
PA   (GEND-) GENDAQ LTD.
XX
PI   Choo Y,  Ullman CG,  Moore M;
XX
DR   WPI; 2001-457607/49.
XX
PT   Selecting switching system components comprising first molecule, second
PT   molecule and ligand, involves determining degree of binding between the
PT   molecules in the presence and absence of the ligand.
XX
PS   Example 3; Page 146; 193pp; English.
XX
CC   The invention relates to a method of selecting components of a switching
CC   system comprising first molecule (M1), selecting (I) a ligand (L2) which
CC   is capable of modulating the interaction between a nucleic acid binding
CC   molecule (NBM) and a target nucleic acid (TN). NBM, TN and the ligands
CC   are useful for regulating a biological process selected from sub-cellular
CC   trafficking and signal transduction, and for regulating transcription or
CC   translation from a nucleic acid sequence comprising TN to which NBM binds
CC   in a manner modulatable by the ligand. They are also useful for
CC   modulating a biological process affecting one or more genes, such as in
CC   transcription, translation, phosphorylation, replication, transport,
CC   splicing, integration and recombination, in a host cell. The polypeptides
CC   or ligands selected from (S) are useful for regulating a biological
CC   process involving binding of first polypeptide with second polypeptide,
CC   selected from sub-cellular trafficking and signal transduction. (I) is
CC   also useful for screening any or all the components of the gene switch
CC   system or protein switch system, and for modulating the interaction
CC   between the components of the switching system. The binding molecules are
CC   useful as diagnostic and research tools, and for switching or modulating
CC   gene expression, especially in gene therapy applications and agricultural
CC   technology applications. The ligands are also useful in the treatment of
CC   diseases. Multiple target nucleic acids or polypeptides could be used in
CC   a single selective step, thus enabling multiple nucleic acid or
CC   polypeptide binding molecules to be isolated simultaneously, even in the
CC   same physical vessel. The present sequence represents the selection
CC   oligonucleotide #2 used to mutate the zinc finger DNA binding domain used
CC   in the method of the invention
XX
SQ   Sequence 16 BP; 12 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 3779
AAA89332/c
ID   AAA89332 standard; DNA; 16 BP.
XX
AC   AAA89332;
XX
DT   23-APR-2001  (first entry)
XX
DE   DNA ligand modulatable restriction enzyme cleavage site.
XX
```

```
KW   Molecular switch; gene switch; protein switch; zinc finger;
KW   restriction endonuclease; ss.
XX
OS   Synthetic.
XX
PN   WO200100815-A1.
XX
PD   04-JAN-2001.
XX
PF   30-MAY-2000; 2000WO-GB002080.
XX
PR   28-MAY-1999;   99GB-00012635.
PR   24-JAN-2000; 2000GB-00001582.
XX
PA   (GEND-) GENDAQ LTD.
XX
PI   Choo Y,  Ullman CGU;
XX
DR   WPI; 2001-123005/13.
XX
PT   Selecting gene or protein switches for use in modulating gene expression,
PT   comprises selecting complexes of two molecules and a ligand whose binding
PT   differs in the presence or absence of the ligand.
XX
PS   Example 3; Page 93; 125pp; English.
XX
CC   The present sequence is that of the DNA recognition sequence of a novel
CC   DNA ligand modulatable restriction enzyme. Phage-selected or rationally
CC   designed zinc finger domains which bind target DNA sequences in a manner
CC   modulatable by a ligand can be converted to restriction enzymes which
CC   cleave DNA containing the target sequence in a manner modulatable by the
CC   ligand. This is achieved by coupling a zinc finger to a cleavage domain
CC   of a restriction enzyme or other nucleic acid cleaving moiety. In this
CC   case, a fusion was made between the catalytic domain of FokI and a zinc
CC   finger. Fusion of the zinc finger nucleic acid-binding domain to the FokI
CC   restriction enzyme resulted in a novel endonuclease which cleaved DNA
CC   adjacent to the present DNA recognition sequence. The DNA-ligand
CC   modulatable restriction enzyme can be used in novel molecular switches of
CC   the invention that are used to modulate gene expression e.g. in gene
CC   therapy or in transgenic plants
XX
SQ   Sequence 16 BP; 12 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              ||||||| ||||||||
Db         16 TTTTTTCGCCTTTTTT 1


RESULT 3780
ABL57076
ID   ABL57076 standard; DNA; 16 BP.
XX
AC   ABL57076;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence (single mismatch).
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    9
FT                   /*tag=  a
FT                   /note= "mismatch site"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 30; 62pp; English.
XX
CC   The present sequence is that of a single mismatch target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Experiments with the present
CC   sequence and a perfectly-matched target (see ABL57071) showed that
CC   hybridisation was very specific to the matched target. The invention
CC   relates generally to the use of metal surface quenchers such as particles
CC   or films for high sensitivity applications in, for example, detection and
CC   diagnostic systems
XX
SQ   Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||||||| |||||||
Db          1 GAAAAAAACAAAAAAA 16


RESULT 3781
ABK87931
ID   ABK87931 standard; DNA; 16 BP.
XX
AC   ABK87931;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Anchored oligo-dT primer, H-T11G, used for differential display.
XX
KW   Human; PCR; primer; H-T11G; ss; CC214; cervical cancer 2; HCCR-2;
KW   protooncogene; cytostatic; tumourigenesis; cervical cancer; cancer;
KW   leukaemia; lymphoma; antisense; gene therapy; carcinogen; anticancer;
KW   antioxidant.
XX
OS   Synthetic.
XX
PN   WO200244370-A1.
XX
PD   06-JUN-2002.
XX
PF   09-JUL-2001; 2001WO-KR001172.
XX
PR   28-NOV-2000; 2000KR-00071202.
XX
PA   (KIMJ/) KIM J W.
```

```
XX
PI   Kim JW;
XX
DR   WPI; 2002-557542/59.
XX
PT   Novel human cervical cancer 2 protooncogene protein and polynucleotide
PT   encoding it useful for diagnosing various cancers e.g. leukemia, lymphoma
PT   or uterine cervix cancer, and for producing transformed animals.
XX
PS   Disclosure; Page 47; 49pp; English.
XX
CC   The invention discloses a human cervical cancer 2 (HCCR-2) protooncogene
CC   and encoded protein. The protooncogene was discovered using mRNA
CC   differential display, identifying it as being amplified in cancer cells
CC   and, more specifically, involved in the tumourigenesis of cervical
CC   cancer. HCCR-2 is useful for preventing, diagnosing or treating cancer,
CC   including leukaemia, lymphoma, colon, breast, kidney, stomach, lung,
CC   ovary or uterine cervix cancer. HCCR-2 is also useful for producing
CC   antibodies which are useful as diagnostic tools. HCCR-2 protooncogene is
CC   useful in the diagnosis of various cancers, in antisense gene therapy and
CC   for producing transformed animals which are useful in screening for
CC   carcinogens or anticancer agents, such as antioxidants. The protooncogene
CC   is also useful for establishing a continuous viable cancer cell line
CC   which is useful in searching for anticancer agents. The sequence
CC   presented is the anchored oligo-dT primer, H-T11G, which was used to
CC   amplify cDNA for differential display. This technique identified a cDNA
CC   fragment, designated CC214, which was then used as a probe to isolate the
CC   full length cDNA (cervical cancer 2 (HCCR-2) protooncogene) from a human
CC   lung embryonic fibroblast cDNA library
XX
SQ   Sequence 16 BP; 2 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||| ||||||||||||
Db          1 AAGTTTTTTTTTTTTG 16


RESULT 3782
AAD44143
ID   AAD44143 standard; DNA; 16 BP.
XX
AC   AAD44143;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #3 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2181
              | |||||||||||||||
Db          1 TVTTTTTTTTTTTTTT 16


RESULT 3783
AAD44143/c
ID   AAD44143 standard; DNA; 16 BP.
XX
AC   AAD44143;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #3 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
```

```
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              |||||||||||||| |
Db         16 AAAAAAAAAAAAAABA 1


RESULT 3784
AAD57846
ID   AAD57846 standard; DNA; 16 BP.
XX
AC   AAD57846;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Target oligonucleotide #3 used in nonlinear optical technique.
XX
KW   Nonlinear optical technique; screening; ss.
XX
OS   Unidentified.
XX
PN   WO2003064991-A2.
XX
PD   07-AUG-2003.
XX
PF   17-JUL-2002; 2002WO-US022681.
XX
PR   17-JUL-2001; 2001US-0306040P.
PR   23-OCT-2001; 2001US-0347821P.
PR   06-FEB-2002; 2002US-0354668P.
XX
PA   (SALA/) SALAFSKY J S.
XX
PI   Salafsky JS;
XX
DR   WPI; 2003-646172/61.
XX
PT   Screening candidate binding partner(s) for binding to test molecule by
PT   applying external force field to sample in homogeneous phase,
PT   illuminating sample with light beam(s) at fundamental frequencies, and
PT   measuring physical properties.
XX
PS   Disclosure; Fig 20-B; 146pp; English.
XX
CC   The present invention relates to a method for detecting interactions
CC   between biological components using a nonlinear optical technique. The
CC   invention is used for screening candidate binding partner(s) for binding
CC   to test molecule. It can also be used to detect changes in orientation or
CC   conformation of the probe and/or target. The present sequence is a target
CC   oligonucleotide used in nonlinear optical technique
XX
SQ   Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||||||| |||||||
Db          1 GAAAAAAACAAAAAAA 16


RESULT 3785
AAA25453/c
ID   AAA25453 standard; DNA; 17 BP.
XX
AC   AAA25453;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              | ||||||||||||||
Db         16 ACAAAAAAAAAAAAAA 1


RESULT 3786
AAQ30741
ID   AAQ30741 standard; DNA; 17 BP.
XX
AC   AAQ30741;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1993  (first entry)
XX
DE   DNA/RNA expression inhibiting modified oligomer.
XX
KW   Treatment; cancer; viral; bacterial; infection; diagnosis; therapy; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    3. .4
FT                   /*tag= e
FT                   /note= "3' thioformacetal linkage"
FT   modified_base   5
FT                   /*tag= a
FT                   /mod_base= m5c
FT   misc_feature    7. .8
FT                   /*tag= f
FT                   /note= "3' thioformacetal linkage"
FT   modified_base   9
FT                   /*tag= b
FT                   /mod_base= m5c
FT   modified_base   11
FT                   /*tag= c
FT                   /mod_base= m5c
FT   modified_base   12
FT                   /*tag= d
FT                   /mod_base= m5c
FT   misc_feature    13. .14
FT                   /*tag= g
FT                   /note= "3' thioformacetal linkage"
FT   misc_feature    15. .16
FT                   /*tag= h
FT                   /note= "3' thioformacetal linkage"
FT   misc_feature    17
FT                   /*tag= i
FT                   /note= "T - anthraquinone pseudonucleoside"
XX
PN   WO9219637-A1.
XX
PD   12-NOV-1992.
XX
PF   24-APR-1992;    92WO-US003385.
XX
PR   24-APR-1991;    91US-00690786.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Matteucci M,  Jones B,  Lin K;
XX
DR   WPI; 1992-398793/48.
XX
PT   New modified oligomers contg. thio:acetal linkages - inhibit DNA and RNA
PT   expression, useful for treating viral diseases, malignancy, bacterial
PT   diseases and in diagnosis.
XX
PS   Claim 1; Page 42; 69pp; English.
XX
CC   The sequence is that of an oligonucleotide analogue, contg.
CC   internucleoside thioacetal linkages, which is capable of binding DNA or
CC   RNA. It is useful for therapeutic or diagnostic purposes, e.g. for
CC   treating cancer or viral or bacterial infections. It also has the ability
CC   to inhibit gene expression. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 17 BP; 0 A; 4 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTT 2170
              ||| ||||||||||||
Db          2 TTTCTTTCTCCTTTTT 17


RESULT 3787
AAX69795
ID   AAX69795 standard; RNA; 17 BP.
XX
AC   AAX69795;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1090.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;    96WO-US017480.
XX
PR   26-OCT-1995;    95US-0005974P.
PR   11-JAN-1996;    96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 3 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   12.5%;  Pred. No. 2.6e+03;
  Matches    2;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTT 2176
              :|: |::::::::::::
Db          2 UCUACUUUUUUUUUUU 17


RESULT 3788
AAX69805/c
ID   AAX69805 standard; RNA; 17 BP.
XX
AC   AAX69805;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1100.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
```

OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 80; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 0 G; 0 T; 12 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2783 TTGAAAAAAAAAAAAA 2798
              ||| ||||||||||||
Db         16 TTGGAAAAAAAAAAAA 1
```

RESULT 3789
AAX71230
ID AAX71230 standard; RNA; 17 BP.
XX
AC AAX71230;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #242.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 104; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 10 A; 0 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1511 AGGAAATAAAATTGGA 1526
              ||||||:||||::| |
Db          2 AGGAAAUAAAAUUGAA 17
```

RESULT 3790
AAV97632/c
ID AAV97632 standard; RNA; 17 BP.
XX
AC AAV97632;
XX
DT 17-MAR-1999 (first entry)
XX
DE Human EGF-R target sequence nucleotide position 3517.
XX
KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW cancer; genetic drift; detection; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO9833893-A2.
XX
PD 06-AUG-1998.
XX
PF 14-JAN-1998; 98WO-US000730.
XX
PR 31-JAN-1997; 97US-0036476P.
PR 04-DEC-1997; 97US-00985162.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (UYAS-) UNIV ASTON.
XX
PI Akhtar S, Fell P, Mcswiggen JA;
XX
DR WPI; 1998-437449/37.
XX
PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and for
PT treating cancers.
XX
PS Claim 5; Page 76; 109pp; English.
XX

```
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC   represent specifically claimed target sequence from human EGF-R. AAV98044
CC   to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC   hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
CC   cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC   expression levels e.g. to inhibit cell proliferation in the prevention or
CC   treatment of cancers. The NAMs can also be used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of EGF-R RNA in a cell
XX
SQ   Sequence 17 BP; 5 A; 5 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1424 CTGATTGTCATAGACA 1439
              |||||||| |||||||
Db         17 CTGATTGTGATAGACA 2


RESULT 3791
AAX14657
ID   AAX14657 standard; DNA; 17 BP.
XX
AC   AAX14657;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix third strand of dystrophin gene nucleotides 12923-12939.
XX
KW   Triplex formation; DNA detection; triple helix; identification; bacteria;
KW   oncogene; virus; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 15-16; 168pp; English.
XX
CC   The present sequence represents a polynucleotide that is able to form a
CC   triple helix with a double stranded sequence. Cytosine bases in the
CC   present can be replaced with 5-methylcytosine for increased triplex
CC   stability. The present sequence is used in the assay of the invention,
CC   where it can be part of the anchor DNA or reporter DNA sequence. The
CC   assay comprises adding a sample containing double-stranded DNA test
CC   sequences to an aqueous medium containing at least one complex of anchor
CC   DNA, attached to a solid support, and reporter DNA, where either a part
CC   of the anchor DNA or reporter DNA is designed to form a triple-strand
CC   structure with part of the test sequence. Triplex formation results in
CC   displacement of the reporter DNA which is detected as an indication of
CC   the presence of the DNA test sequence. The method is used to detect DNA
CC   sequences, particularly for identification of bacteria (by detecting
CC   genes for ribosomal RNA) in clinical samples, but also detection of
CC   oncogenes and Hepatitis B virus
XX
SQ   Sequence 17 BP; 0 A; 5 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTT 2171
              |||||||||||| ||||
Db          1 TTTTTTCTCCTCTTTT 16


RESULT 3792
AAX14656/c
ID   AAX14656 standard; DNA; 17 BP.
XX
AC   AAX14656;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 12923-12939 of the dystrophin gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 15-16; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 17 BP; 12 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTT 2173
              |||||||| ||||||
Db         16 TTTTCTCCTCTTTTTT 1
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```
RESULT 3793
AAA25454
ID   AAA25454 standard; DNA; 17 BP.
XX
AC   AAA25454;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTTGTA 16
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RESULT 3794

```
AAC72830/c
ID   AAC72830 standard; DNA; 17 BP.
XX
AC   AAC72830;
XX
DT   09-FEB-2001  (first entry)
XX
DE   Single nucleotide polymorphism PCR primer #1773.
XX
KW   Single nucleotide polymorphism; SNP; human; genetic disease;
KW   disease susceptibility; cardiovascular system; endocrine system;
KW   neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058519-A2.
XX
PD   05-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-US008440.
XX
PR   31-MAR-1999;   99US-0127248P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Altshuler D,  Cargill M,  Daley GQ,  Ireland JS,  Lander ES;
PI   Lipshutz RJ,  Patil N,  Sklar P;
XX
DR   WPI; 2000-611722/58.
XX
PT   Nucleic acid selected from one of 106 genes comprising single nucleotide
PT   polymorphisms, allele-specific oligonucleotides to the genes are useful
PT   for phenotypic correlations, forensics, paternity testing, medicine and
PT   genetic analysis.
XX
PS   Claim 8; Fig 5; 214pp; English.
XX
CC   The present invention is concerned with a number of human single
CC   nucleotide polymorphisms (SNPs) which the inventors identified in human
CC   genes. These SNPs can be used in disease diagnosis and prediction of an
CC   individual's susceptibility to disease, in forensic and paternity testing
CC   and in genetic mapping. In particular, the SNPs of the invention can be
CC   used to diagnose susceptibility to diseases of the cardiovascular,
CC   endocrine and neurological systems, such as coronary artery disease,
CC   schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC   diseases
XX
SQ   Sequence 17 BP; 2 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        800 GAGCTGGTGGGGGCCG 815
              ||||||||||| ||||
Db         17 GAGCTGGTGGGAGCCG 2
```

```
RESULT 3795
AAF06381
ID   AAF06381 standard; DNA; 17 BP.
XX
AC   AAF06381;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #3178.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 42; Page 128; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 2 A; 0 C; 1 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   18.8%;  Pred. No. 2.6e+03;
  Matches    3;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2178 TTTTTTTTTAACTTTG 2193
              ::::::::::|| :::|
Db          1 UUUUUUUUUAAUUUUG 16


RESULT 3796
AAF02423
ID   AAF02423 standard; DNA; 17 BP.
XX
AC   AAF02423;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #718.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 37; Page 72; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 3 A; 0 C; 4 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2734 TAATTGTTGTGTGTAT 2749
              |||||||||| |||||
Db          2 TAATTGTTGTTTGTAT 17


RESULT 3797
AAF06380
ID   AAF06380 standard; DNA; 17 BP.
XX
AC   AAF06380;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #3177.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 42; Page 128; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   18.8%;  Pred. No. 2.6e+03;
  Matches    3;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       2178 TTTTTTTTTAACTTTG 2193
              ::::::::::|| :::|
Db          2 UUUUUUUUUAAUUUUG 17
```

RESULT 3798
AAF02617/c
ID AAF02617 standard; DNA; 17 BP.
XX
AC AAF02617;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #912.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 76; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 0 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1040 GGGAGGCGGAAAGCCG 1055
              |||||||||| |||||
Db         17 GGGAGGCGGACAGCCG 2
```

RESULT 3799
AAF06327/c
ID AAF06327 standard; DNA; 17 BP.
XX
AC AAF06327;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #3124.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 42; Page 127; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 7 A; 1 C; 2 G; 0 T; 7 U; 0 Other;

 Query Match 0.5%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.6e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1970 TTTACCTTGAAAAAAA 1985
              |||||||||||| ||||
Db         17 TTTACCTTGAATAAAA 2
```

RESULT 3800
ABK02790/c
ID ABK02790 standard; RNA; 17 BP.
XX
AC ABK02790;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CD20 Hammerhead ribozyme #89.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.

XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 30; Page 141; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^2^+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targetting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg^2^+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
XX
SQ Sequence 17 BP; 8 A; 1 C; 0 G; 0 T; 8 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2465 AATTTTAATATTAACT 2480
||||||||||||| |
Db 17 AATTTTAATATTAAGT 2

RESULT 3801
ABS76195
ID ABS76195 standard; DNA; 17 BP.
XX
AC ABS76195;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human PAPP-Eb associated 17-mer SEQ ID 1721.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-00827998.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Shannon ME;
XX
DR WPI; 2002-697817/75.
XX
PT New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX
PS Example 2; Page 301; 353pp; English.
XX
CC This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX
SQ Sequence 17 BP; 1 A; 3 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2315 ATTTGTTGCTGCTTGT 2330
| ||||||||||||||
Db 2 AGTTGTTGCTGCTTGT 17

RESULT 3802
ABS75130
ID ABS75130 standard; DNA; 17 BP.
XX
AC ABS75130;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 656.
XX
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-00827998.

```
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 161; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAG 466
              |||||| |||||||||
Db          1 CACAGGTAGCCAGCAG 16


RESULT 3803
ABS75129
ID   ABS75129 standard; DNA; 17 BP.
XX
AC   ABS75129;
XX
DT   24-DEC-2002  (first entry)
XX
DE   Human PAPP-Ea associated 17-mer SEQ ID 655.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 161; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 5 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        451 CACAGGCAGCCAGCAG 466
              |||||| |||||||||
Db          2 CACAGGTAGCCAGCAG 17


RESULT 3804
ABS76196
ID   ABS76196 standard; DNA; 17 BP.
XX
AC   ABS76196;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Eb associated 17-mer SEQ ID 1722.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 301; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
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```
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 6 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2315 ATTTGTTGCTGCTTGT 2330
              | ||||||||||||||
Db          1 AGTTGTTGCTGCTTGT 16


RESULT 3805
ACA99707
ID   ACA99707 standard; DNA; 17 BP.
XX
AC   ACA99707;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #200.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 224; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2110 CCTTCTGGTTTTAGGA 2125
              ||||||||| ||||||
Db          2 CCTTCTGGTCTTAGCA 17


RESULT 3806
ACA99708
ID   ACA99708 standard; DNA; 17 BP.
XX
AC   ACA99708;
XX
DT   28-JUL-2003  (first entry)
XX
DE   G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #201.
XX
KW   Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW   G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003031621-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032599.
XX
PR   12-OCT-2001; 2001US-0329000P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI   Zhang J;
XX
DR   WPI; 2003-381720/36.
XX
PT   New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT   investigating and/or treating disorders associated with aberrant
PT   expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS   Example 2; SEQ ID NO 225; 156pp; English.
XX
CC   The invention describes an isolated nucleic acid encoding a G protein
CC   coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC   2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC   409 residue amino acid sequence, all given in the specification, with or
CC   without conservative amino acid substitutions, or complements of the
CC   sequence of them. The encoding nucleic acid is not more than 100 kbase in
CC   length. The methods and compositions of the present invention are useful
CC   for diagnosing, investigating and/or treating disorders associated with
CC   aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC   This sequence represents an oligonucleotide used to analyse the gene
CC   encoding human G-protein coupled receptor GPCR-A-1
XX
SQ   Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2110 CCTTCTGGTTTTAGGA 2125
              ||||||||| ||||||
Db          1 CCTTCTGGTCTTAGGA 16


RESULT 3807
ABT35038/c
ID   ABT35038 standard; DNA; 17 BP.
XX
AC   ABT35038;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Tumour suppression related human fukutin oligo SEQ ID No 675.
XX
KW   Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW   antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW   schizophrenia; protein chip; gene therapy; tumour suppression;
KW   human fukutin; ds.
```

XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 113; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 9 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2263 CATATTTATTTCAGAT 2278
              ||| ||||||||||||
Db         17 CATTTTTATTTCAGAT 2
```

RESULT 3808
ADB04268
ID ADB04268 standard; DNA; 17 BP.
XX
AC ADB04268;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5254.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5254; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2163 TCCTTTTTTTTTTTTT 2178
              | ||||||||||||||
Db          2 TTCTTTTTTTTTTTTT 17
```

RESULT 3809
ADB04268/c
ID ADB04268 standard; DNA; 17 BP.
XX
AC ADB04268;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5254.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.

XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5254; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2801
||||||||||||| ||
Db 17 AAAAAAAAAAAAAGAA 2

RESULT 3810
ADB04274
ID ADB04274 standard; DNA; 17 BP.
XX
AC ADB04274;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5260.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5260; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTA 2187
||||||||||||||| |
Db 1 TTTTTTTTTTTTTTGA 16

RESULT 3811
ADB04274/c
ID ADB04274 standard; DNA; 17 BP.
XX
AC ADB04274;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5260.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5260; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is

```
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAA 2799
              | ||||||||||||||
Db         16 TCAAAAAAAAAAAAAA 1


RESULT 3812
ABZ65389
ID   ABZ65389 standard; RNA; 17 BP.
XX
AC   ABZ65389;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human HER2 DNAzyme substrate #846.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 4; Page 149; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 1 A; 8 C; 5 G; 0 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 2.6e+03;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGCC 618
              ||||||:||:| :|||
Db          2 CCGACCUGCUGGUGCC 17


RESULT 3813
ABZ61368
ID   ABZ61368 standard; RNA; 17 BP.
XX
AC   ABZ61368;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human H-Ras DNAzyme target #159.
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 114; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 0 A; 6 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         52 CGGCGGGGGCGGCGGC 67
              |||||| |||||||||
```

```
Db          1 CGGCGGCGGCGGCGGC 16


RESULT 3814
ACD58402/c
ID   ACD58402 standard; RNA; 17 BP.
XX
AC   ACD58402;
XX
DT   24-SEP-2003  (first entry)
XX
DE   HCV DNAzyme substrate sequence #820.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 248; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HCV
CC   DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC   invention
XX
SQ   Sequence 17 BP; 3 A; 5 C; 9 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 2.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1385 GCCGCGGTGTCTGCCC 1400
              ||||||||||||| |||
Db         16 GCCGCGGTGTCTCCCC 1


RESULT 3815
ACD64268
ID   ACD64268 standard; RNA; 17 BP.
XX
AC   ACD64268;
XX
DT   30-SEP-2003  (first entry)
XX
DE   HCV minus strand DNAzyme substrate sequence #1459.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Claim 1; Page 301; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
```

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 0 A; 9 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1385 GCCGCGGTGTCTGCCC 1400
||||||| :|:|: |||
Db 1 GCCGCGGUGUCUCCCC 16

RESULT 3816
ACC68555/c
ID ACC68555 standard; DNA; 17 BP.
XX
AC ACC68555;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour supression, SEQ ID 5802.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 709; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 2 A; 13 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 110 GGGGGCTGGGGGGATC 125
||||| ||||||||||
Db 16 GGGGGGTGGGGGGATC 1

RESULT 3817
ADB44223
ID ADB44223 standard; DNA; 17 BP.
XX
AC ADB44223;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #4546.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 563; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 7 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+03;

```
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||| ||||||||||||
Db          2 ATCTATTAAATACATT 17


RESULT 3818
AAQ67045
ID   AAQ67045 standard; DNA; 18 BP.
XX
AC   AAQ67045;
XX
DT   25-MAR-2003  (revised)
DT   14-FEB-1995  (first entry)
XX
DE   Polynucleotide directed against A raf gene consensus.
XX
KW   Raf gene; hybridisation; vascular smooth muscle cell; proliferation; SMC;
KW   vascular stenosis; post angioplasty restenosis; atherosclerosis;
KW   cardiac hypertrophy; organ transplant; ss.
XX
OS   Synthetic.
XX
PN   WO9415645-A1.
XX
PD   21-JUL-1994.
XX
PF   28-DEC-1993;   93WO-US012603.
XX
PR   31-DEC-1992;   92US-00999710.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Rege AA,  Dixon RAF;
XX
DR   WPI; 1994-248908/30.
XX
PT   Antisense polynucleotides to the raf gene - used for inhibiting vascular
PT   smooth muscle cell proliferation, partic. for treating restenosis.
XX
PS   Claim 4; Page 8; 40pp; English.
XX
CC   The sequence is an antisense molecule directed against a raf gene family
CC   consensus sequence. The polynucleotide can be used for inhibiting
CC   vascular smooth muscle cell proliferation and for treating a disease e.g.
CC   vascular stenosis, post angioplasty restenosis, atherectomy,
CC   atherosclerosis, atrial venous shunt failure, cardiac hypertrophy,
CC   vascular surgery and organ transplant. See also AAQ67034-47. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        508 GCCCTCGCACCACGGG 523
              |||||||||||||  ||
Db          1 GCCCTCGCACCACTGG 16


RESULT 3819
AAQ90172
ID   AAQ90172 standard; DNA; 18 BP.
XX
AC   AAQ90172;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   Pollen allergen gene probe 5.
XX
KW   Japanese cedar; pollen; allergen; allergy; therapy; diagnostic;
KW   desensitizer; Cryptomeria japonica; hybridization; probe; ss.
XX
OS   Synthetic.
XX
PN   EP655500-A1.
XX
PD   31-MAY-1995.
XX
PF   03-NOV-1994;   94EP-00308117.
XX
PR   05-NOV-1993;   93JP-00299151.
PR   20-DEC-1993;   93JP-00344596.
PR   27-DEC-1993;   93JP-00346814.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Namba M,  Torigoe K,  Kurimoto M;
XX
DR   WPI; 1995-195588/26.
XX
PT   New Japanese cedar pollen allergen polypeptide - and DNA coding for it,
PT   useful for treatment and diagnosis of cedar pollen allergy.
XX
PS   Disclosure; Page 11; 41pp; English.
XX
CC   The primers given in AAQ90166-69, based on a portion of cDNA clone SC09
CC   or on previously isolated sequences, were used for the PCR amplification
CC   of cDNA derived from Japanese cedar pollen, to obtain clone SC50 bearing
CC   a partial sequence (nt 1-198 of the sequence given in AAQ90156) of the
CC   pollen allergen gene. The product was was detected using the probe given
CC   in AAQ90172. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 18 BP; 7 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2303 AGGCACGAAGCAATTT 2318
              ||||| ||||||||||
Db          2 AGGCAGGAAGCAATTT 17


RESULT 3820
AAX32945
ID   AAX32945 standard; DNA; 18 BP.
XX
AC   AAX32945;
XX
DT   30-JUN-1999  (first entry)
XX
DE   Seq ID No: 12 of US5495009.
XX
KW   OCH2O linkage; analogue; 2,6-diethylpyridine; DEP; molecular sieve;
KW   tetrabutylammonium fluoride; TBAF; tetrahydrofuran; chemical synthesis;
KW   THF; thioformacetal linkage; diagnostic agent; ss.
XX
OS   Synthetic.
XX
PN   US5495009-A.
XX
PD   27-FEB-1996.
XX
PF   24-APR-1992;   92US-00874334.
XX
PR   24-OCT-1989;   89US-00426286.
PR   11-DEC-1989;   89US-00448941.
PR   30-JUL-1990;   90US-00559957.
PR   24-APR-1991;   91US-00690786.
XX
PA   (GILE-) GILEAD SCI INC.
XX
```

PI Lin K, Jones B, Matteucci M;
XX
DR WPI; 1996-178794/18.
XX
PT Prodn. of nucleoside dimers with methylenedioxy linkage - by reacting 5'-
PT protected nucleoside 3'-methylthio:methyl ether and 3'-protected
PT nucleoside with bromine.
XX
PS Example 2; Col 27; 27pp; English.
XX
CC The invention relates to a method for linking a first nucleoside or
CC oligonucleotide to a second nucleoside or nucleotide through an OCH2O
CC linkage, starting with a 5'-protected nucleoside or nucleotide which is
CC derivatised in the 3' position with an OCH2SMe group. The method
CC comprises (a) treating the derivatised nucleoside or nucleotide and a 3'-
CC protected nucleoside or nucleotide with bromine in the presence of 2,6-
CC diethylpyridine (DEP) and molecular sieves; and (b) treating the product
CC with tetrabutylammonium fluoride (TBAF) in tetrahydrofuran (THF). The
CC OCH2O-linked dimers can be used in the synthesis of oligonucleotide
CC analogues (containing thioformacetal linkages) e.g. useful as diagnostic
CC agents (see WO9106629)
XX
SQ Sequence 18 BP; 0 A; 4 C; 0 G; 13 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTT 2170
|||| ||||||||||||
Db 2 TTTCTTTCTCCTTTTT 17

RESULT 3821
AAX63290/c
ID AAX63290 standard; RNA; 18 BP.
XX
AC AAX63290;
XX
DT 16-JUL-1999 (first entry)
XX
DE Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1165.
XX
KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
OS Zea mays.
XX
PN WO9710328-A2.
XX
PD 20-MAR-1997.
XX
PF 12-JUL-1996; 96WO-US011689.
XX
PR 13-JUL-1995; 95US-0001135P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (DOWC) DOWELANCO.
XX
PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
PI Young SA, Folkerts O, Merlo DJ;
XX
DR WPI; 1997-202224/18.
XX
PT Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX
PS Claim 40; Page 93; 155pp; English.
XX
CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX
SQ Sequence 18 BP; 0 A; 12 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGGCGGCGG 66
||||||| ||||||||
Db 18 GCGGCGGCGGCGGCGG 3

RESULT 3822
AAZ48497/c
ID AAZ48497 standard; DNA; 18 BP.
XX
AC AAZ48497;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18890.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW inflammation; tumour formation; TNFR1; anticancer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-00106038.
XX
PR 26-JUN-1998; 98US-00106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM;
XX
DR WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors.
XX
PS Claim 1; Col 24; 34pp; English.
XX
CC The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic acid
CC molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. Sequences AAZ48482-565
CC represent antisense oligos used for inhibition of the human TNFR1 mRNA
XX
SQ Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;

```
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         605 GACCTGCTGCTGCCCC 620
               ||||||||||||||| |
Db          17 GACCTGCTGCTGCCGC 2


RESULT 3823
ABL57566
ID   ABL57566 standard; DNA; 18 BP.
XX
AC   ABL57566;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly w.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 7; Page 24; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the effects of
CC   the kind of bases in each target nucleic acid, and the kind of bases in
CC   its corresponding invention nucleic acid probe
XX
SQ   Sequence 18 BP; 0 A; 6 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        2162 CTCCTTTTTTTTTTTT 2177
               | ||||||||||||||
Db           3 CCCCTTTTTTTTTTTT 18


RESULT 3824
ABA82471/c
ID   ABA82471 standard; DNA; 18 BP.
XX
AC   ABA82471;
XX
DT   25-JAN-2002  (first entry)
XX
DE   Zmax1 gene region physical map preparation STS marker #430.
XX
KW   Human; high bone mass; HBM gene; Zmax1 gene; chromosome 11; 11q13.3;
KW   sequence tagged site; STS; osteoporosis; osteopathic; gene therapy;
KW   antisense therapy; vaccine; bone disorder; Paget's disease; adapter;
KW   sclerostosis; osteomalacia; fibrous dysplasia; PCR primer; linker; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177327-A1.
XX
PD   18-OCT-2001.
XX
PF   21-JUN-2000; 2000WO-US016951.
XX
PR   05-APR-2000; 2000US-00543771.
PR   05-APR-2000; 2000US-00544398.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Carulli JP,  Little RD,  Recker RR,  Johnson ML;
XX
DR   WPI; 2001-657171/75.
XX
PT   New high bone mass (HBM) and Zmax1 genes and proteins useful for
PT   modulating bone mass for the treatment of e.g. osteoporosis.
XX
PS   Disclosure; Page 36; 443pp; English.
XX
CC   The present invention describes the human Zmax1 gene and the high bone
CC   mass (HBM) gene,which are found on chromosome 11q13.3. The Zmax1 and HBM
CC   genes have osteopathic activities. The genes can be used in gene therapy,
CC   antisense therapy and in the production of vaccines. They can be used in
CC   the diagnosis and treatment of bone disorders including osteoporosis,
CC   Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
CC   ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
CC   the exemplification of the present invention
XX
SQ   Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        2210 ATGGGAGACTCTTTGA 2225
               ||||||||| ||||||
Db          16 ATGGGAGACGCTTTGA 1


RESULT 3825
ABT04993/c
ID   ABT04993 standard; DNA; 18 BP.
XX
AC   ABT04993;
XX
DT   11-OCT-2002  (first entry)
XX
DE   TNFR1 expression modulation related antisense oligo SEQ ID No 23.
```

XX
KW Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW human; ds.
XX
OS Homo sapiens.
XX
PN WO200248168-A1.
XX
PD 20-JUN-2002.
XX
PF 22-OCT-2001; 2001WO-US051224.
XX
PR 24-OCT-2000; 2000US-00695451.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Cowsert LM, Zhang H, Dean NM;
XX
DR WPI; 2002-583481/62.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
PS Example 10; Page 44; 121pp; English.
XX
CC The invention relates to an antisense compound 8 to 30 nucleotides in
CC length targeted to nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC TNFR1. The antisense compound is useful for inhibiting the expression of
CC TNFR1 in cells or tissues. The antisense compound is also useful for
CC treating an animal (preferably human) having a disease or condition
CC associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC the expression of TNFR1. The antisense compound is useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC This polynucleotide sequence represents a human oligonucleotide relating
CC to the TNFR1 of the invention
XX
SQ Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 605 GACCTGCTGCTGCCCC 620
||||||||||||||| |
Db 17 GACCTGCTGCTGCCGC 2

RESULT 3826
AAD40585/c
ID AAD40585 standard; DNA; 18 BP.
XX
AC AAD40585;
XX
DT 30-OCT-2002 (first entry)
XX
DE HIV-1 LTR luciferase reporter gene mutant fragment, A3.
XX
KW Human immunodeficiency virus; HIV; infection; transcriptional repressor;
KW OTK18; brain; polymorphonuclear blood mononucleocyte; neuronal injury;
KW CD4+ T cell; antiretroviral; mononuclear phagocyte; MP; macrophage;
KW gene therapy; anti-HIV; mutant; ds.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
PN WO200235981-A2.
XX
PD 10-MAY-2002.
XX
PF 06-NOV-2001; 2001WO-US044336.
XX
PR 06-NOV-2000; 2000US-0246331P.
PR 06-APR-2001; 2001US-00828648.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Ikezu T, Leisman G, Carlson KA, Gendelman HE;
XX
DR WPI; 2002-519218/55.
XX
PT New truncated OTK18 transcriptional repressor protein, useful for
PT treating human immunodeficiency virus infection and for identifying OTK18
PT expression in a biological sample.
XX
PS Example 2; Fig 11A; 96pp; English.
XX
CC The invention relates to methods and compositions for the treatment of
CC human immunodeficiency virus (HIV) infection. The invention also relates
CC to OTK18 transcriptional repressor protein and its corresponding nucleic
CC acid. An antibody to OTK18 is useful for identifying OTK18 expression in
CC a biological sample (e.g. polymorphonuclear blood mononucleocytes, brain
CC tissue, macrophages and CD4+ T cells). OTK18 is used for treating HIV
CC infection. It is useful for screening molecules that modulate or affect
CC its activity. Its antibody is useful for identifying multinuclear giant
CC cells in HIV encephalitic brains or immune activated mononuclear
CC phagocytes (MP) in the brains, for fluorescent activated cell sorting
CC (FACS) analysis of peripheral blood cells to evaluate the antiretroviral
CC reaction of MP and for immunoprecipitating proteins from a sample
CC containing a mixture of proteins and other biological molecules. OTK18
CC molecules are useful in the treatment and diagnosis of HIV infection, as
CC research tools to identify the control of gene expression in response to
CC HIV infection and subsequent neuronal injury. OTK18 DNA is useful in gene
CC therapy. The present sequence is HIV-1 LTR luciferase reporter gene
CC derived mutant DNA fragment used to illustrate the method of the
CC invention
XX
SQ Sequence 18 BP; 3 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1899 TAGATCAACAGATCAA 1914
|||||| |||||||||
Db 18 TAGATCCACAGATCAA 3

RESULT 3827
ABA97651
ID ABA97651 standard; DNA; 18 BP.
XX
AC ABA97651;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly w nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX

PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 7; Page 19; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 18 BP; 0 A; 6 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2162 CTCCTTTTTTTTTTT 2177
| ||||||||||||||
Db 3 CCCCTTTTTTTTTTT 18

RESULT 3828
ABK23268/c
ID ABK23268 standard; DNA; 18 BP.
XX
AC ABK23268;
XX
DT 09-APR-2002 (first entry)
XX
DE Human Zmax1 cDNA reverse PCR primer #215.
XX
KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
KW bone development disorder; antiarteriosclerotic; cardiovascular;
KW osteopathic; cerebroprotective.
XX
OS Homo sapiens.
XX
PN WO200192891-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016946.
XX
PR 26-MAY-2000; 2000US-00578900.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
XX
PI Carulli JP, Little RD, Recker RR, Johnson ML;
XX
DR WPI; 2002-097784/13.
XX
PT Identifying molecules involved in lipid regulation, useful for
PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
PT identifying a molecule that binds to high bone mass gene or its
PT corresponding wild type gene.
XX
PS Disclosure; Page 41; 409pp; English.
XX
CC The invention relates to a method for identifying a molecule involved in
CC lipid regulation comprising identifying a molecule that binds to or
CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
CC gene, Zmax1. Compounds identified by the method are useful for treating,
CC diagnosing, preventing or screening for normal and abnormal lipid-
CC associated conditions, including arteriosclerosis, cardiovascular
CC disease, stroke, and osteoporosis. The compounds may also be used in the
CC treatment or prevention of diabetic atherosclerosis, neurovascular
CC conditions caused by plaque build-up, poor circulation due to plaque
CC build-up and associated poor wound healing. The methods may be used in
CC gene therapy, pharmaceutical development, and diagnostic assays for bone
CC development disorders. Molecules identified by comparison of Zmax1 and
CC HBM systems can be used as surrogate markers in pharmaceutical
CC development, in diagnosis of human or animal bone disease, and in the
CC treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
CC and adapters of the invention
XX
SQ Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2210 ATGGGAGACTCTTTGA 2225
||||||||| ||||||
Db 16 ATGGGAGACGCTTTGA 1

RESULT 3829
ABL95913
ID ABL95913 standard; DNA; 18 BP.
XX
AC ABL95913;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly w for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 14; Page 64; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis

```
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 18 BP; 0 A; 6 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2177
              | ||||||||||||||
Db          3 CCCCTTTTTTTTTTT 18


RESULT 3830
ACA60581/c
ID   ACA60581 standard; DNA; 18 BP.
XX
AC   ACA60581;
XX
DT   11-JUN-2003  (first entry)
XX
DE   Antisense inhibition of human cyclin D2 related oligonucleotide #18.
XX
KW   Human; cyclin D2; diagnostic; therapeutic; prophylaxis;
KW   cyclin 2 inhibition; ss.
XX
OS   Homo sapiens.
XX
PN   US6492173-B1.
XX
PD   10-DEC-2002.
XX
PF   01-AUG-2001; 2001US-00920760.
XX
PR   01-AUG-2001; 2001US-00920760.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2003-361492/34.
XX
PT   Novel antisense compound useful for treating diseases associated with
PT   Cyclin D2 expression, comprises an oligonucleotide comprising up to 50
PT   nucleobases in length, which inhibits expression of Cyclin D2 in cells or
PT   tissues in vitro.
XX
PS   Claim 1; Col 45-46; 40pp; English.
XX
CC   The invention describes a compound (I) of up to 50 nucleobases in length,
CC   which inhibits the expression of Cyclin D2. (I) is useful for inhibiting
CC   the expression of Cyclin D2 in cells or tissues in vitro. (I) is thus
CC   useful for treating disease associated with Cyclin D2 expression. (I) is
CC   useful for diagnostics, therapeutics, prophylaxis and as research
CC   reagents and kits. This sequence represents human cyclin D2 inhibition
CC   associated oligonucleotide
XX
SQ   Sequence 18 BP; 0 A; 11 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        491 CAGGAGGGAGCGGGGC 506
              |||||||||| |||||
Db         17 CAGGAGGGAGAGGGGC 2


RESULT 3831
ACF62964
ID   ACF62964 standard; DNA; 18 BP.
XX
AC   ACF62964;
XX
DT   09-OCT-2003  (first entry)
XX
DE   Human p16 PCR primer SEQ ID NO:213.
XX
KW   Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
KW   progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
KW   characterisation; classification; diagnosis; differentiation;
KW   colon cell proliferative disorder; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003014388-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-EP008939.
XX
PR   09-AUG-2001; 2001DE-01039283.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Distler J,  Model F,  Taubert H;
XX
DR   WPI; 2003-256600/25.
XX
PT   Determining methylation status of CpG dinucleotides using modified
PT   genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
PT   characterization, grading, staging and/or diagnosis of colon cancer.
XX
PS   Claim 26; Page 159; 219pp; English.
XX
CC   The present invention describes a method for determining the methylation
CC   status of CpG dinucleotides within the genes for oestrogen receptor, p21,
CC   p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erB2, p53
CC   and/or CEA, which comprises contacting the target nucleic acid with a
CC   reagent that distinguishes between methylated and non-methylated CpG
CC   dinucleotides, and determining from the methylation status of the CpG
CC   positions the presence of a colon cancer. A set of oligomers or peptide
CC   nucleic acid (PNA)-oligomers can be used as probes for determining the
CC   cytosine methylation state and/or single nucleotide polymorphisms (SNP)
CC   of a corresponding genomic DNA by analysis of a chemically pretreated
CC   genomic DNA. The pretreated genomic DNA is useful for the determination
CC   of the methylation status of a corresponding genomic DNA and/or detection
CC   of SNPs. The methods and pretreated genomic DNA are also useful for the
CC   characterisation, classification, diagnosis and differentiation of colon
CC   cell proliferative disorders. ACF62752 to ACF63278 represent sequences
CC   used in the exemplification of the present invention
XX
SQ   Sequence 18 BP; 6 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 18;
  Best Local Similarity   93.8%;  Pred. No. 2.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1832 TTTAAATACATTCCCT 1847
              |||||||||||||| ||
Db          1 TTTAAATACATTCACT 16


RESULT 3832
ACF62962/c
ID   ACF62962 standard; DNA; 18 BP.
XX
AC   ACF62962;
XX
DT   09-OCT-2003  (first entry)
XX
DE   Human p16 PCR primer SEQ ID NO:211.
XX
KW   Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
```

KW progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
KW characterisation; classification; diagnosis; differentiation;
KW colon cell proliferative disorder; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003014388-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-EP008939.
XX
PR 09-AUG-2001; 2001DE-01039283.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Distler J, Model F, Taubert H;
XX
DR WPI; 2003-256600/25.
XX
PT Determining methylation status of CpG dinucleotides using modified
PT genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
PT characterization, grading, staging and/or diagnosis of colon cancer.
XX
PS Claim 26; Page 158; 219pp; English.
XX
CC The present invention describes a method for determining the methylation
CC status of CpG dinucleotides within the genes for oestrogen receptor, p21,
CC p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erB2, p53
CC and/or CEA, which comprises contacting the target nucleic acid with a
CC reagent that distinguishes between methylated and non-methylated CpG
CC dinucleotides, and determining from the methylation status of the CpG
CC positions the presence of a colon cancer. A set of oligomers or peptide
CC nucleic acid (PNA)-oligomers can be used as probes for determining the
CC cytosine methylation state and/or single nucleotide polymorphisms (SNP)
CC of a corresponding genomic DNA by analysis of a chemically pretreated
CC genomic DNA. The pretreated genomic DNA is useful for the determination
CC of the methylation status of a corresponding genomic DNA and/or detection
CC of SNPs. The methods and pretreated genomic DNA are also useful for the
CC characterisation, classification, diagnosis and differentiation of colon
CC cell proliferative disorders. ACF62752 to ACF63278 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 BP; 8 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1832 TTTAAATACATTCCCT 1847
||||||||||||| ||
Db 18 TTTAAATACATTCACT 3

RESULT 3833
ABZ10570/c
ID ABZ10570 standard; DNA; 18 BP.
XX
AC ABZ10570;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related oligonucleotide #710.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; probe; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 15; Page 50; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 18 BP; 8 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1832 TTTAAATACATTCCCT 1847
||||||||||||| ||
Db 18 TTTAAATACATTCACT 3

RESULT 3834
ACC45851/c
ID ACC45851 standard; DNA; 18 BP.
XX
AC ACC45851;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human HBM STS marker reverse primer #215.
XX
KW Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
KW gene therapy; bone density modulation; bone strength; trabecular number;
KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.
XX
OS Homo sapiens.
XX

PN WO200292764-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014876.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Babij P, Bex FJ, Yaworsky PJ, Bodine PV;
XX
DR WPI; 2003-129278/12.
XX
PT New transgenic animals (e.g. mice), useful as models for studying bone
PT density modulation, developing drugs for treating or preventing bone
PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by
PT reduced bone density.
XX
PS Disclosure; Page 57; 603pp; English.
XX
CC The invention relates to novel transgenic animals expressing the high
CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,
CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing
CC an LRP5 that is modulated by an altered gene control sequence introduced
CC by homologous or non-homologous recombination. The transgenic animals are
CC for the study of bone density modulation or bone mass modulation. The
CC invention has osteopathic and cytostatic activity. The polynucleotides of
CC the invention may have a use in gene therapy. The transgenic animals and
CC nucleic acids are for the study of bone density modulation, where the
CC bone mass is modulated relative to non-transgenic animals of the same
CC species in more than one parameter selected from bone density, bone
CC strength, trabecular number, bone size, or bone tissue connectivity. The
CC transgenic animals, nucleic acids and methods are useful for identifying
CC molecules involved in bone development, and for developing pharmaceutical
CC compositions, which may be employed for treating or preventing bone
CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
CC neoplasms of the bone. The transgenic animals and nucleic acids are also
CC useful in methods for diagnosing diseases involved in bone development,
CC or characterised by reduced bone density or mass. The present sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2210 ATGGGAGACTCTTTGA 2225
||||||||| ||||||
Db 16 ATGGGAGACGCTTTGA 1

RESULT 3835
ADB98549/c
ID ADB98549 standard; DNA; 18 BP.
XX
AC ADB98549;
XX
DT 04-DEC-2003 (first entry)
XX
DE Sequence tagged site #430 used to prepare Zmax1 (LRP5) gene region map.
XX
KW Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.
XX
OS Homo sapiens.
XX
PN WO200292000-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US014877.
XX
PR 11-MAY-2001; 2001US-0290071P.
PR 17-MAY-2001; 2001US-0291311P.
PR 01-FEB-2002; 2002US-0353058P.
PR 04-MAR-2002; 2002US-0361293P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
XX
PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
XX
DR WPI; 2003-129214/12.
XX
PT New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
PT diagnosing a HBM-like phenotype in a subject and for preparing a
PT composition for modulating bone mass and/or lipid levels in a subject
PT suffering from e.g. osteoporosis.
XX
PS Example 2; Page 64; 629pp; English.
XX
CC The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
CC level modulation. The invention is useful for diagnosing a HBM-like
CC phenotype in a subject and for preparing a composition for modulating
CC bone mass and/or lipid levels in a subject suffering from e.g.
CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)
CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
CC region.
XX
SQ Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2210 ATGGGAGACTCTTTGA 2225
||||||||| ||||||
Db 16 ATGGGAGACGCTTTGA 1

RESULT 3836
ADB54572/c
ID ADB54572 standard; DNA; 18 BP.
XX
AC ADB54572;
XX
DT 04-DEC-2003 (first entry)
XX
DE Hybridisation oligonucleotide 110 used to analyse genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
KW probe.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP002035.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;

XX
DR WPI; 2003-731620/69.
XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
PS Claim 36; Page 32; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the hybridisation
CC oligonucleotide of the invention which was used to analyse the genomic
CC DNA region.
XX
SQ Sequence 18 BP; 8 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1832 TTTAAATACATTCCCT 1847
||||||||||||| ||
Db 18 TTTAAATACATTCACT 3

RESULT 3837
ADC70087/c
ID ADC70087 standard; DNA; 18 BP.
XX
AC ADC70087;
XX
DT 18-DEC-2003 (first entry)
XX
DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 577).
XX
KW PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
KW adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
KW cytosine methylation state.
XX
OS Unidentified.
XX
PN WO2003052135-A2.
XX
PD 26-JUN-2003.
XX
PF 10-DEC-2002; 2002WO-EP014026.
XX
PR 14-DEC-2001; 2001DE-01061625.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;
PI Nimmrich I;
XX
DR WPI; 2003-533029/50.
XX
PT Detecting and differentiating cytosine methylation state of genomic DNA,
PT useful for diagnosing, treating prognosticating and/or monitoring lung
PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
PT carcinoma.
XX
PS Claim 15; SEQ ID NO 577; 58pp; English.
XX
CC This invention relates to a novel method for detecting and
CC differentiating between lung cell proliferative disorders associated with
CC at least one gene and/or their regulatory regions. Specifically, it
CC refers to a method comprising contacting a target nucleic acid in a
CC biological sample with at least one reagent, wherein the reagent is able
CC to distinguish between methylated and non-methylated CpG dinucleotides
CC present in the target DNA. As such, it is possible to further
CC differentiate and diagnose medical conditions including adenocarcinoma
CC and squamous cell carcinoma, and their respective adjacent lung tissue.
CC The present invention describes cytostatic oligomers and PNA-oligomers
CC that are useful as probes for determining the cytosine methylation state
CC or single nucleotide polymorphisms (SNPs) of the target sequence. This
CC oligonucleotide sequence is a primer oligomer used for the analysis of
CC CpG positions within genomic DNA, used in an exemplification of the
CC invention.
XX
SQ Sequence 18 BP; 8 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1832 TTTAAATACATTCCCT 1847
||||||||||||| ||
Db 18 TTTAAATACATTCACT 3

RESULT 3838
AAQ79881/c
ID AAQ79881 standard; cDNA; 19 BP.
XX
AC AAQ79881;
XX
DT 25-MAR-2003 (revised)
DT 17-JUL-1995 (first entry)
XX
DE Adrenodoxin-reductase primer 6.
XX
KW P450scc; P450 side chain cleavage enzyme; fusion enzyme;
KW electron-transfer protein; transgenic animal; cholesterol;
KW atherosclerosis; adrenodoxin-reductase; AdRed; adrenodoxin; Adx;
KW polymerase chain reaction; PCR; amplification; primer; ss.
XX
OS Synthetic.
XX
PN WO9429434-A1.
XX
PD 22-DEC-1994.
XX
PF 09-JUN-1994; 94WO-US006698.
XX
PR 09-JUN-1993; 93US-00075193.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Miller WL, Harikrishna JA, Black SM;
XX
DR WPI; 1995-036464/05.
XX
PT Fusion enzyme comprising P450scc and an electron-transfer protein - used
PT in the production of transgenic livestock with reduced cholesterol meat.
XX
PS Example 1; Page 37; 91pp; English.
XX
CC The primers given in AAQ79878-85 were used to engineer human cDNAs for
CC P450scc, adrenodoxin-reductase (AdRed) and adrenodin (Adx) for the
CC construction of P450scc-AdRed, P450scc-Adx-AdRed and P450scc-AdRed-Adx
CC fusion enzymes capable of cholesterol disposal. AdRed cDNA is amplified
CC using primers 5-8 (AAQ79880-83, respectively). (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

```
SQ   Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        691 CGAGGTGCAGAATGTC 706
              ||||||| ||||||||
Db         17 CGAGGTGAAGAATGTC 2


RESULT 3839
AAV44620
ID   AAV44620 standard; DNA; 19 BP.
XX
AC   AAV44620;
XX
DT   24-NOV-1998  (first entry)
XX
DE   Human uncoupling protein-2 UCP2 gene primer hUCP2.CDSR1.
XX
KW   Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
KW   obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
KW   hypothermia; wasting; cachexia; anorexia; inflammation; fever;
KW   hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9831396-A1.
XX
PD   23-JUL-1998.
XX
PF   22-APR-1997;   97WO-US006864.
XX
PR   15-JAN-1997;   97US-0034960P.
XX
PA   (UYDU-) UNIV DUKE.
PA   (REGC ) UNIV CALIFORNIA.
PA   (CNRS ) CENT NAT RECH SCI.
XX
PI   Surwit RS,  Collins SA,  Warden CH,  Seldin MF,  Ricquier D;
PI   Bouillaud F;
XX
DR   WPI; 1998-413823/35.
XX
PT   Method for treating disease associated with altered UCP-2 expression - by
PT   administering agent which enhances or inhibits UCP-2 activity,
PT   effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT   etc.
XX
PS   Disclosure; Fig 1F; 98pp; English.
XX
CC   Primer hUCP2.CDSR1 is used with forward primer hUCP2.CDSF1 (see AAV44619)
CC   in the PCR amplification of a 1098 bp region of the human uncoupling
CC   protein-2 (UCP2) gene coding sequence (see also AAV44595). The invention
CC   relates to a method for treating diseases associated with altered UCP2
CC   expression, such as obesity, diabetes, syndrome X, hypothermia,
CC   hyperinsulinaemia, glucose intolerance, wasting, anorexia, inflammation,
CC   cachexia, fever or hyperthermia
XX
SQ   Sequence 19 BP; 7 A; 0 C; 12 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1541 GGAGAGTAGGGAAGGA 1556
              |||||| |||||||||
Db          1 GGAGAGAAGGGAAGGA 16


RESULT 3840
AAX79665/c
ID   AAX79665 standard; DNA; 19 BP.
XX
AC   AAX79665;
XX
DT   12-AUG-1999  (first entry)
XX
DE   Human LKB1 gene primer/probe.
XX
KW   LKB1 gene; human; serine protease; Peutz-Jeghers syndrome; PJ syndrome;
KW   variation detection; therapy; diagnosis; primer; probe; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9928459-A1.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-JP005357.
XX
PR   27-NOV-1997;   97JP-00344256.
PR   01-OCT-1998;   98JP-00280357.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Jenne DE,  Nezu J;
XX
DR   WPI; 1999-358129/30.
XX
PT   Primers and probes for use in diagnosis of Peutz-Jeghers syndrome.
XX
PS   Claim 2; Page 94; 107pp; Japanese.
XX
CC   This sequence represents a primer/probe sequence of the invention. The
CC   primer and probe sequences are derived from the sequence of the human
CC   serine protease gene LKB1, and are used to detect variations in LKB1
CC   leading to Peutz-Jeghers (PJ) syndrome. The primers and probes can be
CC   used for the diagnosis, investigation and treatment of diseases in which
CC   variations in the LKB1 gene are implicated, such as PJ syndrome
XX
SQ   Sequence 19 BP; 3 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        247 GCGGGTCCCCCACCTC 262
              |||||||| |||||||
Db         19 GCGGGTCCACCACCTC 4


RESULT 3841
AAZ57803
ID   AAZ57803 standard; DNA; 19 BP.
XX
AC   AAZ57803;
XX
DT   11-APR-2000  (first entry)
XX
DE   HSV-2 ICP4 gene forward PCR primer.
XX
KW   Fine array transcript mapping; FAT mapping; FATMap; HSV-2;
KW   differential expression; ICP4; PCR primer; ss.
XX
OS   Herpes simplex virus 2.
XX
PN   WO9967422-A1.
XX
PD   29-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013813.
XX
```

```
PR   24-JUN-1998;   98US-0090464P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Leary JJ,  Tal-Singer R;
XX
DR   WPI; 2000-147217/13.
XX
PT   Novel analytical method designated Fine Array Transcript Mapping, useful
PT   for detecting and measuring RNA molecules transcribed from a genome,
PT   differential expression, and sequence mapping.
XX
PS   Example 1; Page 16; 53pp; English.
XX
CC   This sequence represents a forward PCR primer targeted at the ICP4 gene
CC   of herpes simplex virus type 2 (HSV-2) SB5 (ATCC VR 2546). It was used
CC   for semi-quantitative PCR analysis of SB5 cDNA. PCR using the ICP4 primer
CC   pair generated a 111 bp product, and allowed detection of 1 HSV copy from
CC   45 cycles (or 1000 copies from 35 cycles). The invention provides a novel
CC   genetic analysis method termed Fine Array Transcript Mapping (FAT
CC   Mapping) for detecting and measuring RNA molecules transcribed from a
CC   genome, differential expression, and mapping of the 5' sequence of a
CC   transcript. FAT mapping involves probing a test grid containing an array
CC   of 100s to 1000s of overlapping genomic clones or DNA fragments with
CC   probes consisting of labeled cDNAs representing the RNA transcripts from
CC   test populations. The system allows quantitative measurements of the
CC   expression of rare transcripts, and enables the analysis of 100s of genes
CC   within a genomic sequence in a single run. The method can be used to
CC   measure the differential expression of transcripts between 2 or more
CC   different viral, tissue or cell populations which share a common genomic
CC   sequence, or to determine whether a particular open reading frame is
CC   expressed under certain conditions. The FATMap technique has been applied
CC   to the HSV-2 genome
XX
SQ   Sequence 19 BP; 3 A; 8 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        268 CGCCGGGCAGCACCTC 283
              || ||||||||||||||
Db          4 CGGCGGGCAGCACCTC 19


RESULT 3842
AAA27545/c
ID   AAA27545 standard; DNA; 19 BP.
XX
AC   AAA27545;
XX
DT   15-AUG-2000  (first entry)
XX
DE   Fas ligand promoter PCR primer -340.
XX
KW   Fas ligand; promoter; polymorphism; systemic lupus erythematosus;
KW   rheumatoid arthritis; autoimmune disease; cancer; diagnosis; haplotyping;
KW   C/EBP-beta; human; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200023623-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-US024148.
XX
PR   16-OCT-1998;   98US-0104644P.
PR   17-JUN-1999;   99US-0139659P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Kimberly RP;
XX
DR   WPI; 2000-339717/29.
XX
PT   Determining autoimmune disease or cancer susceptibility especially useful
PT   for promoting early therapeutic intervention and for gene therapy
PT   comprises haplotyping an individual in a Fas promoter and Fas ligand
PT   promoter region.
XX
PS   Disclosure; Fig 10; 106pp; English.
XX
CC   The present sequence is that of a primer based on the nucleotide -340
CC   region of the Fas ligand promoter. It was used in the PCR amplification
CC   and sequencing of Fas ligand promoter sequences using genomic DNA from
CC   systemic lupus erythematosus (SLE) and healthy donors. Single nucleotide
CC   polymorphisms in the Fas ligand promoter are associated with SLE (see
CC   also AAA27529-40)
XX
SQ   Sequence 19 BP; 5 A; 0 C; 13 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        344 TTTCCCCCTCCCTACC 359
              | ||||||||||||||
Db         17 TCTCCCCCTCCCTACC 2


RESULT 3843
ADC65121/c
ID   ADC65121 standard; DNA; 19 BP.
XX
AC   ADC65121;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Methylobacillus epsA-related PCR primer #2.
XX
KW   Saccharide; epsA; epsB; epsC; PCR; primer; ss.
XX
OS   Methylobacillus sp.
XX
PN   JP2003159073-A.
XX
PD   03-JUN-2003.
XX
PF   26-NOV-2001; 2001JP-00359154.
XX
PR   26-NOV-2001; 2001JP-00359154.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
DR   WPI; 2003-818679/77.
XX
PT   Novel saccharide producing DNA which encodes a protein, useful for
PT   improving saccharide production.
XX
PS   Example 4; SEQ ID NO 11; 15pp; Japanese.
XX
CC   The present invention relates to proteins involved in saccharide
CC   production and their coding sequences (ADC65111-ADC65116) from
CC   Methylobacillus bacteria. The sequences are useful for overproducing or
CC   suppressing saccharide production. A DNA fragment of 4-8kb was obtained
CC   from the genome library of wild-strain 12S of Methylobacillus and was
CC   cloned in a plasmid pUC19. Transposon Tn5 inserted in the Ma1 strain of
CC   Methylobacillus bacteria was determined using the DNA fragment of pTMS3
CC   as probe. Colonies which hybridized to the genome library were assumed as
CC   positive clones and were named as pUMS1-X. The base sequence of the
CC   inserted DNA fragments were determined and it was found that all three
CC   open reading frames (orf) existed in the same direction and were named as
CC   orf1 (epsA; ADC65111), orf2 (epsB; ADC65113) and orf3 (epsC; ADC65115)
CC   respectively. The DNA fragment containing orf1 (epsA) was amplified by
CC   PCR using pUMS1 as template and primers ADC65120 and ADC65121. The
```

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CC   amplified DNA fragments were introduced into two plasmid vectors namely
CC   pT7 Blue (R) vector and an extensive host- range vector pBBR122 to obtain
CC   pTepsA and PBBA. The transformed vectors were introduced into 12S strain
CC   of Methylobacillus bacteria. Bacteria were inoculated into a culture
CC   medium containing methanol as the sole source of carbon, and cultured at
CC   30 degrees C for seven days. Supernatant liquid of the culture medium was
CC   obtained and the amount of saccharide produced in the culture medium was
CC   determined by phenol sulfuric acid method. It was found that the 12S
CC   strain of Methylobacillus produced different kinds of saccharides. The
CC   yield was 1.4 times greater than the wild-strain. From this observation,
CC   it was found that orf1 epsA gene was useful in improving saccharide
CC   synthesis. The present sequence is a PCR primer, which was used in an
CC   example from the invention.
XX
SQ   Sequence 19 BP; 3 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 3.3e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        324 AATATCAGCCGCCACC 339
              ||||| ||||||||||
Db         18 AATATTAGCCGCCACC 3


RESULT 3844
AAL62328
ID   AAL62328 standard; DNA; 20 BP.
XX
AC   AAL62328;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128182.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 2 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2185 TTAACTTTGAAAGTTA 2200
              |||||||| |||||||
Db          5 TTAACTTTCAAAGTTA 20


RESULT 3845
AAV22586/c
ID   AAV22586 standard; DNA; 20 BP.
XX
AC   AAV22586;
XX
DT   08-JUL-1998  (first entry)
XX
DE   Antisense oligonucleotide designed to target the R1 message.
XX
KW   R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;
KW   antisense; growth; inhibition; sensitivity; hydroxyurea;
KW   chemotherapeutic drug; methotrexate; PALA; treatment; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9805769-A2.
XX
PD   12-FEB-1998.
XX
PF   01-AUG-1997;   97WO-CA000540.
XX
PR   02-AUG-1996;   96US-0023040P.
PR   07-MAR-1997;   97US-0039959P.
XX
PA   (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI   Wright JA,  Young AH;
XX
DR   WPI; 1998-145609/13.
XX
PT   Antisense oligonucleotides to ribonucleotide reductase genes - used to
PT   modulate tumour growth and inhibit tumour cell proliferation.
XX
PS   Claim 8; Page 49; 79pp; English.
XX
CC   AAV22531-89 represent antisense oligonucleotides which are targeted
CC   against the mRNA of the R1 subunit sequence of ribonucleotide reductase.
CC   Aberrant expression of the R2 gene, which encodes the second subunit of
CC   the ribonucleotide reductase gene, can determine the malignant
CC   characteristics of cells. Suppression of R2 and R1 gene expression was
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CC   found to reduce transformed properties of tumour cells. The antisense
CC   oligonucleotides can be used for modulating tumour cell growth, or for
CC   inhibiting tumour cell proliferation. They can also be used for
CC   increasing the sensitivity of neoplastic cells to chemotherapeutic drugs
CC   (especially to hydroxyurea, methotrexate (MTX), and PALA). The antisense
CC   oligonucleotides may be used to treat proliferative disorders including
CC   leukaemias, lymphomas, sarcomas, melanomas, various other forms of
CC   cancer, papillomas, arthrosclerosis, psoriasis, polythemia, mastocytosis,
CC   autoimmune diseases, angiogenesis, bacterial infections and viral
CC   infections (including HIV hepatitis, or herpes infections)
XX
SQ   Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||||| ||||||||||
Db         20 AAAAAGAAAAAAAAAA 5


RESULT 3846
AAA90815/c
ID   AAA90815 standard; DNA; 20 BP.
XX
AC   AAA90815;
XX
DT   20-DEC-2000  (first entry)
XX
DE   Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.
XX
KW   Antisense oligonucleotide; ribonucleotide reductase; R1 protein;
KW   R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200047733-A1.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-CA000120.
XX
PR   11-FEB-1999;   99US-00249730.
XX
PA   (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI   Wright JA,  Young AH;
XX
DR   WPI; 2000-558216/51.
XX
PT   New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
PT   tumor cell growth.
XX
PS   Example 3; Page 32; 137pp; English.
XX
CC   The present sequence is an antisense oligonucleotide directed against the
CC   mRNA encoding the R1 component of mammalian ribonucleotide reductase.
CC   Ribonucleotide reductase catalyses the conversion of ribonucleotides to
CC   their corresponding deoxyribonucleotides and thus plays an important role
CC   in DNA synthesis and cell proliferation. Regulation of ribonucleotide
CC   reductase is altered in cultured malignant cells and increased levels of
CC   R2 protein and R2 mRNA have been found in pre-malignant and malignant
CC   tissues as compared to normal control tissue samples. The present
CC   antisense sequence is therefore useful for inhibiting tumourigenicity of
CC   neoplastic cells and inhibiting metastasis of tumour cells. It is also
CC   useful for increasing sensitivity of neoplastic cells to chemotherapeutic
CC   drugs, thus allowing chemotherapeutic treatments to be used in patients
CC   who have become resistant or less sensitive to chemotherapy. The sequence
CC   may be RNA or DNA and may comprise a modified backbone and/or nucleotide
CC   analogues
XX
SQ   Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2801
              ||||| ||||||||||
Db         20 AAAAAGAAAAAAAAAA 5


RESULT 3847
AAX32010/c
ID   AAX32010 standard; DNA; 20 BP.
XX
AC   AAX32010;
XX
DT   14-JUN-1999  (first entry)
XX
DE   MSH2 gene specific primer.
XX
KW   Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW   CFTR; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW   Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW   colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW   BAP1 gene; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9906598-A2.
XX
PD   11-FEB-1999.
XX
PF   04-AUG-1998;   98WO-US016574.
XX
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 1999-153820/13.
XX
PT   Determining common functional alleles in a population - useful in the
PT   diagnosis of disease associated with allelic heterogeneity.
XX
PS   Example 1; Page 24; 78pp; English.
XX
CC   The invention relates to methods of determining a functional allele
CC   profile of a gene in a population. Functional allele profiles comprise
CC   the commonly occurring alleles in a population, and the relative
CC   frequencies at which such alleles of a given gene occur. The methods are
CC   used to identify and determine the frequency of the functional alleles of
CC   genes which display extensive allelic heterogeneity, particularly those
CC   implicated in disease or conditions, such as the BRCA1 gene associated
CC   with breast cancer, CFTR associated with cystic fibrosis, dystrophin
CC   associated with Duchenne muscular dystrophy and Becker muscular
CC   dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
CC   also be employed for diseases where allelic and genetic heterogeneity
CC   exist, such as breast cancer, neurofibromatosis, and hereditary non-
CC   polyposis colorectal cancer. Identification of functional alleles is
CC   necessary for identification of mutations which may be implicated in the
CC   disease. Sequences AAX32001-172 represent primers for determining the
CC   functional allele profiles of various genes. The primers are specific for
CC   genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2800
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```
              | ||||||||||||||||
Db         16 GTAAAAAAAAAAAAAA 1


RESULT 3848
ADA45251/c
ID   ADA45251 standard; DNA; 20 BP.
XX
AC   ADA45251;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MSH2 gene PCR primer #10.
XX
KW   Functional allele profile; genetic inheritance; haplotype; population;
KW   disease; pharmacogenetic application; selective pressure; human; MSH2;
KW   MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2003096236-A1.
XX
PD   22-MAY-2003.
XX
PF   08-AUG-2001; 2001US-00923327.
XX
PR   12-FEB-1996;   96US-00598591.
PR   12-FEB-1997;   97US-00798691.
PR   04-AUG-1997;   97US-00905772.
PR   22-MAY-1998;   98US-00084471.
PR   04-AUG-1998;   98US-00129134.
PR   14-MAR-2000; 2000US-00524794.
XX
PA   (ONCO-) ONCORMED INC.
XX
PI   Murphy PD;
XX
DR   WPI; 2003-576875/54.
XX
PT   Determining a functional allele profile of a gene in a population by
PT   identifying the nucleotide sequence of a gene of genomic DNA from each of
PT   the individuals with a family history of functional alleles of the gene
PT   of interest.
XX
PS   Example 1; Page 9; 28pp; English.
XX
CC   The present invention relates to a method for determining a functional
CC   allele profile of a gene in a population. The method comprises
CC   identifying the nucleotide sequence of a gene of interest out of genomic
CC   DNA from each of a population of individuals identified as having a
CC   family history which indicates inheritance of functional alleles of the
CC   gene of interest, and rank ordering the frequency of occurrence of each
CC   haplotype, where the identity of the alleles containing each haplotype
CC   and the determination of their relative frequencies constitutes the
CC   functional allele profile of the gene of interest in the population. The
CC   method is useful for determining functional allele profiles which are
CC   useful in the treatment and diagnosis of diseases, for genetic and
CC   pharmacogenetic applications, and for evaluating the degree to which the
CC   gene(s) are under selective pressure. The present sequence represents a
CC   PCR primer used in the method of the invention.
XX
SQ   Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              | ||||||||||||||||
Db         16 GTAAAAAAAAAAAAAA 1


RESULT 3849
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AAC82924
ID   AAC82924 standard; DNA; 20 BP.
XX
AC   AAC82924;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #8.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 2 A; 3 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAA 2188
              ||||||||||||| ||
Db          1 TTTTTTTTTTTTCAA 16


RESULT 3850
ABZ89440
ID   ABZ89440 standard; DNA; 20 BP.
XX
AC   ABZ89440;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
```

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4682; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAA 2799
| ||||||||||||||
Db 5 TCAAAAAAAAAAAAA 20

RESULT 3851
AAC82917/c
ID AAC82917 standard; DNA; 20 BP.
XX
AC AAC82917;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human S-9 derived oligonucleotide #1.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
PS Example; Fig 1; 8pp; German.
XX
CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
SQ Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAA 2798
|| ||||||||||||||
Db 16 TTTAAAAAAAAAAAAA 1

RESULT 3852
AAC82918/c
ID AAC82918 standard; DNA; 20 BP.
XX
AC AAC82918;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human S-9 derived oligonucleotide #2.
XX
KW Recognition system; screening; identification; pharmaceutical; toxin;
KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS Homo sapiens.
XX
PN DE19923966-A1.
XX
PD 30-NOV-2000.
XX
PF 25-MAY-1999; 99DE-01023966.
XX
PR 25-MAY-1999; 99DE-01023966.
XX
PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI Boekenkamp D, Hoppe H, Burgstaller P;
XX
DR WPI; 2001-050938/07.
XX
PT Recognition system, e.g. for identifying nucleic acids, comprises at

```
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 3 A; 1 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 3853
AAC82919/c
ID   AAC82919 standard; DNA; 20 BP.
XX
AC   AAC82919;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #3.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 4 A; 1 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 3854
AAC82920/c
ID   AAC82920 standard; DNA; 20 BP.
XX
AC   AAC82920;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human S-9 derived oligonucleotide #4.
XX
KW   Recognition system; screening; identification; pharmaceutical; toxin;
KW   plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW   herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
OS   Homo sapiens.
XX
PN   DE19923966-A1.
XX
PD   30-NOV-2000.
XX
PF   25-MAY-1999;   99DE-01023966.
XX
PR   25-MAY-1999;   99DE-01023966.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Boekenkamp D,  Hoppe H,  Burgstaller P;
XX
DR   WPI; 2001-050938/07.
XX
PT   Recognition system, e.g. for identifying nucleic acids, comprises at
PT   least one recognition unit comprising a region with a defined structure
PT   adjacent to a region with a randomized structure.
XX
PS   Example; Fig 1; 8pp; German.
XX
CC   This invention describes a novel recognition system comprising at least 1
CC   recognition unit bound to a support, each recognition unit comprising a
CC   region A with a defined structure adjacent to a region B with a
CC   randomized structure. The recognition system is useful for screening,
CC   identifying, or characterizing at least 1 component of a sample,
CC   especially nucleic acids and/or proteins, and for screening for and/or
CC   identifying cellular or synthetic binding partners, preferably proteins,
CC   peptides, nucleic acids, chemical agents, preferably organic compounds,
CC   pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC   teratogens, herbicides, fungicides or pesticides
XX
SQ   Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
              || |||||||||||||
Db         16 TTTAAAAAAAAAAAAA 1


RESULT 3855
ABZ85313
ID   ABZ85313 standard; DNA; 20 BP.
```

```
XX
AC   ABZ85313;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 555; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 4 A; 3 C; 1 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||||||||| |||
Db          1 TTTTTTTTTTTTCAAC 16


RESULT 3856
ABZ89178
ID   ABZ89178 standard; DNA; 20 BP.
XX
AC   ABZ89178;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4420; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 13 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAA 2798
                || ||||||||||||
Db          5 TTTAAAAAAAAAAAAA 20


RESULT 3857
AAQ52305
ID   AAQ52305 standard; cDNA; 20 BP.
```

```
XX
AC   AAQ52305;
XX
DT   25-MAR-2003  (revised)
DT   03-JUN-1994  (first entry)
XX
DE   FKBP12C PCR primer VX10201.
XX
KW   Transplant rejection; monitoring; FK506 immunosuppressant therapy;
KW   tissue specific; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9323548-A2.
XX
PD   25-NOV-1993.
XX
PF   20-MAY-1993;   93WO-US004916.
XX
PR   20-MAY-1992;   92US-00886611.
XX
PA   (VERT-) VERTEX PHARM INC.
XX
PI   Peattie DA;
XX
DR   WPI; 1993-386579/48.
XX
PT   New cDNA for tissue specific FK506 binding proteins - and detection of
PT   its mRNA to monitor transplant rejection and effect or FK506
PT   immunosuppressant therapy.
XX
PS   Example 4; Page 35; 54pp; English.
XX
CC   The sequence is that of a PCR primer VX10201 which was used to amplify
CC   DNA specific to FKBP12C. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 1 A; 11 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        409 AGCGTACGCCGCCGCC 424
              ||||| ||||||||||
Db          5 AGCGTCCGCCGCCGCC 20


RESULT 3858
AAQ53303
ID   AAQ53303 standard; DNA; 20 BP.
XX
AC   AAQ53303;
XX
DT   25-MAR-2003  (revised)
DT   17-JUN-1994  (first entry)
XX
DE   Probe 5 based on sake yeast alcohol acetyl transferase peptide.
XX
KW   AATase; Saccharomyces cerevisiae; sake yeast; alcohol production;
KW   fermentation; alcoholic beverage; enriched ester flavour; ss.
XX
OS   Synthetic.
XX
PN   EP574941-A2.
XX
PD   22-DEC-1993.
XX
PF   18-JUN-1993;   93EP-00109775.
XX
PR   18-JUN-1992;   92JP-00184328.
PR   26-FEB-1993;   93JP-00062997.
XX
PA   (KIRI ) KIRIN BEER KK.
XX
PI   Fujii T,  Iwamatsu A,  Yoshimoto H,  Minetoki T,  Bogaki T;
PI   Nagasawa N;
XX
DR   WPI; 1993-407311/51.
XX
PT   New alcohol acetyl transferase(s) with specified sequences derived from
PT   yeast - useful for transforming yeast to produce alcoholic beverage with
PT   enriched ester flavour.
XX
PS   Example 4; Page 13; 38pp; English.
XX
CC   An AATase was isolated from sake yeast (Kyokai #7), purified and
CC   partially sequenced. Two degenerate probe pools were designed based on
CC   partial peptide sequences. The probes (AAQ53303 and AAQ53304) were used
CC   to screen a sake yeast cDNA library. The DNA sequence of the gene
CC   encoding AATase was obtained (see AAQ53305). (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 20 BP; 8 A; 1 C; 3 G; 2 T; 0 U; 6 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 3.6e+03;
  Matches   12;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        194 AAGTACGAAGAGGACTGCGA 213
              ||:||:||:||:||:| : |
Db          1 AARTAYGARGARGAYTAYCA 20


RESULT 3859
AAQ40165
ID   AAQ40165 standard; DNA; 20 BP.
XX
AC   AAQ40165;
XX
DT   25-MAR-2003  (revised)
DT   10-AUG-1993  (first entry)
XX
DE   DiGeorge syndrome critical region from chromosome 22q11 PCR primer #5.
XX
KW   DiGeorge syndrome; PCR primer; chromosome 22q11; ss.
XX
OS   Synthetic.
XX
PN   WO9307293-A1.
XX
PD   15-APR-1993.
XX
PF   02-SEP-1992;   92WO-US007536.
XX
PR   04-OCT-1991;   91US-00770758.
PR   10-JUL-1992;   92US-00911534.
XX
PA   (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Emanuel BS,  Budarf ML,  Driscoll DA;
XX
DR   WPI; 1993-134478/16.
XX
PT   Detecting genetic deletions and mutation(s) - by determining the number
PT   of functional copies of the DiGeorge syndrome critical region loci.
XX
PS   Claim 5; Page 39; 43pp; English.
XX
CC   The invention comprises the steps of preparing primer pairs effective to
CC   amplify a region of chromosome 22q11 shown to be unique sequences in the
CC   DiGeorge syndrome critical region; synthesizing DNA substantially
CC   complementary to a region of normal human genomic DNA or cDNA by PCR
CC   amplification using said primer pairs; and isolating a DiGeorge syndrome
CC   critical region probe from a library containing human chromosome 22 using
CC   said substantially complementary DNA. In preferred embodiments the
```

```
CC   primers are selected from the group consisting of the sequences in
CC   AAQ40161-6. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        257 CACCTCTCCTCCGCCG 272
              ||||| ||||||||||
Db          5 CACCTATCCTCCGCCG 20


RESULT 3860
AAQ77670
ID   AAQ77670 standard; DNA; 20 BP.
XX
AC   AAQ77670;
XX
DT   13-JUL-1995  (first entry)
XX
DE   Probe for alcohol acetyl transferase expression control sequence.
XX
KW   Yeast; alcohol acetyl transferase; AATase; inhibition; reduction;
KW   ester-flavour reduced spirits; ss.
XX
OS   Synthetic.
XX
PN   JP06253826-A.
XX
PD   13-SEP-1994.
XX
PF   26-FEB-1993;   93JP-00062998.
XX
PR   26-FEB-1993;   93JP-00062998.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 1994-328981/41.
XX
PT   Transformed yeast where alcohol acetyl-transferase activity is reduced or
PT   inhibited - is useful for prodn. of ester-flavoured spirits obtd. by
PT   sugar fermentation using the yeast.
XX
PS   Example 4; Page 11; 27pp; Japanese.
XX
CC   Two degenerate probe pools (AAQ77670 and AAQ77671) were designed for use
CC   in cloning sequences which control expression of alcohol acetyl-
CC   transferase enzyme (AATase). Yeast in which the AATase activity is
CC   reduced or inhibited are useful for production of ester flavour- reduced
CC   spirits
XX
SQ   Sequence 20 BP; 8 A; 1 C; 3 G; 2 T; 0 U; 6 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 3.6e+03;
  Matches   12;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        194 AAGTACGAAGAGGACTGCGA 213
              ||:||:||:||:||:| : |
Db          1 AARTAYGARGARGAYTAYCA 20


RESULT 3861
AAT87898
ID   AAT87898 standard; DNA; 20 BP.
XX
AC   AAT87898;
XX
DT   12-JAN-1998  (first entry)
XX
DE   Lower primer for exon 2 of human interleukin 9 gene.
XX
KW   Human; interleukin 9; asthma associated factor 1; IL-9; primer;
KW   atopic allergy; asthma; bronchial hyperesponsiveness; BHR; eczema;
KW   rhinitis; urticaria; allergic inflammation; bowel; amplification;
KW   polymorphism; polymerase chain reaction; PCR; exon 2; ss.
XX
OS   Synthetic.
XX
PN   WO9708321-A1.
XX
PD   06-MAR-1997.
XX
PF   23-AUG-1996;   96WO-US012757.
XX
PR   24-AUG-1995;   95US-0002765P.
PR   06-AUG-1996;   96US-0023800P.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Levitt RC,  Lee MW,  Prasad KU,  Nicholas N;
XX
DR   WPI; 1997-179278/16.
XX
PT   Human interleukin-9 variant with Met at position 117 - useful for
PT   treating atopic allergy, esp. asthma.
XX
PS   Disclosure; Page 42; 142pp; English.
XX
CC   The present sequence is a primer for the PCR amplification of exon 2 from
CC   the human interleukin 9 (hIL-9), also known as asthma associated factor
CC   1, gene. hIL-9 plays a role in atopic allergy, asthma and related
CC   disorders, e.g. bronchial hyperesponsiveness (BHR), rhinitis, urticaria,
CC   allergic inflammatory disorders of the bowel and various forms of eczema.
CC   A naturally occurring polymorphism has been identified at position 117 of
CC   hIL-9, individuals homozygous for Met at position 117 demonstrate, e.g. a
CC   lack of asthma and low serum immunoglobulin E (IgE) levels, while Thr/Thr
CC   homozygotes and Thr/Met heterozygotes are susceptible to asthma
XX
SQ   Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1641 TTAAAGAGCCTTCACT 1656
              ||||||||| ||||||
Db          5 TTAAAGAGCATTCACT 20


RESULT 3862
AAV41334
ID   AAV41334 standard; DNA; 20 BP.
XX
AC   AAV41334;
XX
DT   06-OCT-1998  (first entry)
XX
DE   Interleukin-9 (IL-9) gene exon 2 specific lower primer.
XX
KW   Interleukin; IL-9; AAF1; asthma associated factor; human; IBD;
KW   inflammatory bowel disease; Th2 mediated immune response; lupus;
KW   Crohn's disease; chronic non-specific ulcerative colitis; diabetes;
KW   multiple sclerosis; arthritis; autoimmune disease; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9827997-A1.
XX
PD   02-JUL-1998.
XX
PF   22-DEC-1997;   97WO-US023527.
XX
```

```
PR   20-DEC-1996;   96US-0034331P.
PR   19-DEC-1997;   97US-00994986.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Levitt RC,  Nicolaides NC;
XX
DR   WPI; 1998-377404/32.
XX
PT   Treating inflammatory bowel diseases, e.g. Crohn's disease - and chronic
PT   non-specific ulcerative colitis by administering compounds up-regulating
PT   function of interleukin-9 or its receptor.
XX
PS   Disclosure; Page 23; 61pp; English.
XX
CC   Sequences shown in AAV41331 to AAV41340 represent exon specific primers
CC   of human interleukin (IL-9) gene. The invention provides a method for the
CC   treatment of inflammatory bowel disease (IBD) or related disorders that
CC   comprises administering a compound that up-regulates the function of IL-9
CC   or the IL-9 receptor. A method for monitoring humans undergoing IBD
CC   treatment with polypeptides with human IL-9 sequence (or fragments), by
CC   evaluating IL-9 levels in samples taken at different times, and a method
CC   for screening for cells expressing the IL-9 receptor by detecting binding
CC   of a specific ligand are also provided. Compounds up-regulating the
CC   function of IL-9 or the IL-9 receptor can be used therapeutically (in
CC   pharmaceutical compositions, optionally with acceptable carriers) to
CC   treat IBD and other related inflammatory disorders. IBDs (which include
CC   Crohn's diseases and chronic non-specific ulcerative colitis) are
CC   diseases characterised by an inappropriate inflammatory response to
CC   environmental stimuli. Immune responses to antigens are classified as Th1
CC   or Th2 responses, and evidence suggests that IBDs are dominated by a Th1
CC   mediated, antigen induced, inflammatory response. Other related Th1
CC   mediated diseases include multiple sclerosis, diabetes, arthritis, lupus
CC   and autoimmune diseases. The method is based on the observation that the
CC   Th2 response is up-regulated by IL-9
XX
SQ   Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1641 TTAAAGAGCCTTCACT 1656
              ||||||||| ||||||
Db          5 TTAAAGAGCATTCACT 20


RESULT 3863
AAX95502/c
ID   AAX95502 standard; DNA; 20 BP.
XX
AC   AAX95502;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1753; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 4 A; 1 C; 9 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1567 AAAAATCCTTCTCCAC 1582
              ||||||||| ||||||
Db         20 AAAAATCCTCCTCCAC 5


RESULT 3864
AAX93519/c
ID   AAX93519 standard; DNA; 20 BP.
XX
AC   AAX93519;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1598; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
```

```
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        898 GGCTGAAGTACAGAGG 913
              ||||||||||||||| |
Db         20 GGCTGAAGTACAGAAG 5


RESULT 3865
AAX93371
ID   AAX93371 standard; DNA; 20 BP.
XX
AC   AAX93371;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1584; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1481 AACAAAACCCTGGAGA 1496
              ||||| ||||||||||
Db          5 AACAATACCCTGGAGA 20


RESULT 3866
AAX96785
ID   AAX96785 standard; DNA; 20 BP.
XX
AC   AAX96785;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1853; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 10 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1556 AACAGGACTGCAAAAA 1571
              || |||||||||||||
Db          4 AAGAGGACTGCAAAAA 19


RESULT 3867
AAA55978
ID   AAA55978 standard; DNA; 20 BP.
XX
AC   AAA55978;
XX
DT   05-SEP-2000  (first entry)
XX
DE   Human G713 PCR primer SEQ ID NO:17.
```

XX
KW Human; chromosome 13; G713; chromosome 13q31-q33; schizophrenia;
KW biallelic marker; polymorphism; central nervous disease; detection;
KW neuroleptic; G713 gene expression inhibitor; genotyping; PCR primer;
KW brain disorder; psychiatric disorder; bipolar disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200022122-A2.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-IB001730.
XX
PR 13-OCT-1998; 98US-0103955P.
PR 30-OCT-1998; 98US-0106457P.
XX
PA (GEST) GENSET.
XX
PI Blumenfeld M, Bougueleret L, Chumakov I, Cohen D, Essioux L;
XX
DR WPI; 2000-317979/27.
XX
PT Novel polynucleotide of human G713 gene useful for diagnosis and
PT prophylactic treatment of brain, psychiatric disorders like schizophrenia
PT and bipolar disorders.
XX
PS Disclosure; Page 26; 271pp; English.
XX
CC The present invention describes an isolated, purified or recombinant
CC polynucleotide (PN) (I) comprising a contiguous span of 8 to 50
CC nucleotides, where the span includes a G713 or chromosome 13q31-q33
CC related biallelic marker. (I) has neuroleptic activity and can be used as
CC a G713 gene expression inhibitor. (I) can be used genotyping to estimate
CC the frequency of an allele of a G713 or chromosome 13q31-q33 related
CC biallelic marker in a population, and of a haplotype for a set of
CC biallelic markers in a population. (I) is also useful in detecting an
CC association between a haplotype and a trait. The frequency is used for
CC detecting an association between a genotype and a trait being
CC schizophrenia. The genotype is used to determine whether an individual is
CC at risk of developing schizophrenia. (I) can also be used as a medicament
CC against several disorders preferably brain, psychiatric disorders such as
CC schizophrenia and bipolar disorder. Early identification of risk of
CC developing schizophrenia is possible, which would enable early and/or
CC prophylactic treatment. AAA55964 to AAA55966 represent human G713 genomic
CC DNA sequences; AAA55967 encodes the human G713 protein AAY90962; AAA55968
CC encodes the murine G713 protein AAY90963; AAA55992 to AAA56030 represent
CC human chromosome 13q31-q33 locus biallelic markers A12 to A49; AAA55969
CC to AAA55991, and AAA56031 and AAA56032 represent PCR primers used in the
CC exemplification of the present invention
XX
SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAAC 2189
||||||||||||| ||
Db 1 TTTTTTTTTTTTTGAC 16

RESULT 3868
AAZ77152
ID AAZ77152 standard; DNA; 20 BP.
XX
AC AAZ77152;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11508.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 2684; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 1 A; 7 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2160 TTCTCCTTTTTTTTTT 2175
||||||| ||||||||
Db 1 TTCTCCTCTTTTTTTT 16

RESULT 3869
AAZ70964
ID AAZ70964 standard; DNA; 20 BP.
XX
AC AAZ70964;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5320.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.

```
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 1365; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 20 BP; 9 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2543 TTAAGAATTAAGAGGA 2558
              ||||||| ||||||||
Db          2 TTAAGAAGTAAGAGGA 17


RESULT 3870
AAD11331/c
ID   AAD11331 standard; DNA; 20 BP.
XX
AC   AAD11331;
XX
DT   24-SEP-2001  (first entry)
XX
DE   Human cot oncogene antisense oligonucleotide, ISIS 116372.
XX
KW   Human; cot oncogene; antisense therapy; inflammation; cancer; antisense;
KW   immune system disorder; prophylaxis; cytostatic; immunomodulator; Tpl-2;
KW   est; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residues"
FT   modified_base   1
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   3
FT                   /*tag=  e
FT                   /mod_base= m5c
FT   modified_base   5
FT                   /*tag=  f
FT                   /mod_base= m5c
FT   modified_base   6
FT                   /*tag=  g
FT                   /mod_base= m5c
FT   modified_base   12
FT                   /*tag=  h
FT                   /mod_base= m5c
FT   modified_base   14
FT                   /*tag=  i
FT                   /mod_base= m5c
FT   modified_base   15
FT                   /*tag=  j
FT                   /mod_base= m5c
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residues"
FT   modified_base   20
FT                   /*tag=  k
FT                   /mod_base= m5c
XX
PN   US6265216-B1.
XX
PD   24-JUL-2001.
XX
PF   20-JAN-2000; 2000US-00489868.
XX
PR   20-JAN-2000; 2000US-00489868.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Wyatt J;
XX
DR   WPI; 2001-463936/50.
XX
PT   New antisense oligonucleotides for modulating cot oncogene expression,
PT   particularly useful for diagnosing or treating diseases associated with
PT   expression of cot oncogene, such as inflammation, cancer or immune system
PT   disorders.
XX
PS   Claim 3; Col 41; 39pp; English.
XX
CC   The invention relates to antisense oligonucleotides, compositions and
CC   methods for modulating cot oncogene expression. The cot oncogene is also
CC   known as Tpl-2 and est. The compositions comprise antisense compounds,
CC   particularly antisense oligonucleotides, targetted to nucleic acids
CC   encoding cot oncogene. The antisense oligonucleotides are useful for
CC   modulating the expression of cot oncogene and for treating diseases
CC   associated with expression of cot oncogene, e.g. inflammation, cancer or
CC   disorders of the immune system. The antisense oligonucleotides are also
CC   useful for diagnosis or prophylaxis or as research reagents and kits. The
CC   present sequence is human cot oncogene antisense oligonucleotide, ISIS
CC   116372. This sequence was targetted towards the coding region of human
CC   cot oncogene
XX
SQ   Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1490 CTGGAGAAAATGGAGA 1505
              ||||||||| ||||||
Db         17 CTGGAGAAACTGGAGA 2
```

```
RESULT 3871
AAF23315
ID   AAF23315 standard; DNA; 20 BP.
XX
AC   AAF23315;
XX
DT   06-AUG-2003  (revised)
DT   19-MAR-2001  (first entry)
XX
DE   Oligonucleotide for detection of Mycobacterium farcinogen.
XX
KW   ITS; internal transcribed spacer region; Mycobacterium fortuitum;
KW   Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
KW   Mycobacterium flavescens; Mycobacterium asiaticum; tuberculosis;
KW   Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
KW   Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
XX
OS   Mycobacterium farcinogenes.
XX
PN   WO200073436-A1.
XX
PD   07-DEC-2000.
XX
PF   16-MAY-2000; 2000WO-KR000477.
XX
PR   29-MAY-1999;   99KR-00019631.
PR   29-MAY-1999;   99KR-00019632.
PR   29-MAY-1999;   99KR-00019633.
PR   29-MAY-1999;   99KR-00019634.
PR   29-MAY-1999;   99KR-00019635.
PR   07-APR-2000; 2000KR-00018189.
XX
PA   (SJHI-) SJ HIGHTECH CO LTD.
PA   (KIMC/) KIM C M.
PA   (PARK/) PARK H K.
XX
PI   Kim CM,  Park HK,  Jang HJ;
XX
DR   WPI; 2001-061527/07.
XX
PT   Novel oligonucleotide sequences of internal transcribing spacer region of
PT   non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT   detecting and identifying mycobacteria and distinguish TB complex from
PT   NTM.
XX
PS   Claim 32; Page 75; 89pp; English.
XX
CC   The present sequence is an oligonucleotide developed using a
CC   Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC   sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC   M. vaccae, M. flavescens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC   diernhoferi genes were identified. The oligonucleotides derived from
CC   these sequences were used to develop PCR primers and hybridisation probes
CC   for detection and identification of Mycobacterium. ITS has a more
CC   polymorphic region than 16S rRNA and also has a conserved region. It is
CC   therefore highly effective as a target DNA for distinction of genotype.
CC   The oligonucleotide probes, attached to solid substrate, hybridise only
CC   with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC   can detect and identify the specific mycobacteria sensitively. The
CC   oligonucleotides can also detect and identify the specific mycobacteria
CC   by PCR amplification. Using the oligonucleotide primers or probes made
CC   from ITS of mycobacteria, it is possible to detect mycobacteria,
CC   distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC   (NTM), and to identify mycobacteria species accurately and effectively.
CC   (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 20 BP; 0 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTT 2120
             ||||||||||| |||||
Db          2 GGGGGCCTTCGGGTTT 17


RESULT 3872
AAH80592
ID   AAH80592 standard; cDNA; 20 BP.
XX
AC   AAH80592;
XX
DT   11-SEP-2003  (revised)
DT   19-SEP-2001  (first entry)
XX
DE   Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 556.
XX
KW   Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW   disease diagnosis; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6251588-B1.
XX
PD   26-JUN-2001.
XX
PF   10-FEB-1998;   98US-00021701.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2001-424456/45.
XX
PT   Predicting the potential of an oligonucleotide to hybridize to a target
PT   nucleotide sequence, useful for evaluating oligonucleotide probe
PT   sequences, by identifying a oligonucleotides based on the evaluation of
PT   parameters.
XX
PS   Example 2; Col 65; 342pp; English.
XX
CC   The present invention describes a method for predicting the potential of
CC   an oligonucleotide to hybridise to a (complementary) target nucleotide
CC   sequence, involving identifying a subset of oligonucleotides within the
CC   predetermined number of unique oligonucleotides based on the evaluation
CC   of the parameter. Oligonucleotides in the subset are identified that are
CC   clustered along a region of the nucleotide sequence that is hybridisable
CC   to the target nucleotide sequence. This is useful for evaluating
CC   oligonucleotide probe sequences. The present sequence is an
CC   oligonucleotide described in the exemplification of the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 20 BP; 3 A; 4 C; 1 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
              |||||| |||||||||
Db          3 TTTTTTCTTTTTTAAC 18


RESULT 3873
AAH80591
ID   AAH80591 standard; cDNA; 20 BP.
XX
AC   AAH80591;
XX
DT   11-SEP-2003  (revised)
DT   19-SEP-2001  (first entry)
XX
DE   Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 555.
```

```
XX
KW   Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW   disease diagnosis; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6251588-B1.
XX
PD   26-JUN-2001.
XX
PF   10-FEB-1998;   98US-00021701.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2001-424456/45.
XX
PT   Predicting the potential of an oligonucleotide to hybridize to a target
PT   nucleotide sequence, useful for evaluating oligonucleotide probe
PT   sequences, by identifying a oligonucleotides based on the evaluation of
PT   parameters.
XX
PS   Example 2; Col 65; 342pp; English.
XX
CC   The present invention describes a method for predicting the potential of
CC   an oligonucleotide to hybridise to a (complementary) target nucleotide
CC   sequence, involving identifying a subset of oligonucleotides within the
CC   predetermined number of unique oligonucleotides based on the evaluation
CC   of the parameter. Oligonucleotides in the subset are identified that are
CC   clustered along a region of the nucleotide sequence that is hybridisable
CC   to the target nucleotide sequence. This is useful for evaluating
CC   oligonucleotide probe sequences. The present sequence is an
CC   oligonucleotide described in the exemplification of the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||  |||||||||
Db          4 TTTTTTCTTTTTTAAC 19


RESULT 3874
AAH80593
ID   AAH80593 standard; cDNA; 20 BP.
XX
AC   AAH80593;
XX
DT   11-SEP-2003  (revised)
DT   19-SEP-2001  (first entry)
XX
DE   Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 557.
XX
KW   Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW   disease diagnosis; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6251588-B1.
XX
PD   26-JUN-2001.
XX
PF   10-FEB-1998;   98US-00021701.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2001-424456/45.
XX
PT   Predicting the potential of an oligonucleotide to hybridize to a target
PT   nucleotide sequence, useful for evaluating oligonucleotide probe
PT   sequences, by identifying a oligonucleotides based on the evaluation of
PT   parameters.
XX
PS   Example 2; Col 65; 342pp; English.
XX
CC   The present invention describes a method for predicting the potential of
CC   an oligonucleotide to hybridise to a (complementary) target nucleotide
CC   sequence, involving identifying a subset of oligonucleotides within the
CC   predetermined number of unique oligonucleotides based on the evaluation
CC   of the parameter. Oligonucleotides in the subset are identified that are
CC   clustered along a region of the nucleotide sequence that is hybridisable
CC   to the target nucleotide sequence. This is useful for evaluating
CC   oligonucleotide probe sequences. The present sequence is an
CC   oligonucleotide described in the exemplification of the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 20 BP; 3 A; 4 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||  |||||||||
Db          2 TTTTTTCTTTTTTAAC 17


RESULT 3875
AAH80590
ID   AAH80590 standard; cDNA; 20 BP.
XX
AC   AAH80590;
XX
DT   11-SEP-2003  (revised)
DT   19-SEP-2001  (first entry)
XX
DE   Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 554.
XX
KW   Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW   disease diagnosis; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6251588-B1.
XX
PD   26-JUN-2001.
XX
PF   10-FEB-1998;   98US-00021701.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2001-424456/45.
XX
PT   Predicting the potential of an oligonucleotide to hybridize to a target
PT   nucleotide sequence, useful for evaluating oligonucleotide probe
PT   sequences, by identifying a oligonucleotides based on the evaluation of
PT   parameters.
XX
PS   Example 2; Col 65; 342pp; English.
XX
CC   The present invention describes a method for predicting the potential of
```

```
CC   an oligonucleotide to hybridise to a (complementary) target nucleotide
CC   sequence, involving identifying a subset of oligonucleotides within the
CC   predetermined number of unique oligonucleotides based on the evaluation
CC   of the parameter. Oligonucleotides in the subset are identified that are
CC   clustered along a region of the nucleotide sequence that is hybridisable
CC   to the target nucleotide sequence. This is useful for evaluating
CC   oligonucleotide probe sequences. The present sequence is an
CC   oligonucleotide described in the exemplification of the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||  |||||||||
Db          5 TTTTTTCTTTTTTAAC 20


RESULT 3876
ABK90289
ID   ABK90289 standard; DNA; 20 BP.
XX
AC   ABK90289;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Bcl-2-targeting antisense oligonucleotide #22.
XX
KW   Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;
KW   cAMP response element; bacterial infection; viral infection;
KW   inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;
KW   autoimmune disorder; parasitic infection; virucide; hyperplasia;
KW   tumourigenesis; hepatitis B infection; human.
XX
OS   Homo sapiens.
XX
PN   WO200257480-A2.
XX
PD   25-JUL-2002.
XX
PF   22-JAN-2002; 2002WO-US001967.
XX
PR   22-JAN-2001; 2001US-0263244P.
XX
PA   (GENT-) GENTA INC.
XX
PI   Klem RE;
XX
DR   WPI; 2002-590754/63.
XX
PT   Hybrid oligomer comprises a cyclic AMP response element sequence and a
PT   sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for
PT   preventing or treating cell-proliferative disorders e.g., cancer.
XX
PS   Disclosure; Page 13; 78pp; English.
XX
CC   The invention relates to a hybrid oligomer comprising a cyclic AMP
CC   response element (CRE) sequence and a sequence that hybridises to the bcl
CC   -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of
CC   cancer cells in vitro, which comprises contacting the cancer cells with a
CC   hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;
CC   (2) treating or preventing cancer in a human, which comprises
CC   administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE
CC   decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid
CC   oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a
CC   carrier. The pharmaceutical composition of the invention is useful for
CC   preventing or treating cell-proliferative disorders e.g., cancer,
CC   hyperplasia or tumourigenesis and also bacterial infection, viral
CC   infection, inflammation, anaphylaxis, allergy, arthritis, asthma,
CC   autoimmune disorders and parasitic infection. The CRE decoy oligomer and
CC   bcl-2 antisense oligomer are also useful for preventing or treating
CC   hepatitis B virus infection. The hybrid oligomers can also be used for
CC   screening candidate transcription factors or other molecules e.g., gene
CC   regulatory proteins or for diagnostic assays. The present sequence is a
CC   Bcl-2 antisense oligonucleotide
XX
SQ   Sequence 20 BP; 2 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         54 GCGGGGGCGGCGGCAG 69
                ||||  ||||||||||
Db          2 GCGGCGGCGGCGGCAG 17


RESULT 3877
AAD33529/c
ID   AAD33529 standard; DNA; 20 BP.
XX
AC   AAD33529;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Actin specific RT-PCR upstream primer.
XX
KW   Upregulated by nitric oxide; NO; rno; differentiation; death; cancer;
KW   acute myeloid leukaemia; AML; cytostatic; RT-PCR; reverse transcription;
KW   actin; primer; ss.
XX
OS   Unidentified.
XX
PN   US2001029033-A1.
XX
PD   11-OCT-2001.
XX
PF   06-MAR-2001; 2001US-00799983.
XX
PR   06-MAR-2000; 2000US-0186971P.
XX
PA   (SHAM/) SHAMI P J.
PA   (PARK/) PARKER C J.
XX
PI   Shami PJ,  Parker CJ;
XX
DR   WPI; 2002-009982/01.
XX
PT   Novel polypeptide regulated by nitric oxide useful for inducing acute
PT   myeloid leukemia cell differentiation and apoptosis.
XX
PS   Example 6; Page 8; 23pp; English.
XX
CC   The present invention relates to novel genes which are upregulated by
CC   nitric oxide (NO), designated as rno and their corresponding proteins.
CC   The invention also relates to the isolation and characterisation of three
CC   isoforms of rno gene, rno-1, rno-2, rno-3. rno proteins of the invention
CC   are useful for inducing differentiation and death in a cancer cell.
CC   Diagnosing acute myeloid leukaemia (AML) comprises detecting the
CC   expression of a rho gene comprising the nucleotides coding for rno
CC   protein. The present DNA sequence is actin specific reverse transcription
CC   (RT)-PCR primer. This primer is used in the exemplification of the
CC   invention
XX
SQ   Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        703 TGTCGACGACCAGCAC 718
                ||||||||||||| |
Db         20 TGTCGACGACCAGCGC 5
```

```
RESULT 3878
ABQ65350/c
ID   ABQ65350 standard; DNA; 20 BP.
XX
AC   ABQ65350;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Human gene methylation status determination method PCR primer #90.
XX
KW   Toxicological diagnosis; DNA methylation; methylation status;
KW   toxic response; human; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200240710-A2.
XX
PD   23-MAY-2002.
XX
PF   08-NOV-2001; 2001WO-EP012951.
XX
PR   14-NOV-2000; 2000DE-01056802.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-463571/49.
XX
PT   Toxicological diagnosis, useful for diagnosis and prognosis of adverse
PT   reactions, based on effect of test compounds on methylation status of
PT   selected genes, involves determining changes in DNA methylation status.
XX
PS   Example 2; Page 104; 113pp; German.
XX
CC   The present invention relates to a method of toxicological diagnosis,
CC   involving taking a DNA-containing sample from an organism or cell culture
CC   that has been treated with a test compound and determining any changes in
CC   the DNA methylation status or pattern caused by said test compound. The
CC   method is used for diagnosis and prognosis of adverse toxic responses in
CC   individuals. The present sequence is a PCR primer used to demonstrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 9 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1535 AGGTTAGGAGAGTAGG 1550
              || |||||||||||||
Db         19 AGATTAGGAGAGTAGG 4


RESULT 3879
AAD36554
ID   AAD36554 standard; DNA; 20 BP.
XX
AC   AAD36554;
XX
DT   09-AUG-2002  (first entry)
XX
DE   Human Her-1 antisense oligonucleotide ISIS #122163.
XX
KW   Human; epidermal growth factor receptor; hyperproliferative disease;
KW   Her1; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
KW   tumour; cancer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    3
FT                    /*tag=  d
FT                    /mod_base= m5c
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    17
FT                    /*tag=  e
FT                    /mod_base= m5c
XX
PN   WO200226758-A1.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-US030551.
XX
PR   29-SEP-2000; 2000US-00676610.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Wyatt JR,  Freier SM;
XX
DR   WPI; 2002-394234/42.
XX
PT   Novel antisense oligonucleotide that specifically hybridizes with and
PT   inhibits nucleic acid encoding epidermal growth factor receptor, useful
PT   for treating hyperproliferative disease such as cancer or psoriasis.
XX
PS   Claim 1; Page 45; 169pp; English.
XX
CC   The invention relates to an antisense oligonucleotide targetted to a
CC   nucleic acid molecule encoding human epidermal growth factor receptor
CC   (Her1) to inhibit its expression. The antisense compounds are useful for
CC   treating diseases or conditions associated with Her-1 such as
CC   hyperproliferative diseases especially cancer (lung, ovarian, colon or
CC   prostrate cancer) and psoriasis. They are also useful as research
CC   reagents, diagnostics, therapeutics, kits and prophylactically e.g. to
CC   prevent or delay tumour formation. The present sequence is an antisense
CC   oligonucleotide targetted to human Her-1
XX
SQ   Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1424 CTGATTGTCATAGACA 1439
              |||||||| |||||||
Db          3 CTGATTGTGATAGACA 18


RESULT 3880
ABK34138/c
ID   ABK34138 standard; DNA; 20 BP.
XX
AC   ABK34138;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human MHC PCR primer #14.
XX
KW   Human; ss; astrocytoma; cytostatic; staging; cysteine methylation; CpG;
KW   bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;
```

KW matrix assisted laser desorption/ionization mass spectrometry; primer.
XX
OS Homo sapiens.
XX
PN WO200202808-A2.
XX
PD 10-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007538.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-171649/22.
XX
PT Novel chemically modified genomic DNA sequences, useful in the
PT characterization, classification, differentiation, grading, staging,
PT treatment and/or diagnosis of astrocytomas or predisposition to
PT astrocytomas.
XX
PS Example; Page 25; 37pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence (I) of at
CC least 18 bases in length of a segment of chemically pre-treated genomic
CC DNA which has any one of the sequences of (ABK33919-ABK34032) or its
CC complement. Also included are an oligonucleotide or peptide nucleic acid
CC (or set thereof) of at least 9 nucleotides which hybridises to (I),
CC primers for (I), probes for detecting cytosine methylation or single-
CC nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide
CC nucleic acids for analysing diseases associated with the methylation
CC states of the CpG dinucleotides of (I). The array is useful for
CC determining genetic and/or epigenetic parameters, classification,
CC differentiation, grading, staging, treatment and/or diagnosis of
CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine
CC methylations, involves obtaining a biological sample containing genomic
CC DNA, extracting the genomic DNA, converting cytosine bases which are
CC unmethylated at the 5-position, in the genomic DNA sample, to uracil or
CC another base which is dissimilar to cytosine in terms of hybridisation
CC behaviour, by chemical treatment and amplifying chemically pre-treated
CC genomic DNA fragments using the array and a polymerase, where the
CC amplificates carry a detectable label. The method further involves
CC identifying methylation status of one or more cytosine positions, and
CC analysing methylation status of the cytosine positions by reference to
CC one or more data sets. The genomic DNA is chemically treated by using a
CC bisulphite, hydrogen sulphite or disulphite. The amplification step
CC amplifies DNA which is of particular interest in astrocytoma or brain
CC tissue, based on the specific genomic methylation status of brain
CC tissues, as opposed to background DNA. The amplificates carry a
CC fluorescent label or radionuclide. Optionally, the labels of the
CC amplificates are detachable molecule fragments having a typical mass
CC which are detected in a mass spectrometer. The fragments of chemically
CC pre-treated genomic DNA to be amplified, have a single positive or
CC negative charge for a better detectability in the mass spectrometer.
CC Preferably, the amplificates or fragments of the amplificates are
CC detected by matrix assisted laser desorption/ionization mass spectrometry
CC (MALDI) or using electron spray mass spectrometry (ESI). The present
CC sequence is a PCR primer used to amplify a region containing a methylated
CC cytosine from one of the chemically pre-treated reference DNA samples of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 9 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1535 AGGTTAGGAGAGTAGG 1550
|| ||||||||||||||
Db 19 AGATTAGGAGAGTAGG 4

RESULT 3881
ABZ26083/c
ID ABZ26083 standard; DNA; 20 BP.
XX
AC ABZ26083;
XX
DT 27-MAR-2003 (first entry)
XX
DE Mitochondrial cytochrome B PCR primer 1.
XX
KW Mitochondria; cytochrome B; animal fodder; PCR; primer; ss.
XX
OS Synthetic.
XX
PN DE10105056-A1.
XX
PD 08-AUG-2002.
XX
PF 05-FEB-2001; 2001DE-01005056.
XX
PR 05-FEB-2001; 2001DE-01005056.
XX
PA (CONG-) CONGEN BIOTECHNOLOGIE GMBH.
XX
PI Kuhn M, Mergemeier S;
XX
DR WPI; 2002-667979/72.
XX
PT Species-specific detection of animal DNA, useful for analyzing foods and
PT feeds, by amplifying gene common to all animals, then testing amplicon
PT with specific probes.
XX
PS Claim 13; Page 15; 24pp; German.
XX
CC The invention relates to a method for determining the absence or presence
CC of DNA of a particular animal species in a sample by polymerase chain
CC reaction (PCR) amplification using a primer mixture (ABZ26083-ABZ26085)
CC that includes a labeled primer that hybridises to conserved regions of a
CC gene present in all species being tested for. The amplicon is then tested
CC for hybridisation with species-specific probes (ABZ26086-ABZ26095). The
CC method is especially used to determine the origin of foods and animal
CC fodder. The method requires neither restriction enzymes nor gel
CC electrophoresis, provides high sample throughput (including analysis in
CC parallel) and produces few incorrect results and can be applied to
CC practically all foods
XX
SQ Sequence 20 BP; 7 A; 7 C; 1 G; 4 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.6e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2682 GGGTGAAATGGAGATTTG 2699
|||||:|||||| ||||
Db 20 GGGTGRAATGGAATTTTG 3

RESULT 3882
AAD24274
ID AAD24274 standard; DNA; 20 BP.
XX
AC AAD24274;
XX
DT 07-MAR-2002 (first entry)
XX
DE Human chromosome 22q11 region amplifying primer #5.
XX
KW Human; genetic deletion; translocation; mutation; conotruncal defect;
KW DiGeorge syndrome; DGS; CHARGE association; Velocardiofacial syndrome;

KW Shprintzen syndrome; cleft palate; chromosome 22q11; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6303294-B1.
XX
PD 16-OCT-2001.
XX
PF 07-JUN-1995; 95US-00473319.
XX
PR 04-OCT-1991; 91US-00770758.
PR 10-JUL-1992; 92US-00911534.
PR 22-NOV-1993; 93US-00156672.
XX
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Emanuel BS, Budarf ML, Driscoll D;
XX
DR WPI; 2002-033211/04.
XX
PT Novel methods to detect genetic changes associated with DiGeorge
PT syndrome, Velocardiofacial syndrome, CHARGE association, conotruncal
PT defect and/or cleft palate are useful for prenatal screening for the
PT diseases.
XX
PS Claim 8; Col 40; 56pp; English.
XX
CC The invention relates to methods of detecting genetic deletions,
CC translocations and mutations associated with at least one condition
CC selected from the group consisting of DiGeorge syndrome (DGS), CHARGE
CC association, Velocardiofacial (Shprintzen) syndrome (VCF), conotruncal
CC defect and/or cleft palate in a human patient. DGS is linked to
CC chromosomal deletion of chromosome 22. The method involves identifying in
CC a sample DNA if there are less than 2 functional copies of chromosome
CC 22q11 and including locus D22S36 to locus BCRL2, indicating a genetic
CC deletion or mutation associated with the conditions. The method is useful
CC for diagnosing DGS, VCF, CHARGE association, conotruncal defect and/or
CC cleft palate, particularly in prenatal monitoring. The present sequence
CC is a PCR primer used to amplify a region of human chromosome 22q11
XX
SQ Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 257 CACCTCTCCTCCGCCG 272
||||| ||||||||||
Db 5 CACCTATCCTCCGCCG 20

RESULT 3883
ABQ78545
ID ABQ78545 standard; DNA; 20 BP.
XX
AC ABQ78545;
XX
DT 25-NOV-2002 (first entry)
XX
DE Antisense oligodeoxynucleotide of the human bcl-2 gene.
XX
KW Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;
KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;
KW autoimmune disease; ss.
XX
OS Homo sapiens.
XX
PN US6414134-B1.
XX
PD 02-JUL-2002.
XX
PF 28-NOV-2000; 2000US-00724426.
XX
PR 22-DEC-1988; 88US-00288692.
PR 21-FEB-1992; 92US-00840716.
PR 20-SEP-1993; 93US-00124256.
PR 05-JUN-1995; 95US-00465485.
PR 18-MAY-1998; 98US-00080285.
PR 17-AUG-1999; 99US-00375514.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Reed JC;
XX
DR WPI; 2002-641579/69.
XX
PT Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia
PT -2 mRNA, useful for inhibiting cancer cell growth, for treating
PT autoimmune disorders, and for ex vivo bone marrow purging.
XX
PS Disclosure; Fig 13C; 41pp; English.
XX
CC The present sequence represents an antisense oligonucleotide
CC complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense
CC oligonucleotide is useful for inhibiting cancer cell (lymphoma or
CC leukemia cells) growth, for increasing the sensitivity of cancer cells to
CC cancer chemotherapeutic agents, or for inducing cancer cell death alone
CC or in combination with any one or more cancer chemotherapeutic agents. It
CC is also useful for reducing the bcl-2 gene expression or impairing bcl-2
CC protein function, for ex vivo bone marrow purging, for removing residual
CC malignant cells from the bone marrow, for inhibiting cancer of neoplastic
CC cell growth, and for treating autoimmune disease
XX
SQ Sequence 20 BP; 2 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 54 GCGGGGGCGGCGGCAG 69
|||| ||||||||||||
Db 2 GCGGCGGCGGCGGCAG 17

RESULT 3884
ABK28076/c
ID ABK28076 standard; DNA; 20 BP.
XX
AC ABK28076;
XX
DT 09-APR-2002 (first entry)
XX
DE Human MHC methylation state PCR primer #14.
XX
KW Human; ss; astrocytoma; oligoastrocytoma; oligodendroglioma; antitumour;
KW cytostatic; cytosine methylation state; single nucleotide polymorphism;
KW SNP; CpG; brain tumour; PCR; primer.
XX
OS Homo sapiens.
XX
PN WO200200705-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007539.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-139900/18.
XX

```
PT   Oligonucleotide for diagnosing and treating tumors and cancer especially
PT   gliomas, astrocytomas and oligodendromas, comprises chemically modified
PT   genomic sequences of genes associated with tumors and cancers.
XX
PS   Example 4; Page 22; 31pp; English.
XX
CC   The invention relates to a nucleic acid (I) comprising a sequence of at
CC   least 18 bases of a segment of chemically pretreated genomic DNA (II)
CC   according to one of the sequences (S1) selected from 120 sequences, and
CC   its complementary sequences. Also included are an oligomer (III),
CC   especially an oligonucleotide or peptide nucleic acid (PNA)-oligomer,
CC   comprising a sequence of at least 9 nucleotides which hybridises to or is
CC   identical to (II), and complementary sequences, a set of oligomers (IV)
CC   comprising at least two (III) and their use for detecting the cytosine
CC   methylation state and/or single nucleotide polymorphisms (SNPs) in (II),
CC   and manufacturing (M1) an arrangement of different oligomers (array)
CC   fixed to a carrier material for analysing diseases associated with the
CC   methylation state of the CpG dinucleotide of (S1), where at least one
CC   oligomer is coupled to solid phase. The set of oligomers (IV) are useful
CC   as primer oligonucleotides for the amplification of (II) especially for
CC   characterising classifying and differentiating oligodendroglioma,
CC   astrocytoma and oligoastrocytoma tumours (by ascertaining genetic and/or
CC   epigenetic parameters of genomic DNA by analysing cytosine methylation
CC   and single nucleotide polymorphisms). The present sequence is a PCR
CC   primer used to amplify the modified genomic sequence from a gene
CC   associated with brain tumours
XX
SQ   Sequence 20 BP; 3 A; 9 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1535 AGGTTAGGAGAGTAGG 1550
              || |||||||||||||
Db         19 AGATTAGGAGAGTAGG 4


RESULT 3885
ABK69560
ID   ABK69560 standard; DNA; 20 BP.
XX
AC   ABK69560;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Rat phosphorylase kinase alpha-1 antisense oligonucleotide #66.
XX
KW   Human; rat; antisense; phosphorylase kinase alpha 1; ss;
KW   antiinflammatory; cytostatic; antimicrobial; antidiabetic;
KW   metabolic disorder; diabetes; infection; inflammation; tumour; probe.
XX
OS   Rattus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER = phosporothioate backbone, all cytidine
FT                   residues are 5-methyl cytidine"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methoxyethyl"
FT   modified_base   5. .15
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2' deoxynucleotide"
FT   modified_base   15. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER = 2'-O-methoxyethyl"
XX
PN   WO200220546-A1.
XX
PD   14-MAR-2002.
XX
PF   24-AUG-2001; 2001WO-US026608.
XX
PR   07-SEP-2000; 2000US-00657452.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Wyatt JR;
XX
DR   WPI; 2002-351759/38.
XX
PT   New antisense compound which is targeted to nucleic acid encoding
PT   phosphorylase kinase alpha 1 and inhibits expression of kinase protein,
PT   useful for treating a condition associated with kinase, e.g. diabetes.
XX
PS   Claim 3; Page 91; 140pp; English.
XX
CC   This invention relates to a novel antisense nucleic acid compound
CC   targeted to a nucleic acid molecule encoding phosphorylase kinase alpha-1
CC   which specifically hybridises with and inhibits expression of
CC   phosphorylase kinase alpha-1. The compound of the invention is useful for
CC   inhibiting the expression of phosphorylase kinase alpha-1 in cells or
CC   tissues, and for treating an animal having a disease condition associated
CC   with phosphorylase kinase alpha-1, e.g. a metabolic disorder such as
CC   diabetes. The compounds are also useful prophylactically, e.g. to prevent
CC   or delay infection, inflammation or tumour formation. The antisense
CC   compounds are also useful as therapeutic, diagnostic and research
CC   reagent, for distinguishing functions of various members of a biological
CC   pathway, and in antisense gene therapy. The present sequence represents
CC   an antisense oligonucleotide probe used to create the phosphorylase
CC   kinase alpha-1 inhibiting compound of the invention
XX
SQ   Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1462 CCAGAGTCCAGCTGAT 1477
              |||||||||||||| ||
Db          3 CCAGAGTCCAGCTCAT 18


RESULT 3886
ABL54173
ID   ABL54173 standard; DNA; 20 BP.
XX
AC   ABL54173;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Oligonucleotide.
XX
KW   B cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma;
KW   leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
KW   breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;
KW   hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;
KW   testicular cancer; lung carcinoma; bladder carcinoma; melanoma;
KW   head and neck cancer; brain cancer; cytostatic; human; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200217852-A2.
XX
PD   07-MAR-2002.
XX
PF   23-AUG-2001; 2001WO-US026414.
XX
```

PR 25-AUG-2000; 2000US-0227970P.
PR 29-SEP-2000; 2000US-0237009P.
PR 10-NOV-2000; 2000US-00709170.
XX
PA (GENT-) GENTA INC.
XX
PI Warrel RP, Klem RE, Fingert H;
XX
DR WPI; 2002-371796/40.
XX
PT Treating or preventing cancer, tumors and carcinomas, comprises
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at
PT high doses for short period for time with one or more cancer
PT therapeutics.
XX
PS Disclosure; Page 64; 64pp; English.
XX
CC The present invention is related to the use of a B cell
CC lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly
CC G3139 (see ABL54148), to treat and prevent bcl-2 related disorders.
CC Administration at high doses results in significant therapeutic
CC responses, including low toxicity, high tolerance and prolonged survival.
CC Administration at high doses for short periods of time (less than 14
CC days) also provides significant therapeutic responses in the treatment of
CC cancer. The bcl-2 antisense oligomer may also be used to increase the
CC sensitivity of a subject to cancer therapeutics, and in combination with
CC hormone treatment or gene therapy. Conditions that may be treated or
CC prevented include cancer of the haematopoietic system, skin, bone and
CC soft tissue, reproductive system, genitourinary system, breast, endocrine
CC system, brain, central nervous system, peripheral nervous system, kidney,
CC lung, respiratory system, thorax, gastrointestinal and alimentary canal,
CC lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary
CC site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon
CC carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate,
CC cervical, testicular, head and neck or brain cancer, renal cell
CC carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung
CC carcinoma, bladder carcinoma and melanoma (all claimed). Note: The
CC present sequence is given in the Sequence Listing from the present
CC invention but the Seq ID No. is not referred to within the specification
XX
SQ Sequence 20 BP; 2 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 54 GCGGGGGCGGCGGCAG 69
|||| ||||||||||
Db 2 GCGGCGGCGGCGGCAG 17

RESULT 3887
ABZ85693
ID ABZ85693 standard; DNA; 20 BP.
XX
AC ABZ85693;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 935; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 10 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2330 TCACCCCCAAGTCCCC 2345
||| ||||||||||||
Db 1 TCAGCCCCAAGTCCCC 16

RESULT 3888
ABZ90754/c
ID ABZ90754 standard; DNA; 20 BP.
XX
AC ABZ90754;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5996; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 1 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2176 TTTTTTTTTTTAACTT 2191
||||||||| ||||||
Db 20 TTTTTTTTTGTAACTT 5

RESULT 3889
ABZ88617
ID ABZ88617 standard; DNA; 20 BP.
XX
AC ABZ88617;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3859; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAA 2798
|| ||||||||||||||
Db 5 TTCAAAAAAAAAAAAA 20

RESULT 3890
ABZ88617/c
ID ABZ88617 standard; DNA; 20 BP.
XX
AC ABZ88617;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3859; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAA 2188
||||||||||||| ||
Db 20 TTTTTTTTTTTTTGAA 5

RESULT 3891
ABZ90451
ID ABZ90451 standard; DNA; 20 BP.
XX
AC ABZ90451;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5693; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 12 C; 4 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 286 CAGCCCCGCGCCACCCC 302
|||||||| |||| |||
Db 3 CAGCCCCGAGCCANCCC 19

RESULT 3892
ABZ91600/c
ID ABZ91600 standard; DNA; 20 BP.
XX
AC ABZ91600;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6842; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2761 AATAAAAGTATTCTTG 2776
||||||||| ||||||
Db 20 AATAAAAGTCTTCTTG 5

RESULT 3893
ABZ88121
ID ABZ88121 standard; DNA; 20 BP.
XX
AC ABZ88121;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3363; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 11 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2757 GTATAATAAAAGTATT 2772
||| ||||||||||
Db 2 GTAAAATAAAAGTATT 17

RESULT 3894
ABZ85508/c
ID ABZ85508 standard; DNA; 20 BP.
XX
AC ABZ85508;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 750; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 7 A; 0 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 CTTTCCCCCTCCCTAC 358
||||||||| ||||||
Db 17 CTTTCCCCCACCCTAC 2

RESULT 3895
ABZ93178
ID ABZ93178 standard; DNA; 20 BP.
XX
AC ABZ93178;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.

XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8420; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 9 A; 2 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2356 TGTATTTTAAGAAACA 2371
||| |||||||||||||
Db 5 TGTCTTTTAAGAAACA 20

RESULT 3896
ABQ77172
ID ABQ77172 standard; DNA; 20 BP.
XX
AC ABQ77172;
XX
DT 24-APR-2003 (first entry)
XX
DE Human ABCC12 intron 5/exon 6 boundary.
XX
KW Adenosine triphosphate (ATP)-binding cassette transporter subfamily C12;
KW cystic fibrosis transmembrane conductance regulator; human; CFTR/MRP;
KW multidrug resistance-like subgroup; somatic gene therapy; ABCC12;
KW paroxysmal kinesigenic choreoathetosis; cysteinyl leukotriene;
KW anionic drug; methotrexate; neutral drug; glutathione; glucuronate;
KW sulphate conjugated drug; ds.
XX
OS Homo sapiens.
XX
PN WO200285943-A2.
XX
PD 31-OCT-2002.

XX
PF 05-MAR-2002; 2002WO-EP003320.
XX
PR 05-MAR-2001; 2001US-0272759P.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosier-Montus M, Prades C, Arnould-Reguigne I, Denefle P, Dean M;
PI Allikmets R;
XX
DR WPI; 2003-093101/08.
XX
PT New ATP-binding cassette transporter gene subfamily C12, ABCC12
PT polypeptide, useful for preventing or treating paroxysmal kinesigenic
PT choreoathetosis.
XX
PS Disclosure; Page 44; 122pp; English.
XX
CC This invention describes a novel human ABCC12 (adenosine triphosphate
CC (ATP)-binding cassette transporter gene subfamily C12, i.e. cystic
CC fibrosis transmembrane conductance regulator/multidrug resistance-like
CC subgroup (CFTR/MRP) family) polypeptide and its encoding polynucleotides
CC The polypeptide is useful for screening agonists and antagonist of the
CC ABCC12 polypeptide. The products of the invention are useful for
CC screening an active ingredient for preventing and treating paroxysmal
CC kinesigenic choreoathetosis or pathologies linked to dysfunction of
CC transport of organic anion transporters such as cysteinyl leukotriene,
CC anionic drugs, such as methotrexate, neutral drugs conjugated to acidic
CC ligands, such as glutathione, glucuronate or sulphate conjugated drugs
CC and can be used for somatic gene therapy. This sequence represents a
CC region corresponding to an exon/intron boundary from the gene encoding a
CC human ABCC12 isoform described in the disclosure of the invention
XX
SQ Sequence 20 BP; 4 A; 1 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2267 TTTATTTCAGATGTTT 2282
|| ||||||||||||
Db 1 TTGATTTCAGATGTTT 16

RESULT 3897
ADA20513/c
ID ADA20513 standard; DNA; 20 BP.
XX
AC ADA20513;
XX
DT 20-NOV-2003 (first entry)
XX
DE Prostate tumour related gene MLH1 PCR primer #2.
XX
KW cytostatic; gene therapy; genetic marker; epigenetic parameter;
KW classification; differentiation; diagnosis; prostate tumour;
KW prostate cancer; cytosine methylation; uracil;
KW single nucleotide polymorphism; SNP; prostate carcinoma; ss; primer; PCR.
XX
OS Homo sapiens.
XX
PN WO2002103042-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-EP006605.
XX
PR 14-JUN-2001; 2001DE-01028508.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Distler J, Model F, Adorjan P;
XX
DR WPI; 2003-167536/16.
XX
PT Determining genetic and/or epigenetic parameters, useful for the
PT classification, differentiation and/or diagnosis of prostate tumors or a
PT predisposition to prostate cancer, comprises analyzing cytosine
PT methylation.
XX
PS Example 2; Page 17; 376pp; English.
XX
CC The invention relates to a method of determining genetic and/or
CC epigenetic parameters for the classification, differentiation and/or
CC diagnosis of prostate tumours or the predisposition to prostate cancer,
CC by analysing cytosine methylation in a sample of genomic DNA. The method
CC comprises chemically treating unmethylated cytosine bases at the 5-
CC position to uracil or another base, which is dissimilar to cytosine in
CC terms of hybridization behaviour; followed by amplifying at least one
CC fragment of the chemically pre-treated genomic DNA using sets of primer
CC oligonucleotides and a polymerase. The oligomers or probes derived from
CC them are useful for detecting the methylation state of all CpG
CC dinucleotides and/or single nucleotide polymorphisms (SNPs) in a
CC chemically pre-treated genomic DNA. They are all useful for treating
CC prostate carcinoma. This sequence represents an oligonucleotide used to
CC amplify a gene possibly involved in predisposition to prostate cancer
CC which may contain methylated or unmethylated CpG dinucleotides.
XX
SQ Sequence 20 BP; 3 A; 9 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1535 AGGTTAGGAGAGTAGG 1550
|| ||||||||||||||
Db 19 AGATTAGGAGAGTAGG 4

RESULT 3898
ADA84316/c
ID ADA84316 standard; DNA; 20 BP.
XX
AC ADA84316;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human G6E PCR primer 2.
XX
KW renal cancer; prostate cancer; cytosine methylation;
KW single nucleotide polymorphism; histological; cytological; ss; primer;
KW PCR.
XX
OS Homo sapiens.
XX
PN WO2002103041-A2.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-EP006603.
XX
PR 14-JUN-2001; 2001DE-01028509.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Distler J, Model F, Adorjan P;
XX
DR WPI; 2003-183991/18.
XX
PT Method for characterizing, classifying and/or differentiating renal and
PT prostate cancers, by analyzing the genetic and/or epigenetic parameters
PT of genomic DNA, particularly by determining its cytosine methylation
PT status.
XX
PS Example 2; Page 17; 211pp; English.

```
XX
CC   The invention relates to a novel method for characterising, classifying
CC   and/or differentiating renal and prostate cancer. The method comprises
CC   extracting genomic DNA from a biological sample, converting cytosine
CC   bases (by chemical treatment) that are unmethylated at the 5-position to
CC   uracil or another base, and amplifying at least one fragment of the
CC   chemically pretreated genomic DNA using sets of primer oligonucleotides
CC   and a polymerase. The method is useful for detecting the cytosine
CC   methylation state and/or single nucleotide polymorphisms in genomic DNA,
CC   particularly for characterising, classifying and/or differentiating renal
CC   and prostate cancers. The oligomers are useful as primer oligonucleotides
CC   for the amplification of any of the 112 DNA sequences of the invention.
CC   The set of oligomer probes is useful for detecting the cytosine
CC   methylation state and/or single nucleotide polymorphisms in any of the
CC   112 chemically pretreated genomic DNA sequences. The method is also
CC   useful for identifying the tissue of origin of cancer cells. The method
CC   allows the classification, differentiation and/or diagnosis of cancer
CC   tissues using minute samples which would be inadequate for histological
CC   or cytological analysis. The present sequence is used in the
CC   exemplification of the invention.
XX
SQ   Sequence 20 BP; 3 A; 9 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1535 AGGTTAGGAGAGTAGG 1550
                || ||||||||||||||
Db         19 AGATTAGGAGAGTAGG 4


RESULT 3899
AAL53963/c
ID   AAL53963 standard; DNA; 20 BP.
XX
AC   AAL53963;
XX
DT   18-FEB-2003  (first entry)
XX
DE   DNA mutation detection related oligo, SEQ ID No 13.
XX
KW   Detecting; point mutation; hybridising; target DNA; duplex; RNase H;
KW   single nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   US2002142308-A1.
XX
PD   03-OCT-2002.
XX
PF   30-MAR-2001; 2001US-00823634.
XX
PR   30-MAR-2001; 2001US-00823634.
XX
PA   (DATT/) DATTAGUPTA N.
PA   (TSEN/) TSENG T.
XX
PI   Dattagupta N,  Tseng T;
XX
DR   WPI; 2003-102506/09.
XX
PT   Detecting point mutation in DNA strand, by hybridizing target DNA strand
PT   having mutation with test DNA strand to form duplex, contacting the
PT   duplex with RNase H and determining the cleavage of test strand by RNase
PT   H.
XX
PS   Example 5; Fig 4; 26pp; English.
XX
CC   The invention relates to a novel method for detecting a point mutation in
CC   a DNA strand. The novel method comprises hybridising a target DNA strand
CC   containing or suspected of containing a point mutation with a test
CC   nucleic acid strand complementary to the DNA strand to form a target DNA
CC   strand/test nucleic acid strand duplex, contacting the duplex with an
CC   RNase H, and determining whether the ribonucleotide residues within the
CC   nucleotide sequence are cleaved by RNase H. The method is useful for
CC   detecting a point mutation in a DNA strand, where the point mutation to
CC   be detected is a single nucleotide polymorphism, preferably a
CC   polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian
CC   or human genome. The method is useful to detect any nucleic acids from
CC   any species of organisms such as Acintobacter, Bacillus, Candida,
CC   Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
CC   This polynucleotide sequence represents an oligo relating to the mutation
CC   detecting method of the invention
XX
SQ   Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2177 TTTTTTTTTTAACTTT 2192
                ||||||||| ||||||
Db         20 TTTTTTTTTAAACTTT 5


RESULT 3900
ADB89911/c
ID   ADB89911 standard; DNA; 20 BP.
XX
AC   ADB89911;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Antisense oligonucleotide targeting human C3 component, ISIS140013.
XX
KW   Human; ss; antisense; complement component C3; inflammation;
KW   septic shock; multiple organ failure; hyperacute organ failure;
KW   autoimmune disorder; CNS inflammation; multiple sclerosis;
KW   atherosclerosis; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone and all cytosines are 5
FT                   -methyl cytosines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
XX
PN   US2003096775-A1.
XX
PD   22-MAY-2003.
XX
PF   23-OCT-2001; 2001US-00001076.
XX
PR   23-OCT-2001; 2001US-00001076.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Graham MJ,  Watt AT;
XX
DR   WPI; 2003-606441/57.
XX
PT   New antisense oligonucleotides targeted to a nucleic acid molecule
PT   encoding complement component C3, useful for treating a disease or
PT   condition associated with complement component C3, e.g. autoimmune
PT   disorder or infection.
```

```
XX
PS   Claim 3; Page 26; 72pp; English.
XX
CC   The invention relates to a compound 8-50 nucleobases in length targeted
CC   to a nucleic acid molecule encoding complement component C3. The compound
CC   specifically hybridises with the nucleic acid molecule encoding
CC   complement component C3 and inhibits the expression of complement
CC   component C3, or specifically hybridises with at least an 8-nucleobase
CC   portion of an active site on a nucleic acid molecule encoding complement
CC   component C3. Also included are a composition comprising the compound and
CC   a pharmaceutical carrier or diluent, inhibiting the expression of
CC   complement component C3 in cells or tissues (comprising contacting the
CC   cells or tissues with the compound cited above) and treating an animal
CC   having a disease or condition associated with complement component C3
CC   comprising administering to the animal the compound cited above so that
CC   expression of complement component C3 is inhibited. The antisense
CC   compounds are useful for inhibiting the expression of complement
CC   component C3 in cells or tissues, or for treating an animal having a
CC   disease or condition associated with complement component C3 such as an
CC   autoimmune disorder (e.g. multiple sclerosis), an infection, or
CC   atherosclerosis, inflammation, septic shock, multiple organ failure,
CC   hyperacute organ failure and CNS inflammation. The compounds are also
CC   useful as research reagents and diagnostics, in distinguishing functions
CC   of various members of a biological pathway, or for preventing or delaying
CC   infection, inflammation or tumour formation. The present sequence is an
CC   antisense oligonucleotide targeting human C3.
XX
SQ   Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        358 CCAGCAGCTGGCCTAC 373
              ||||||||||||||| |
Db         17 CCAGCAGCTGGCCTTC 2


RESULT 3901
ADC66070
ID   ADC66070 standard; DNA; 20 BP.
XX
AC   ADC66070;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human CFTR sequencing primer #65.
XX
KW   typing; variable site; cystic fibrosis; human;
KW   cystic fibrosis transmembrane conductance regulator; CFTR; sequencing;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003074737-A1.
XX
PD   12-SEP-2003.
XX
PF   07-MAR-2003; 2003WO-SE000394.
XX
PR   07-MAR-2002; 2002SE-00000695.
XX
PA   (PYRO-) PYROSEQUENCING AB.
XX
PI   Schiller A,  Dunker J;
XX
DR   WPI; 2003-731684/69.
XX
PT   Typing at least two variable sites of at least one nucleic acid molecule
PT   related to cystic fibrosis by simultaneously or sequentially performing
PT   primer extension reactions and determining the pattern of nucleotide
PT   incorporation.
XX
PS   Claim 24; Page 22; 69pp; English.
XX
CC   The present invention describes a method for typing at least two variable
CC   sites of at least one nucleic acid molecule related to cystic fibrosis.
CC   The method comprises: (a) providing at least one nucleic acid molecule of
CC   a gene related to cystic fibrosis; (b) providing at least one extension
CC   primer, which binds to different predetermined sites in the nucleic acid
CC   molecules, where at least one extension primer is designed to extend over
CC   at least two potential variable sites in the nucleic acid molecule, and
CC   nucleotide; (c) simultaneously or sequentially performing primer
CC   extension reactions; and (d) determining the pattern of nucleotide
CC   incorporation to obtain a test pattern; optionally (e) comparing the test
CC   pattern of step (c) with one or more reference patterns, in order to type
CC   the variable sites of the nucleic acid molecules. Also described: (1)
CC   diagnosing the genetic predisposition of states, diseases and drug
CC   response related to the human cystic fibrosis transmembrane conductance
CC   regulator (CFTR) gene; and (2) a kit for use in the method for typing
CC   comprising at least one extension primer. The method is useful for typing
CC   at least two variable sites of at least one nucleic acid molecule related
CC   to cystic fibrosis. The present sequence represents a human CFTR
CC   sequencing primer, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 20 BP; 4 A; 1 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGATG 2279
              || |||||||||||||
Db          5 ATTTTTATTTCAGATG 20


RESULT 3902
ADC66069
ID   ADC66069 standard; DNA; 20 BP.
XX
AC   ADC66069;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human CFTR sequencing primer #64.
XX
KW   typing; variable site; cystic fibrosis; human;
KW   cystic fibrosis transmembrane conductance regulator; CFTR; sequencing;
KW   primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003074737-A1.
XX
PD   12-SEP-2003.
XX
PF   07-MAR-2003; 2003WO-SE000394.
XX
PR   07-MAR-2002; 2002SE-00000695.
XX
PA   (PYRO-) PYROSEQUENCING AB.
XX
PI   Schiller A,  Dunker J;
XX
DR   WPI; 2003-731684/69.
XX
PT   Typing at least two variable sites of at least one nucleic acid molecule
PT   related to cystic fibrosis by simultaneously or sequentially performing
PT   primer extension reactions and determining the pattern of nucleotide
PT   incorporation.
XX
PS   Claim 24; Page 22; 69pp; English.
XX
```

```
CC   The present invention describes a method for typing at least two variable
CC   sites of at least one nucleic acid molecule related to cystic fibrosis.
CC   The method comprises: (a) providing at least one nucleic acid molecule of
CC   a gene related to cystic fibrosis; (b) providing at least one extension
CC   primer, which binds to different predetermined sites in the nucleic acid
CC   molecules, where at least one extension primer is designed to extend over
CC   at least two potential variable sites in the nucleic acid molecule, and
CC   nucleotide; (c) simultaneously or sequentially performing primer
CC   extension reactions; and (d) determining the pattern of nucleotide
CC   incorporation to obtain a test pattern; optionally (e) comparing the test
CC   pattern of step (c) with one or more reference patterns, in order to type
CC   the variable sites of the nucleic acid molecules. Also described: (1)
CC   diagnosing the genetic predisposition of states, diseases and drug
CC   response related to the human cystic fibrosis transmembrane conductance
CC   regulator (CFTR) gene; and (2) a kit for use in the method for typing
CC   comprising at least one extension primer. The method is useful for typing
CC   at least two variable sites of at least one nucleic acid molecule related
CC   to cystic fibrosis. The present sequence represents a human CFTR
CC   sequencing primer, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 20 BP; 4 A; 1 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGATG 2279
                || ||||||||||||
Db          5 ATTTTTATTTCAGATG 20


RESULT 3903
ADD20414
ID   ADD20414 standard; DNA; 20 BP.
XX
AC   ADD20414;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Oreochromis niloticus microsatellite primer  SEQ ID NO:1049.
XX
KW   single nucleotide polymorphism; SNP; fish; Salmo salar;
KW   Orechromis niloticus; Atlantic halibut; microsatellite; cod;
KW   polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW   detection; primer; ss.
XX
OS   Synthetic.
OS   Oreochromis niloticus.
XX
PN   WO2003060160-A2.
XX
PD   24-JUL-2003.
XX
PF   17-JAN-2003; 2003WO-IB000112.
XX
PR   18-JAN-2002; 2002US-0349950P.
PR   16-AUG-2002; 2002US-0404200P.
XX
PA   (GENO-) GENOMAR ASA.
XX
PI   Lie O,  Slettan A,  Hoyum M,  Lingaas F;
XX
DR   WPI; 2003-627388/59.
XX
PT   Novel isolated nucleic acid molecule comprising single nucleotide
PT   polymorphism associated with fish, useful for forming PCR primers which
PT   are used for detecting single nucleotide polymorphisms in fish nucleic
PT   acids.
XX
PS   Claim 18; SEQ ID NO 1049; 233pp; English.
XX
CC   The present invention describes an isolated nucleic acid (I) comprising a
CC   single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
CC   Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
CC   and (ii) a nucleic acid having nucleotide sequence that hybridises to
CC   (i), or its complement under highly stringent hybridisation conditions.
CC   Also described: (1) an isolated oligonucleotide (II) comprising at least
CC   17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites, or their complement; (2)
CC   a primer pair (III) suitable for use in PCR, comprising two (II) capable
CC   of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
CC   niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
CC   polymorphic sites and seabass polymorphic sites; and determining (M1) the
CC   origin of fish sample comprising providing a parentage genotype database
CC   comprising a collection of candidate parent genotypes, where each of the
CC   candidate parent genotype represents a distinct origin, and comparing a
CC   sample genotype to the parentage genotype database, where a match between
CC   the sample genotype and one of the candidate parent genotype identifies
CC   to the origin of the sample. (M1) is useful for determining the origin of
CC   a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
CC   rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
CC   detecting nucleic acid molecule comprising SNP in a sample, which
CC   involves contacting the sample containing nucleic acids with one or more
CC   (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
CC   SNPs, and identifying nucleic acid that hybridises to (II). (II) is
CC   useful for detecting nucleic acid molecule comprising a polymorphic
CC   sequence in a sample, comprising contacting the sample containing nucleic
CC   acids with one or more (II) which is derived from O. niloticus
CC   microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
CC   sites or seabass polymorphic sites, and identifying a nucleic acid that
CC   hybridises to (II). (III) is useful for detecting nucleic acid molecule
CC   comprising a microsatellite sequence in sample. The present sequence is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1453 CCCTGGAGACCAGAGT 1468
                |||||||||  ||||||
Db          1 CCCTGGAGAACAGAGT 16


RESULT 3904
ADD81484
ID   ADD81484 standard; DNA; 20 BP.
XX
AC   ADD81484;
XX
DT   29-JAN-2004  (first entry)
XX
DE   HIV PRT antisense derived probe #413.
XX
KW   ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW   large array; minimum oligonucleotide synthesis; probe.
XX
OS   Human immunodeficiency virus.
XX
PN   US2003054346-A1.
XX
PD   20-MAR-2003.
XX
PF   15-FEB-2001; 2001US-00784674.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (SHAN/) SHANNON K W.
PA   (WOLB/) WOLBER P K.
PA   (DELE/) DELENSTARR G C.
PA   (WEBB/) WEBB P G.
PA   (KINC/) KINCAID R H.
XX
```

PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
DR WPI; 2003-743746/70.
XX
PT Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
PS Example 2; SEQ ID NO 557; 423pp; English.
XX
CC The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridise to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridise
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridise to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC HIV PRT antisense derived probe.
XX
SQ Sequence 20 BP; 3 A; 4 C; 0 G; 13 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAAC 2189
||||||| |||||||||
Db 2 TTTTTTCTTTTTTAAC 17

RESULT 3905
ADD81483
ID ADD81483 standard; DNA; 20 BP.
XX
AC ADD81483;
XX
DT 29-JAN-2004 (first entry)
XX
DE HIV PRT antisense derived probe #412.
XX
KW ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW large array; minimum oligonucleotide synthesis; probe.
XX
OS Human immunodeficiency virus.
XX
PN US2003054346-A1.
XX
PD 20-MAR-2003.
XX
PF 15-FEB-2001; 2001US-00784674.
XX
PR 10-FEB-1998; 98US-00021701.
XX
PA (SHAN/) SHANNON K W.
PA (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINC/) KINCAID R H.
XX
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
DR WPI; 2003-743746/70.
XX
PT Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
PS Example 2; SEQ ID NO 556; 423pp; English.
XX
CC The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridise to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridise
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridise to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC HIV PRT antisense derived probe.
XX
SQ Sequence 20 BP; 3 A; 4 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTAAC 2189
||||||| |||||||||
Db 3 TTTTTTCTTTTTTAAC 18

RESULT 3906
ADD81482
ID ADD81482 standard; DNA; 20 BP.
XX
AC ADD81482;
XX
DT 29-JAN-2004 (first entry)
XX
DE HIV PRT antisense derived probe #411.
XX
KW ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW large array; minimum oligonucleotide synthesis; probe.
XX
OS Human immunodeficiency virus.
XX
PN US2003054346-A1.
XX
PD 20-MAR-2003.
XX
PF 15-FEB-2001; 2001US-00784674.
XX
PR 10-FEB-1998; 98US-00021701.
XX
PA (SHAN/) SHANNON K W.
PA (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINC/) KINCAID R H.
XX
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
DR WPI; 2003-743746/70.
XX
PT Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX
PS Example 2; SEQ ID NO 555; 423pp; English.
XX
CC The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridise to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridise
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridise to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with

```
CC   minimum synthesis of oligonucleotides. The present sequence represents a
CC   HIV PRT antisense derived probe.
XX
SQ   Sequence 20 BP; 3 A; 3 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||  |||||||||
Db          4 TTTTTTCTTTTTTAAC 19


RESULT 3907
ADD81481
ID   ADD81481 standard; DNA; 20 BP.
XX
AC   ADD81481;
XX
DT   29-JAN-2004  (first entry)
XX
DE   HIV PRT antisense derived probe #410.
XX
KW   ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW   large array; minimum oligonucleotide synthesis; probe.
XX
OS   Human immunodeficiency virus.
XX
PN   US2003054346-A1.
XX
PD   20-MAR-2003.
XX
PF   15-FEB-2001; 2001US-00784674.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (SHAN/) SHANNON K W.
PA   (WOLB/) WOLBER P K.
PA   (DELE/) DELENSTARR G C.
PA   (WEBB/) WEBB P G.
PA   (KINC/) KINCAID R H.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2003-743746/70.
XX
PT   Predicting potential of oligonucleotides to hybridize to target
PT   nucleotide sequence comprises determining and evaluating for each
PT   oligonucleotide a parameter predictive of the oligonucleotides ability to
PT   hybridize with target.
XX
PS   Example 2; SEQ ID NO 554; 423pp; English.
XX
CC   The invention relates to a method of predicting the potential of
CC   oligonucleotides to hybridise to target nucleotide sequences. The method
CC   is useful for predicting the potential of an oligonucleotide to hybridise
CC   to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC   contains chemically modified nucleotides. The method is also useful for
CC   predicting the potential of the oligonucleotides to hybridise to a
CC   complementary target nucleotide sequence. The method is useful to predict
CC   efficient hybridisation oligonucleotides for each of multiple target
CC   sequences therefore very large arrays may be constructed and tested with
CC   minimum synthesis of oligonucleotides. The present sequence represents a
CC   HIV PRT antisense derived probe.
XX
SQ   Sequence 20 BP; 3 A; 3 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||  |||||||||
Db          5 TTTTTTCTTTTTTAAC 20


RESULT 3908
AAZ26619/c
ID   AAZ26619 standard; DNA; 21 BP.
XX
AC   AAZ26619;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 808.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 12 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAAC 2189
                ||||||||||||  |||
Db         21 TTTTTTTTTTTTCAAC 6
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```
RESULT 3909
AAT94317/c
ID   AAT94317 standard; DNA; 21 BP.
XX
AC   AAT94317;
XX
DT   04-MAR-1998  (first entry)
XX
DE   Human DPC4 sequence tagged site sense primer y899E8R.
XX
KW   DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;
KW   tumour suppressor gene; proliferative disease; bile duct; bladder;
KW   colorectal; cancer; Crohn's disease; colitis; PCR primer;
KW   sequence tagged site; STS; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9726271-A1.
XX
PD   24-JUL-1997.
XX
PF   17-JAN-1997;   97WO-US000827.
XX
PR   19-JAN-1996;   96US-00588821.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Kern SE,  Hahn SA;
XX
DR   WPI; 1997-385290/35.
XX
PT   Deleted in Pancreatic Cancer locus 4 polypeptide - and related nucleic
PT   acids, used in diagnosis and treatment of proliferative diseases, e.g.
PT   cancer of pancreas or other organs.
XX
PS   Example 2; Page 56; 104pp; English.
XX
CC   The present sequence represents a sequence tagged site (STS) primer used
CC   in the isolation of cosmids from the DPC4 (deleted in pancreatic cancer,
CC   locus 4) region, and gene identification. DPC4 is a tumour suppressor
CC   gene. Detection of truncated DPC4 protein, or of homozygous deletions or
CC   intragenic mutations in the nucleic acid encoding it, is used to diagnose
CC   (in vivo or in vitro) proliferative diseases, especially pancreatic
CC   carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease,
CC   colitis-associated neoplasia or chronic ulcerative colitis. These
CC   conditions, where associated with a homozygous deletion, can be treated
CC   by administering an agent that: (a) modulates DPC4 expression,
CC   specifically a sense DPC4 sequence (particularly in the form of a vector,
CC   i.e. by gene therapy), but also an antisense sequence where DPC4 protein
CC   is over expressed or (b) mimics the activity of DPC4. DPC4 nucleic acid
CC   is also used as hybridisation probes for detecting presence/absence of
CC   human chromosome 18q21.1 fragments. When a homozygous deletion is
CC   detected in this region, an agent can be administered that accumulates
CC   within, or kills, only cells which contain such a deletion. This agent
CC   exploits the absence of an enzyme (or other protein) encoded by a
CC   neighbouring gene and lost by the deletion, i.e. it has a highly
CC   selective action
XX
SQ   Sequence 21 BP; 3 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1483 CAAAACCCTGGAGAAA 1498
              |||||| |||||||||
Db         21 CAAAACTCTGGAGAAA 6


RESULT 3910
AAZ26572
ID   AAZ26572 standard; DNA; 21 BP.
XX
AC   AAZ26572;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 761.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 13 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAA 2797
              |||||| |||||||||
Db          6 ATTGAATAAAAAAAAA 21


RESULT 3911
AAA11454/c
ID   AAA11454 standard; DNA; 21 BP.
XX
AC   AAA11454;
XX
DT   30-JUN-2000  (first entry)
```

XX
DE Human dysferlin PCR primer #99.
XX
KW Dysferlin; anti-dystrophic; gene therapy; muscular dystrophy; human;
KW skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis;
KW limb girdle muscular dystrophy-2B; brain-specific; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200011157-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019395.
XX
PR 25-AUG-1998; 98US-0097927P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;
XX
DR WPI; 2000-237646/20.
XX
PT Novel dysferlin genes and related proteins useful for diagnosis, risk
PT identification and treatment of hereditary muscular dystrophies and other
PT dysferlin related disorders.
XX
PS Claim 8; Page 130; 146pp; English.
XX
CC This invention describes a novel human dysferlin nucleic acid (I) and its
CC encoding protein (II), which has anti-dystrophic activity and can be used
CC for gene therapy. Introduction of (I), a vector comprising (I) or
CC dysferlin into a cell of a mammal can be used to decrease the symptoms of
CC muscular dystrophy. The dysferlin gene is normally expressed in skeletal
CC muscle cells and is selectively mutated in several families with the
CC hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle
CC muscular dystrophy-2B. The primers and oligonucleotides derived from (I)
CC can be used in diagnosis of or risk identification for dysferlin-related
CC disorders in patients, fetus, or pre-embryos. Expression of brain-
CC specific dysferlin may be important as a marker for normal neural
CC development. Dysferlin DNA or subgenomic coding sequences can be used for
CC therapy of the hereditary muscular dystrophies. AAX82919-X82945 represent
CC PCR primers used in the method of the invention
XX
SQ Sequence 21 BP; 5 A; 2 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 543 CCCACCTCTCCGGGCT 558
||||||||||| ||||
Db 21 CCCACCTCTCCTGGCT 6

RESULT 3912
AAA36909/c
ID AAA36909 standard; DNA; 21 BP.
XX
AC AAA36909;
XX
DT 03-AUG-2000 (first entry)
XX
DE Human dysferlin exon amplification primer SEQ ID NO:171.
XX
KW Human; dysferlin; mutant; identification; chromosome 2p12-14; detection;
KW muscular dystrophy; diagnosis; hereditary muscular dystrophy;
KW miyoshi myopathy; limb girdle muscular dystrophy; primer; amplification;
KW screening; ss.
XX
OS Homo sapiens.
XX
PN WO200011016-A1.
XX
PD 02-MAR-2000.
XX
PF 25-AUG-1999; 99WO-US019394.
XX
PR 25-AUG-1998; 98US-0097930P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Brown RH, Liu J, Hoffman E, Chou F;
XX
DR WPI; 2000-246531/21.
XX
PT Dysferlin polynucleotide, its mutant form useful for diagnosis and
PT treatment of hereditary muscular dystrophies e.g. miyoshi myopathy and
PT limb girdle muscular dystrophy.
XX
PS Disclosure; Page 30; 136pp; English.
XX
CC The present invention describes an isolated dysferlin DNA of 20-25
CC nucleotides in length, comprising a nucleotide sequence specifically
CC selected from nucleotides 911-913, 929-948, 1019-1038, 1392-1411, 1424-
CC 1443, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759, 2241-2260,
CC 2864-2883, 2978-2997, 3057-3076, 3198-3217, 3252-3271, 4356-4375, 4665-
CC 4684, 5015-5034, 5610-5629, 5726-5735, 6035-6054, 6179-6198, 6243-6263
CC and 6529-6548 of the human dysferlin nucleotide sequence given in
CC AAA36744. Dysferlin nucleotide sequences containing specific mutations
CC can be used for diagnosing a patient, a foetus or a pre-embryo at risk of
CC developing a dysferlin associated disorder by detecting mutations in the
CC dysferlin gene in biological samples from patients. Alternatively, the
CC biological sample containing genomic DNA can be incubated with a
CC restriction enzyme, preferably BanII, Bsp1286I, RsaI, HhaI, HaeIII,
CC Bsp1286, NlaIV, NlaIII, BcgI, AvaII, BstEII, PleI, HaeI, AluI, ApoI,
CC Tsp509I, SalI, HincII, TaqI, HinfI, TfiI, SfaNI or FokI and the presence
CC or absence of a restriction enzyme site in the sample is detected as an
CC indication of the presence or absence of a particular mutation in the
CC sample. Dysferlin polynucleotides are useful for treating hereditary
CC muscular dystrophies such as miyoshi myopathy (MM) and limb girdle
CC muscular dystrophy-2B (LGMB-2B). MM and LGMB-2B map to the human
CC chromosome 2p12-14 region between the genetic markers D2S292 and D2S286.
CC The present sequence represents a primer for human dysferlin
XX
SQ Sequence 21 BP; 5 A; 2 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 543 CCCACCTCTCCGGGCT 558
||||||||||| ||||
Db 21 CCCACCTCTCCTGGCT 6

RESULT 3913
AAA30231/c
ID AAA30231 standard; DNA; 21 BP.
XX
AC AAA30231;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human housekeeping gene rack1 PCR primer #1.
XX
KW Human; chemokine; chemotaxis; chemokinesis; nutrition;
KW cell proliferation; cell differentiation; immunosuppressant;
KW immunostimulant; haematopoiesis regulation; tissue growth regulation;
KW anti-inflammatory; activin; inhibin; nervous system; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200029439-A1.
XX

```
PD   25-MAY-2000.
XX
PF   16-NOV-1999;   99WO-US027199.
XX
PR   16-NOV-1998;   98US-00193092.
XX
PA   (GEMY ) GENETICS INST INC.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Collins-Racie LA,  Lu Z,  Mi S;
PI   Kelleher K,  Carlin-Duckett M,  Dorf ME;
XX
DR   WPI; 2000-387745/33.
XX
PT   Treating nervous system conditions such as multiple sclerosis, Miller
PT   Fisher syndrome and Spongiform encephalopathy, comprises administering an
PT   inhibitor of endogenous non-ELR CXC chemokine-receptor interactions.
XX
PS   Disclosure; Page 25; 105pp; English.
XX
CC   The present sequence is a PCR primer for the gene for human rack1, which
CC   was used as a control when the expression of H174 and Mig in brain tissue
CC   were being measured. H174 is a member of the non-ELR group of the CXC-
CC   chemokine family, as are Mig and IP10. Two clones of the H174 gene were
CC   isolated by screening a peripheral blood mononuclear cell cDNA library
CC   for cDNAs encoding secreted proteins. IP10 was used in a sequence
CC   alignment with H174, along with Mig. The H174 gene, protein, its
CC   antibodies, agonists and antagonists are useful in diagnosing and
CC   treating the following diseases: AIDS-related dementia, multiple
CC   sclerosis, Miller Fisher syndrome, spongiform encephalopathy, viral
CC   encephalomyelitis, post-rabies-vaccine encaphalomyelitis, postinfectious
CC   encephalomyelitis, paraneoplastic neuronopathy, paraneoplastic cerebellar
CC   degeneration, acute inflammatory demyelinating polyradiculoneuropathy,
CC   Guillain-Barre syndrome, experimental auto-immune neuritis, acute
CC   inflammatory polyneuropathy, chronic inflammatory polyneuropathy, chronic
CC   inflammatory demyelinating polyneuropathy, chronic relapsing inflammatory
CC   polyneuropathy, the polyneuropathy associated with monoclonal gammopathy,
CC   IgM monoclonal anti-myelin-associated glycoprotein-associated
CC   demyelinating polyneuropathy, Lambert-Eaton myasthenic syndrome,
CC   myasthenia grave, multifocal motor neuropathy with or without GM1
CC   antibodies, inflammatory myopathy, stiff-man syndrome and autoimmune
CC   neuromyotonia. Suggested activities include nutritional activities,
CC   cytokine and cell proliferation/differentiation activity, immune
CC   stimulating or suppressing activity, haematopoiesis regulating activity,
CC   tissue growth activity, activin/inhibin activity, haemostatic and
CC   thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppression activity, tumour
CC   inhibition activity and chemotactic/chemokinetic activity
XX
SQ   Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        832 GGTCTTCTGCTCAGTC 847
              |||| ||||||||||||
Db         18 GGTCATCTGCTCAGTC 3


RESULT 3914
AAF95557
ID   AAF95557 standard; DNA; 21 BP.
XX
AC   AAF95557;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #318.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 71; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         27 TGACCCGGACAGCAAG 42
              || ||||||||||||
Db          6 TGCCCCGGACAGCAAG 21


RESULT 3915
AAF95571
ID   AAF95571 standard; DNA; 21 BP.
XX
AC   AAF95571;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #332.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   Variation       replace(11,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 72; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1460 GACCAGAGTCCAGCTG 1475
              | ||||||||||||||
Db          5 GCCCAGAGTCCAGCTG 20


RESULT 3916
AAF87033
ID   AAF87033 standard; DNA; 21 BP.
XX
AC   AAF87033;
XX
DT   18-SEP-2001  (first entry)
XX
DE   Anchored 3' oligo dT12 primer.
XX
KW   Sequencing primer; definitive ectoderm equivalent cell; DEE cell;
KW   cell preparation; early primitive ectoderm-like cell; EPL cell; human;
KW   cell therapy; gene therapy; neuroectoderm cell; organ transplant;
KW   neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW   stroke; spinal cord injury; therapy; ss.
XX
OS   Synthetic.
XX
PN   WO200151610-A1.
XX
PD   19-JUL-2001.
XX
PF   12-JAN-2001; 2001WO-AU000029.
XX
PR   14-JAN-2000; 2000AU-00005098.
PR   20-APR-2000; 2000AU-00007045.
PR   27-APR-2000; 2000AU-00007143.
XX
PA   (BRES-) BRESAGEN LTD.
PA   (LONG/) LONG C L O.
XX
PI   Long CLO,  Rathjen PD,  Rathjen J;
XX
DR   WPI; 2001-432907/46.
XX
PT   Preparing (M1) definitive ectoderm equivalent (DEE) cells in vitro for
PT   treatment of Parkinson's and Alzheimers comprises culturing early
PT   primitive ectoderm-like cells in conditioned medium.
XX
PS   Example; Page 37; 116pp; English.
XX
CC   This sequence represents a sequencing primer used within the scope of the
CC   invention. The invention relates to a method for preparing definitive
CC   ectoderm equivalent (DEE) cells in vitro comprising providing: (a) early
CC   primitive ectoderm-like (EPL) cells; and (b) a conditioned medium or
CC   extract exhibiting neural inducing properties and culturing the EPL cells
CC   for a time to permit controlled differentiation to DEE cells. The DEE
CC   cells, or their differentiated or partially differentiated progeny are
CC   useful in human cell therapy or transgenic animal production and for use
CC   in human or animal gene therapy. The method is useful for preparing DEE
CC   cells in vitro. It can also be used for selectively producing
CC   neuroectoderm cells or surface ectoderm cells from DEE cells. The method
CC   can also be used to produce genetically modified DEE cells. It is also
CC   useful for preparing tissues or organ for transplant. The cells are
CC   useful for treating and curing neurodegenerative diseases such as
CC   Parkinson's disease and Alzheimer's disease and pathological conditions
CC   such as stroke and spinal cord injury by replacing or assisting the
CC   function of normal disease tissues. They are also useful for the
CC   treatment of corneal disorders. The methods are useful for producing
CC   cells as a source for reprogramming and for use in pharmaceutical or
CC   toxicological screening
XX
SQ   Sequence 21 BP; 4 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTA 2187
              || ||||||||||||
Db          6 TTCTTTTTTTTTTTA 21


RESULT 3917
AAF80105/c
ID   AAF80105 standard; DNA; 21 BP.
XX
AC   AAF80105;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Nucleotide sequence of a polymorphism site in a target gene.
XX
KW   Gene inhibitor; cancer; allele specific inhibitor;
KW   proliferative disorder; ss.
XX
OS   Homo sapiens.
XX
PN   US6200754-B1.
XX
PD   13-MAR-2001.
XX
PF   19-MAR-1998;   98US-00045054.
XX
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PR   19-MAR-1998;   98US-00045054.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman DE,  Ledley FD,  Stanton VP;
XX
DR   WPI; 2001-256468/26.
XX
PT   Identifying inhibitor active on conditionally essential gene (EG) subject
PT   to loss of heterozygosity in cancer, useful in cancer treatment, involves
PT   determining two alleles of EG and testing potential allele specific
PT   inhibitor.
XX
PS   Disclosure; Fig 2; 43pp; English.
XX
CC   The specification describes a method for identifying inhibitors active on
CC   conditionally essential genes subject to loss of heterozygosity in
CC   cancer. The method involves determining two alleles of the essential
CC   gene, testing potential allele specific inhibitors to determine whether
CC   the inhibitor is active on at least one but less than all of alleles. The
CC   inhibitors suppress either the synthesis or the biological activity of
CC   the target allelic gene product. The inhibitors are useful for treating
CC   or preventing cancer or other proliferative disorders in a patient. They
CC   are also useful for inhibiting growth of a cell by subjecting the cell to
CC   conditions such that the gene is essential and administering an inhibitor
CC   active on an allele of the conditionally essential gene. Use of allele
CC   specific inhibitors allows specific killing or reduction of growth of
CC   cancer cells. AAF80072-AAF80115 represent the sequences around
CC   polymorphism sites of various target genes
XX
SQ   Sequence 21 BP; 14 A; 3 C; 1 G; 2 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||:|| | |||
Db         21 TTTTTTTTTYTTATGTTA 4


RESULT 3918
ABL57072
ID   ABL57072 standard; DNA; 21 BP.
XX
AC   ABL57072;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Molecular beacon target sequence (single mismatch).
XX
KW   Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    9
FT                   /*tag=  a
FT                   /note= "mismatch site"
XX
PN   WO200218951-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US041941.
XX
PR   29-AUG-2000; 2000US-0228728P.
PR   30-MAR-2001; 2001US-0280350P.
XX
PA   (UYRQ ) UNIV ROCKEFELLER.
XX
PI   Dubertret B,  Calame M,  Libchaber A;
XX
DR   WPI; 2002-404569/43.
XX
PT   Sensitively detecting proximity changes in a system that utilizes an
PT   interacting fluorophore and quencher, for high sensitivity applications,
PT   involves utilizing a metal surface as quencher.
XX
PS   Example 3; Page 62; 62pp; English.
XX
CC   The present sequence is that of a single mismatch target sequence for a
CC   molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC   covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC   a nanoparticle. In the native state, the probe forms a hairpin
CC   conformation with hybridised termini. The proximity of the fluorophore
CC   and quencher (gold nanoparticle) in the molecular beacon results in
CC   little or no detectable fluorescence. Upon hybridisation of the central
CC   complementary stretch of the probe to a target sequence, such as the
CC   present sequence, the hairpin undergoes a conformational change resulting
CC   in an increase in fluorescence, the extent of which is proportional to
CC   the amount of target sequence present. Experiments with the present
CC   sequence and a perfectly-matched target (see ABL57071) showed that
CC   hybridisation was very specific to the matched target. The invention
CC   relates generally to the use of metal surface quenchers such as particles
CC   or films for high sensitivity applications in, for example, detection and
CC   diagnostic systems
XX
SQ   Sequence 21 BP; 14 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2800
              |||||||| |||||||
Db          1 GAAAAAAACAAAAAAA 16


RESULT 3919
ABX11284
ID   ABX11284 standard; DNA; 21 BP.
XX
AC   ABX11284;
XX
DT   29-APR-2003  (first entry)
XX
DE   Mouse P0 gene 5' UTR PCR primer.
XX
KW   Mouse; ss; PCR; primer; P0; myelin structural protein; SCIP; Oct-6;
KW   Tst-1; transcription factor; peripheral nervous system; PNS;
KW   Schwann cell; nerve regeneration; transgenic; Alzheimer's disease;
KW   Pick's disease; Huntington's disease; Parkinson's disease;
KW   cerebral palsy; amyotrophic lateral sclerosis; ALS; muscular dystrophy;
KW   multiple sclerosis; myasthenia gravis; Binswanger's disease;
KW   vascular lesion; brain trauma; spinal chord trauma; cerebral haemorrhage;
KW   intracranial aneurysm; hypertensive encephalopathy; spina bifida;
KW   subarachanoid haemorrhage; developmental disorder;
KW   congenital hydrocephalus; neurodegenerative disorder.
XX
OS   Mus sp.
XX
PN   US2002146395-A1.
XX
PD   10-OCT-2002.
XX
PF   19-APR-1999;   99US-00294764.
XX
PR   19-APR-1999;   99US-00294764.
XX
PA   (WEIN/) WEINSTEIN D E.
XX
PI   Weinstein DE;
XX
DR   WPI; 2003-237963/23.
XX
```

```
PT   Regenerating nervous tissue, involves contacting the tissue with Schwann
PT   cells expressing DeltaSCIP to regenerate the nervous tissue.
XX
PS   Disclosure; Page 5; 21pp; English.
XX
CC   The invention relates to regenerating nervous tissue, involves contacting
CC   the tissue with Schwann cells expressing DeltaSCIP (a mutant form of the
CC   SCIP (not defined) gene under control of the P0 promoter (a myelin
CC   structural protein). SCIP is a transcription factor also known as Oct-6
CC   and Tst-1) to regenerate the nervous tissue. Also included are treating a
CC   subject in need of nervous tissue regeneration, by introducing Schwann
CC   cells expressing DeltaSCIP and inducing nervous tissue regeneration in a
CC   subject in need of such treatment, by administering to the subject,
CC   DeltaSCIP to induce nervous tissue regeneration in the subject. The
CC   methods are useful for useful for regenerating nervous tissue and for
CC   treating a subject in need of nervous tissue regeneration, where the
CC   subject in need of nervous tissue regeneration has a neurodegenerative
CC   disease. The neurodegenerative disease is Alzheimer's disease, Pick's
CC   disease, Huntington's disease, Parkinson's disease, cerebral palsy,
CC   amyotrophic lateral sclerosis (ALS), muscular dystrophy, multiple
CC   sclerosis, myasthenia gravis, or Binswanger's disease. The subject in
CC   need of nervous tissue regeneration has one or more damaged neurons. The
CC   damage to the neurons are caused by vascular lesions of the brain and
CC   spinal chord, trauma to the brain and spinal chord, cerebral haemorrhage,
CC   intracranial aneurysms, hypertensive encephalopathy, subarachanoid
CC   haemorrhage or developmental disorders. The developmental disorder is a
CC   disorder of the brain or spinal cord e.g. congenital hydrocephalus or
CC   spina bifida. The present sequence is a PCR primer used to genotype mice
CC   which are transgenic for the P0/deltaSCIP construct
XX
SQ   Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   93.8%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1576 TCTCCACCGCACAGAC 1591
              ||||||| |||||||
Db          6 TCTCCACCCCACAGAC 21


RESULT 3920
ABS58234/c
ID   ABS58234 standard; DNA; 21 BP.
XX
AC   ABS58234;
XX
DT   05-FEB-2003  (first entry)
XX
DE   Sequence surrounding polymorphism target 1539.21.
XX
KW   Cancer; ss; single nucleotide polymorphism; human; SNP; CEG; LOH;
KW   conditionally essential gene; alternative allele; loss of heterozygosity;
KW   antiproliferative treatment; glutamate-ammonia ligase; chromosome 1q31.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       11
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   US2002127714-A1.
XX
PD   12-SEP-2002.
XX
PF   14-FEB-2001; 2001US-00782837.
XX
PR   19-MAR-1998;   98US-00045054.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman DE,  Ledley FD,  Stanton VP;
XX
DR   WPI; 2003-066906/06.
XX
PT   Inhibitor for treating cancer, is active on allelic form of conditionally
PT   essential gene which has two alternative alleles in a population, and
PT   targets alternative alleles.
XX
PS   Disclosure; Fig 2; 47pp; English.
XX
CC   The invention relates to an inhibitor which is active on an allelic form
CC   of a conditionally essential gene (CEG) comprising at least two
CC   alternative alleles in a population, and where the inhibitor targets at
CC   least one but less than all of the alternative alleles. Also included
CC   are: (1) a method of identifying an inhibitor potentially useful for
CC   treatment of cancer, where the inhibitor is active on CEG, and where the
CC   gene is subject to loss of heterozygosity in a cancer, involves
CC   determining at least two alleles of the gene, testing potential allele
CC   specific inhibitor (AI) to determine whether potential AI is active on
CC   alleles; (2) identifying a potential patient for treatment with an
CC   inhibitor active on alleles of CEG, where the patient is suffering from
CC   cancer, involves: (a) identifying a patient heterozygous for the gene, or
CC   (b) determining whether cancer cells in the patient have undergone loss
CC   of heterozygosity (LOH) of the gene; (3) a nucleic acid probe of at least
CC   12 nucleotides in length which is perfectly complementary to a portion of
CC   a first allelic form of CEG (but not a second), where the portion
CC   comprises a sequence variance site; and (4) selecting a patient for
CC   treatment with an antiproliferative treatment, or selecting an
CC   antiproliferative treatment for a patient suffering from a cancer,
CC   involves determining whether normal somatic cells in a potential patient
CC   are heterozygous for an essential or CEG (which reduces the sensitivity
CC   of the cells to antiproliferative treatment), where a first allelic form
CC   of the gene is more active than a second allelic form, and determining
CC   whether cancer cells of the patient have only the second allelic form of
CC   the gene, where if the somatic cells are heterozygous and the cancer
CC   cells have only the second allelic form, it is indicative that the
CC   patient is suitable for treatment with the antiproliferative treatment or
CC   the antiproliferative treatment is suitable for the patient. The methods
CC   of the invention are useful for preventing development of cancer in a
CC   patient having a precancerous condition, for treating a patient suffering
CC   from a cancer, where the patient is heterozygous for CEG, for inhibiting
CC   growth of a cell (involves subjecting the cell to conditions such that
CC   the gene is essential, and administering at least one inhibitor active on
CC   an allele of CEG). The method inhibits proliferation or kills cells which
CC   have undergone LOH of genes that are not inhibited by the drug and
CC   contain only an allelic form of the essential gene, its RNA transcript,
CC   or its protein product against which the inhibitor is targeted, under the
CC   appropriate altered conditions, recognises more than one linked sequence
CC   variances within a specific allele, and discriminates between two allelic
CC   forms due to a particular single sequence variance between allelic forms
CC   of the target gene. The present sequence shows the sequence surrounding a
CC   polymorphism in an allele of the target gene, glutamate-ammonia ligase
CC   (chromosome 1q31)
XX
SQ   Sequence 21 BP; 14 A; 3 C; 1 G; 2 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.8e+03;
  Matches   15;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||:|| | |||
Db         21 TTTTTTTTTYTTATGTTA 4


RESULT 3921
ABQ80008
ID   ABQ80008 standard; RNA; 21 BP.
XX
AC   ABQ80008;
XX
DT   16-MAY-2003  (first entry)
XX
DE   SiRNA duplex antisense strand, dsRNA/a1 control.
```

```
XX
KW   T2-tryptophanyl-tRNA synthetase; T2-TrpRS; antagonist; neuropilin;
KW   VEGF-mediated activity; neuropilin-mediated disease; cancer; lung; colon;
KW   breast; prostate cancer; injury; nervous system; rheumatoid arthritis;
KW   vascular endothelial growth factor; developmental anomaly; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        3. .21
FT                   /*tag=  a
FT                   /note= "Forms ds region with 1-19 of ABQ80007"
XX
PN   WO2003009813-A2.
XX
PD   06-FEB-2003.
XX
PF   25-JUL-2002; 2002WO-US023868.
XX
PR   26-JUL-2001; 2001US-0307872P.
PR   07-FEB-2002; 2002US-0355551P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Liau G,  Ho D;
XX
DR   WPI; 2003-229618/22.
XX
PT   Treating a neuropilin-mediated disease in a mammal, e.g. cancer, injury
PT   to the nervous system, rheumatoid arthritis, or a developmental anomaly,
PT   comprises administering a T2-tryptophanyl-tRNA synthetase or its
PT   derivative.
XX
PS   Example 5; Page 32; 59pp; English.
XX
CC   The sequences given in ABQ80005-10 form siRNA duplexes which were used to
CC   interfere with suppression of NRP-1 expression. T2-tryptophanyl- tRNA
CC   synthetase (T2-TrpRS) was used in a method for identifying an antagonist
CC   to neuropilin. The method comprises designing molecules that are expected
CC   to bind to a neuropilin based on the chemistry and three-dimensional
CC   structure of neuropilin and the chemistry and three-dimensional structure
CC   of T2-TrpRS, contacting the molecules with neuropilin in an in vitro or
CC   cellular assay, and identifying which molecules bind to neuropilin. There
CC   is a specific interaction between T2-TrpRS and neuropilin and this
CC   binding inhibits VEGF-mediated activity. The method and T2-TrpRS or its
CC   derivative are useful for treating a neuropilin-mediated disease in a
CC   mammal, such as cancer (e.g. lung, colon, breast, or prostate cancer),
CC   injury to the nervous system, rheumatoid arthritis, or a developmental
CC   anomaly. The method is useful for identifying an antagonist to
CC   neuropilin. This duplex is targeted at the a1 region of human Nrp-1
XX
SQ   Sequence 21 BP; 4 A; 5 C; 7 G; 2 T; 3 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 21;
  Best Local Similarity   81.2%;  Pred. No. 3.8e+03;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1123 TGTCTGTGAAGCCGAA 1138
              || |:|:|||||||||
Db          2 TGGCUGUGAAGCCGAA 17


RESULT 3922
AAQ90036
ID   AAQ90036 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ90036;
XX
DT   03-JAN-1996  (first entry)
XX
DE   Human SMP30 gene PCR primer.
XX
KW   SMP30; marker protein; ageing; organ development; ss.
XX
OS   Homo sapiens.
XX
PN   JP07097399-A.
XX
PD   11-APR-1995.
XX
PF   29-SEP-1993;   93JP-00265681.
XX
PR   29-SEP-1993;   93JP-00265681.
XX
PA   (FJRE ) FUJI REBIO KK.
XX
DR   WPI; 1995-175363/23.
XX
PT   Novel polypeptide for detecting human ageing marker protein SMP30 - for
PT   monitoring liver and kidney development in new-born babies.
XX
PS   Example 2; Page 5; 10pp; Japanese.
XX
CC   AAQ90036-Q90039 are PCR primers used to produce the SMP30 gene
CC   (AAQ90035). which encodes the human ageing marker protein, SMP30
CC   (AAR74219). Human SMP30 is found in human organs, tissues, blood, urine
CC   and cerebrospinal fluid. The blood concentration of SMP30 is known to
CC   increase with renal and hepatic deficiencies and to decrease with age. It
CC   is therefore useful in the monitoring of renal or hepatic deficiencies
CC   and for the monitoring of the development of the liver and kidneys in
CC   newborn babies
XX
SQ   Sequence 22 BP; 1 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTT 2177
              | ||||||||||||||
Db          7 CCCCTTTTTTTTTTTT 22


RESULT 3923
AAQ82287/c
ID   AAQ82287 standard; DNA; 22 BP.
XX
AC   AAQ82287;
XX
DT   25-MAR-2003  (revised)
DT   07-SEP-1995  (first entry)
XX
DE   Chromosome 11 (locus D11S1129) STS primer cSRL-4d7-tA.
XX
KW   sequence sampled mapping; genomic analysis; complex genome mapping;
KW   cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS   Synthetic.
XX
PN   WO9429486-A1.
XX
PD   22-DEC-1994.
XX
PF   15-JUN-1994;   94WO-US006810.
XX
PR   15-JUN-1993;   93US-00078471.
PR   07-SEP-1993;   93US-00117952.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Evans GA,  Smith MW;
XX
DR   WPI; 1995-036508/05.
XX
PT   Sequencing complex genomes, present as fragments in a cosmid library - by
PT   sequencing end-specific nucleotides of each clone then correlating with
```

```
PT   spatial relationship of cosmid, esp. for mammalian chromosomes.
XX
PS   Example 4; Page 74; 128pp; English.
XX
CC   Sequences were determined from the ends of chromosome 11-specific cosmids
CC   by automated sequencing without intermediate subcloning. A sample of 371
CC   DNA sequence fragments were determined and of these, 277 were suitable
CC   for STS primer prediction by computer analysis (using the "Primer"
CC   program available from E.Lander, MIT). The STSs and cosmids were mapped
CC   by in situ hybridisation, somatic cell hybrid analysis or both. Using
CC   this method, 370 STSs specific for human chromosome 11 were generated and
CC   most of them were regionally mapped. This procedure illustrates a novel
CC   method for sequencing complex genomes, designated "sequence sampled
CC   mapping". The sequence sampled mapping method is useful for the
CC   completion of high density sequence-based maps, and ultimately, for the
CC   complete sequencing of genomic DNA directly from cosmid clones. See
CC   AAQ82001-Q82706 for STS primers. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 22 BP; 9 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2444 CTTTTTTGAGACATGG 2459
                ||||||||||||  ||
Db         21 CTTTTTTGAGACAGGG 6


RESULT 3924
AAT62686
ID   AAT62686 standard; DNA; 22 BP.
XX
AC   AAT62686;
XX
DT   28-MAY-1997  (first entry)
XX
DE   Primer for human senility marker protein gene amplification.
XX
KW   SMP30; senility marker protein; monoclonal antibody; detection; primer;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   JP08319298-A.
XX
PD   03-DEC-1996.
XX
PF   25-MAY-1995;   95JP-00149791.
XX
PR   25-MAY-1995;   95JP-00149791.
XX
PA   (FJRE ) FUJI REBIO KK.
XX
DR   WPI; 1997-073109/07.
XX
PT   Anti-human senility marker protein monoclonal antibody - useful for
PT   detection of protein.
XX
PS   Disclosure; Page 5; 8pp; Japanese.
XX
CC   AAT62686-89 are primers used to amplify the human senility marker protein
CC   (hSMP30) gene. hSMP30 (AAW14475) has a molecular weight of 30 kDa.
CC   Monoclonal antibodies recognising hSMP30 are claimed and can be used in a
CC   method for detection of the hSMP30 protein in a sample
XX
SQ   Sequence 22 BP; 1 A; 4 C; 5 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTT 2177
                | ||||||||||||||
Db          7 CCCCTTTTTTTTTTT 22


RESULT 3925
AAV51724/c
ID   AAV51724 standard; DNA; 22 BP.
XX
AC   AAV51724;
XX
DT   02-FEB-1999  (first entry)
XX
DE   Zea mays genome reverse PCR primer #20.
XX
KW   Polymorphic marker; allele-specific; probe; amplification; PCR primer;
KW   hybridisation; plant; hybrid certification; genetic contribution;
KW   progeny; back-cross; hybrid; ancestry; corn; ss.
XX
OS   Synthetic.
OS   Zea mays.
XX
PN   WO9824796-A1.
XX
PD   11-JUN-1998.
XX
PF   01-DEC-1997;   97WO-US021782.
XX
PR   02-DEC-1996;   96US-0032069P.
PR   07-MAR-1997;   97US-00813507.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Lemieux B,  Landry BS,  Sapolsky RJ,  Murigneux A;
XX
DR   WPI; 1998-333252/29.
XX
PT   Brassica species allele-specific oligonucleotide probes and primers -
PT   useful for plant breeding.
XX
PS   Example 1; Page 50; 65pp; English.
XX
CC   AAV51705-V52008 are reverse PCR primers used to amplify fragments of the
CC   Zea mays genome in order to detect polymorphic markers. Such markers can
CC   be used in the construction of allele-specific primers and probes for
CC   amplification or hybridisation, e.g. to determine common or disparate
CC   ancestry between 2 or more plants, to monitor the genetic contribution of
CC   an ancestral plant, to trace the progeny of proprietary plants, in
CC   certification of a hybrid plant or to identify the progeny of a back-
CC   crossed plant with an ancestral plant
XX
SQ   Sequence 22 BP; 10 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1916 AATACCTTTTTTTTCA 1931
                ||||||||||||  |||
Db         19 AATACCTTTTTTGTCA 4


RESULT 3926
AAA72031
ID   AAA72031 standard; DNA; 22 BP.
XX
AC   AAA72031;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human cathepsin Y PCR primer Y3.
XX
KW   Human cathepsin Y; cysteine protease; EST; expressed sequence tag;
```

KW monoclonal antibody; drug screening; Alzheimer's disease; pneumonectasis;
KW rheumatoid arthritis; myodystrophy; osteoporosis;
KW neurodegenerative disease; cancer; invasion; metastasis;
KW chromosome 11q13; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000157263-A.
XX
PD 13-JUN-2000.
XX
PF 26-NOV-1998; 98JP-00352110.
XX
PR 26-NOV-1998; 98JP-00352110.
XX
PA (FUJY) FUJI PHARM IND CO LTD.
XX
DR WPI; 2000-468198/41.
XX
PT New human cathepsin Y protein, a gene encoding it and its application.
XX
PS Example 2; Page 31; 48pp; Japanese.
XX
CC The invention relates to human cathepsin Y (AAB11960) and to nucleic
CC acids encoding it. The cDNA (AAA72028) encoding cathepsin Y was derived
CC from ESTs (expressed sequence tags). The gene encoding cathepsin Y is
CC located on chromosome 11q13. Cathepsin Y, like other cathepsins, has
CC cysteine protease activity. The invention also relates to vectors and
CC transformants comprising human cathepsin Y nucleic acid sequences, anti-
CC cathepsin Y antibodies (particularly monoclonal antibodies), and methods
CC and kits for screening potential modulators of cathepsin Y activity.
CC Cathepsin Y, fragments thereof, cathepsin Y nucleotides and cathepsin Y
CC antibodies can be used to study the mechanisms by which various diseases
CC develop. Diseases which may be studied include Alzheimer's disease,
CC pneumonectasis, rheumatoid arthritis, myodystrophy, osteoporosis,
CC neurodegenerative diseases and invasion and metastasis of cancers.
CC Cathepsin Y antibodies and hybridisation probes may also be used for the
CC detection and diagnosis of cancer. Sequences AAA72031-A72032 represent
CC PCR primers used in an exemplification of the invention to amplify human
CC cathepsin Y cDNA
XX
SQ Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 918 TGTCCCCACCTGAATG 933
|| ||||||||||||||
Db 2 TGGCCCCACCTGAATG 17

RESULT 3927
ABS52173/c
ID ABS52173 standard; DNA; 22 BP.
XX
AC ABS52173;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human forward primer Ag781.
XX
KW Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis;
KW cell signal processing; metabolic pathway modulation; metabolic disorder;
KW obesity; diabetes; infectious disease; neurodegenerative disorder; acne;
KW Alzheimer's disease; Parkinson's disease; immune disorder; cancer;
KW haematopoietic disorder; cirrhosis; pancreatitis; learning defect;
KW memory defect; infertility; congenital heart defect; hair growth;
KW pigmentation disorder; endocrine disorder; respiratory disease; health;
KW gastro-intestinal disease; reproductive; neurological disease;
KW bone marrow transplantation; endocrine disease; allergy; inflammation;
KW nephrological disorder; urinary system disorder; age-related disorder;
KW neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4;
KW adipocyte complement-related C1q tumour necrosis factor; out at first;
KW beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter;
KW type 1a membrane sushi-containing domain; butyrophilin;
KW type 1a membrane-sushi domain containing; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200257453-A2.
XX
PD 25-JUL-2002.
XX
PF 19-DEC-2001; 2001WO-US050331.
XX
PR 19-DEC-2000; 2000US-0256704P.
PR 20-DEC-2000; 2000US-0257314P.
PR 02-MAY-2001; 2001US-0288153P.
PR 29-MAY-2001; 2001US-0294075P.
PR 24-JUL-2001; 2001US-0307506P.
PR 10-AUG-2001; 2001US-0311590P.
PR 10-AUG-2001; 2001US-0311613P.
PR 29-AUG-2001; 2001US-0315617P.
PR 14-SEP-2001; 2001US-0322358P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Gangolli EA, Patturajan M, Vernet CAM, Malyankar UM, Kekuda R;
PI Stone DJ, Anderson D, Shimkets RA, Burgess CE, Zerhusen BD, Liu X;
PI Spytek KA, Casman SJ, Boldog FL, Smithson G, Li L, Ji W;
XX
DR WPI; 2002-590744/63.
XX
PT Novel isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease or
PT cancer.
XX
PS Example 2; Page 259; 318pp; English.
XX
CC The present invention relates to new NOVX polypeptides. The invention is
CC useful for treating or preventing a NOVX-associated disorder such as
CC cardiomyopathy or atherosclerosis, where the disorder is related to cell
CC signal processing and metabolic pathway modulation in a subject,
CC preferably human. The invention is also useful for treating metabolic
CC disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative
CC disorders (e.g. Alzheimer's disease, Parkinson's disease), immune
CC disorders, haematopoietic disorders and various cancers. The molecules of
CC the invention are also useful for treating or preventing cirrhosis,
CC pancreatitis, learning and memory defects, infertility, congenital heart
CC defects, acne, hair growth, pigmentation disorders, endocrine disorders,
CC respiratory disease, gastro-intestinal diseases, reproductive, health,
CC neurological diseases, bone marrow transplantation, endocrine diseases,
CC allergy and inflammation, nephrological disorders, urinary system
CC disorders, neuropsychiatric disorders and age-related disorders. The
CC present nucleic acid sequence represents a PCR primer that was used in
CC the methods of the invention to amplify NOVX proteins
XX
SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 360 AGCAGCTGGCCTACTC 375
|||||||| |||||||
Db 18 AGCAGCTGACCTACTC 3

RESULT 3928
ABV73127
ID ABV73127 standard; DNA; 22 BP.
XX
AC ABV73127;
XX

DT 08-JAN-2003 (first entry)
XX
DE N-acetyltransferase NAT1*14 allele specific primer.
XX
KW Immunosuppressive; genotyping; N-acetyltransferase; NAT1; allele; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200273205-A2.
XX
PD 19-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-CA000360.
XX
PR 14-MAR-2001; 2001US-0275489P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2002-740823/80.
XX
PT Characterizing a metabolic phenotype for an immunosuppressant agent,
PT comprises administering a probe substrate specific to a metabolic pathway
PT of the determinant and detecting metabolites of the pathway.
XX
PS Disclosure; Page 79; 225pp; English.
XX
CC The invention relates to characterising a multi-determinant metabolic
CC phenotype (P) for an immunosuppressant agent. The method involves: (a)
CC administering to an individual a probe substrate specific to a metabolic
CC pathway for an immunosuppressant agent; (b) detecting metabolites of MPs
CC in a biological sample from the individual; and (c) characterizing
CC respective phenotypic determinants of (P). The method is useful for
CC characterizing a multi-determinant metabolic phenotype for an
CC immunosuppressant agent such as cyclosporine, Tacrolimus (RTM),
CC Sirolimus, Prednisone, Cellcept (RTM) and OKT3. (P) can be used to
CC individualize a treatment regimen for an immunosuppressant agent for an
CC individual, by determining (P) of the individual using the method, and
CC determining/selecting a safe and therapeutically effective dose of the
CC immunosuppressant agent for treatment based on (P) of the individual. A
CC new method of genotyping individuals to identify those lacking an allelic
CC variation known to prompt toxicity of the immunosuppressant agent, and
CC characterizing (P) of the identified individual to determine each
CC individual's ability to metabolize the immunosuppressant agent is also
CC provided. This is useful for identifying those individuals at high risk
CC for serious adverse events. The present sequence represents an allele-
CC specific primer used for genotyping the N-acetyltransferase (NAT1) gene,
CC by amplifying NAT1*14 allele
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
||||||| ||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3929
ABV74921
ID ABV74921 standard; DNA; 22 BP.
XX
AC ABV74921;
XX
DT 22-JAN-2003 (first entry)
XX
DE NAT1*14 allele specific primer.
XX
KW Naphthalidimide; anticancer; amonafide; phenotype; drug development;
KW N-acetyltransferase; NAT1; allele; genotyping; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200271060-A2.
XX
PD 12-SEP-2002.
XX
PF 28-FEB-2002; 2002WO-CA000256.
XX
PR 28-FEB-2001; 2001US-0271714P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2002-740767/80.
XX
PT Characterizing multi-determinant metabolic phenotypes of N-(aryl
PT substituted)-naphthalidimide compounds, useful for individualizing
PT therapy with amonafide, comprises determining metabolic phenotype from
PT detected metabolites.
XX
PS Disclosure; Page 89; 351pp; English.
XX
CC The invention relates to characterizing a multi-determinant metabolic
CC phenotype for a class of N-(aryl substituted)-naphthalidimide compounds
CC (I) (the phenotypic determinants correspond to respective metabolic
CC characteristics). The method involves (a) administering to an individual
CC a probe substrate specific to metabolic pathway(s) of (I); (b) detecting
CC metabolites of the pathway in a biological sample in response to the
CC probe substrate; and (c) characterizing the determinants of the metabolic
CC phenotype based on detected metabolites. The method is useful for the
CC individualization of treatment with the anticancer drug, amonafide, on
CC the basis of a phenotypic profile of an individual. It may also be used
CC in research and in the development of new drugs. The present sequence
CC represents an allele specific PCR primer for amplifying the NAT1*14
CC allele, used in NAT1 genotyping
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
||||||| ||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3930
ABQ78653/c
ID ABQ78653 standard; DNA; 22 BP.
XX
AC ABQ78653;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer R1.
XX
KW Human; cell growth; inhibitor; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN JP2002186484-A.
XX
PD 02-JUL-2002.
XX
PF 20-DEC-2000; 2000JP-00387898.
XX
PR 20-DEC-2000; 2000JP-00387898.
XX
PA (OSAU) UNIV OSAKA.

```
PA   (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
DR   WPI; 2002-603278/65.
XX
PT   A cell-growth inhibiting gene, a protein inhibiting cell growth, a DNA, a
PT   recombinant vector, a transformed cell, an antibody, gene inspection.
XX
PS   Example 11; Page 14; 34pp; Japanese.
XX
CC   The specification describes a human protein which inhibits cell growth.
CC   The polynucleotide sequence is used as a source of probes and primers,
CC   which are used to examine homologous genes. PCR primers ABQ78651-55 were
CC   used in the course of the invention
XX
SQ   Sequence 22 BP; 6 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2411 TGGGGTCTGTAAATAC 2426
                ||| ||||||||||||
Db         17 TGGAGTCTGTAAATAC 2


RESULT 3931
ABA00253
ID   ABA00253 standard; DNA; 22 BP.
XX
AC   ABA00253;
XX
DT   29-NOV-2002  (first entry)
XX
DE   NAT1 A560G mutation detection primer #4.
XX
KW   Primer; PCR; amplify; multi-determinant; metabolic phenotype;
KW   phenotypic determinant; probe substrate; metabolic pathway; drug therapy;
KW   fast metabolism; inhibitor; ss.
XX
OS   Homo sapiens.
XX
PN   WO200264816-A2.
XX
PD   22-AUG-2002.
XX
PF   08-FEB-2002; 2002WO-CA000161.
XX
PR   09-FEB-2001; 2001US-0267472P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Leyland-Jones B;
XX
DR   WPI; 2002-667012/71.
XX
PT   Characterizing metabolic phenotype based on phenotypic determinants, by
PT   administering a probe substrate specific to a metabolic pathway of the
PT   determinant and detecting metabolites of pathway in response to
PT   substrate.
XX
PS   Disclosure; Page 78; 268pp; English.
XX
CC   The sequences given in ABA00250-87 are primers which were used in the
CC   method of the invention for characterizing multi-determinant metabolic
CC   phenotype based on a number of phenotypic determinants (PDs). The method
CC   comprises administering to an individual a probe substrate (PS) specific
CC   to a metabolic pathway (MP) of each of the PDs, detecting metabolites of
CC   MPs in a biological sample from the individual in response to PS, and
CC   characterizing respective PDs of metabolic phenotypes based on detected
CC   metabolites. This primer is used in the determination of the N-acetyl
CC   transferase (NAT1) alleles NAT1*4 (wt) and the mutant NAT1*14 (A560G).
CC   The first PCR reaction produces a 175 bp fragment which when incubated
CC   with BsaI is cleaved in the presence of NAT1*4, but NAT1*14 is uncleaved.
CC   The NAT1*14 allele is confirmed using the second PCR reaction. Knowledge
CC   of the metabolic phenotype is useful for determining a combination drug
CC   therapy where an individual's phenotype is indicative of a fast
CC   metabolizer, and a corresponding inhibitor is selected for combined
CC   treatment with a drug to improve the therapeutic effect in the
CC   individual. The method of the invention is useful for diagnosing a
CC   disease or condition associated with altered function in a drug
CC   metabolizing enzyme. It is also useful for selecting a treatment for an
CC   individual corresponding to the individual's metabolic phenotype and for
CC   screening a number of individuals for participation in a drug treatment
CC   trial assessing the therapeutic effect of a candidate drug treatment
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||||  |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3932
AAD54260
ID   AAD54260 standard; DNA; 22 BP.
XX
AC   AAD54260;
XX
DT   17-JUN-2003  (first entry)
XX
DE   NAT1 mutant allele (NAT1*14) amplifying primer.
XX
KW   Hyperlipidaemia agent; therapy; N-acetyltransferase; NAT; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200295402-A2.
XX
PD   28-NOV-2002.
XX
PF   17-APR-2002; 2002WO-CA000526.
XX
PR   18-APR-2001; 2001US-0284210P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Leyland-Jones B;
XX
DR   WPI; 2003-120822/11.
XX
PT   Characterizing a multi-determinant metabolic phenotype for a
PT   hyperlipidemia agent, comprises administering a probe substrate specific
PT   to a metabolic pathway for an agent and detecting metabolites of the
PT   pathway.
XX
PS   Disclosure; Page 94; 245pp; English.
XX
CC   The invention relates to a method for characterising a multi-determinant
CC   metabolic phenotype for an hyperlipidaemia agent. The method involves
CC   administering a probe substrate specific to a metabolic pathway for an
CC   agent and detecting metabolites of the pathway. The method is useful for
CC   screening a number of individuals for participation in a drug treatment
CC   trial assessing the therapeutic effect of the hyperlipidaemia agent. The
CC   invention is also useful for treating an individual having a condition
CC   treatable with hyperlipidemia agent. The present sequence is a primer
CC   used to amplify N-acetyltransferase (NAT) mutant allele. This primer is
CC   used to illustrate the method of the invention
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
```

```
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||||  |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3933
ABZ75815
ID   ABZ75815 standard; DNA; 22 BP.
XX
AC   ABZ75815;
XX
DT   15-MAY-2003  (first entry)
XX
DE   NAT1 allele NAT1*14 genotyping primer.
XX
KW   Genotyping; therapy; drug dosing; CYP3A4; CYP2D6; NAT1; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003008637-A2.
XX
PD   30-JAN-2003.
XX
PF   17-JUL-2002; 2002WO-CA001103.
XX
PR   17-JUL-2001; 2001US-0305630P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Leyland-Jones B;
XX
DR   WPI; 2003-239358/23.
XX
PT   Use of genotyping for the individualization of therapy and/or treatment,
PT   and the individual is genotype for a specific metabolic factor and a
PT   corresponding genotypic determinant is characterized.
XX
PS   Disclosure; Page 35; 147pp; English.
XX
CC   The invention relates to the use of genotyping for the individualization
CC   of therapy and/or treatment, where an individual is genotype for a
CC   specific metabolic factor and a corresponding genotypic determinant is
CC   characterized. The method is useful for the individualization of therapy
CC   and/or treatment, for quantifying an individualized dosage regime of a
CC   drug, and to identify an individual having a metabolic incompatibility
CC   with a selected therapy and/or treatment. The method is useful for the
CC   individualization of drug dosing, to identify individuals having a
CC   particular allelic variation known to influence the ability to
CC   effectively metabolize a given drug or class of drugs, to characterize a
CC   metabolic determinant and identify an individualized dosage for a given
CC   drug treatment regime, and for identifying those individuals who is at
CC   risk for a particular drug treatment regime. The method quickly and
CC   accurately determines phenotypic determinants for the CYP3A4 or CYP2D6
CC   metabolic pathway. Sequences ABZ75813-815 represent PCR primers for
CC   genotyping the NAT1 determinants
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||||  |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3934
AAD50983
ID   AAD50983 standard; DNA; 22 BP.
XX
AC   AAD50983;
XX
DT   02-APR-2003  (first entry)
XX
DE   NAT1 allele specific PCR primer #3.
XX
KW   Antibiotic agent; therapy; research development; drug development; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   WO200293162-A2.
XX
PD   21-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-CA000725.
XX
PR   17-MAY-2001; 2001US-0291336P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Leyland-Jones B;
XX
DR   WPI; 2003-112080/10.
XX
PT   Characterization of a multi-determinant metabolic phenotype for at least
PT   one antibiotic agent for treating an individual having a condition
PT   treatable with at least one antibiotic agent.
XX
PS   Disclosure; Col 266; 270pp; English.
XX
CC   The invention relates to a method of characterisation of a multi-
CC   determinant metabolic phenotype for at least one antibiotic agent. The
CC   method involves administering a probe substrate specific to metabolic
CC   pathways for antibiotic agents; detecting metabolites of the metabolic
CC   pathways in response to the probe substrate and characterising respective
CC   phenotypic determinants of the metabolic phenotype based on detected
CC   metabolites. The method is used for characterisation of multi-determinant
CC   metabolic phenotype for at least one antibiotic agent, useful for
CC   treating an individual having a condition treatable with at least one
CC   antibiotic agent with individualisation of the treatment and for
CC   selecting an individual treatment regime. The invention is useful in
CC   research and drug development. The present sequence is NAT1 (N-
CC   acetyltransferase) 1 allele specific PCR primer, used to illustrate the
CC   method of the invention
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||||  |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3935
ABZ20529
ID   ABZ20529 standard; DNA; 22 BP.
XX
AC   ABZ20529;
XX
DT   03-MAR-2003  (first entry)
XX
DE   Human NAT1 genotyping PCR primer #1.
XX
KW   Antiarrhythmic; individualisation of therapy; phenotype; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200284288-A2.
```

XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-CA000525.
XX
PR 18-APR-2001; 2001US-0284191P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-093044/08.
XX
PT Characterization of a multi-determinant metabolic phenotype for at least
PT one antiarrhythmic agent for treating an individual having a condition
PT treatable with at least one antiarrhythmic agent.
XX
PS Disclosure; Page 226; 231pp; English.
XX
CC The present invention relates to the characterisation of a multi-
CC determinant metabolic phenotype. This comprises: (a) administering to an
CC individual a probe substrate specific to metabolic pathway(s) for
CC antiarrhythmic agent(s); (b) detecting metabolites of the metabolic
CC pathway(s) in response to the probe substrate; and (c) characterising
CC respective phenotypic determinants of the multi-determinant metabolic
CC phenotype based on detected metabolites. This useful for treating an
CC individual having a condition treatable with at least one antiarrhythmic
CC agent with individualisation of the treatment and for selecting an
CC individual treatment regime. The present sequence is a PCR primer used to
CC identify an individual's metabolic phenotype
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
||||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3936
ABZ23147
ID ABZ23147 standard; DNA; 22 BP.
XX
AC ABZ23147;
XX
DT 24-MAR-2003 (first entry)
XX
DE PCR primer used to amplify a 175 bp fragment of the human NAT1 gene.
XX
KW N-acetyltransferase-1; NAT2; metabolic phenotype; Alzheimer's disease;
KW acetylcholinesterase inhibitor; nicotinic compound;
KW gamma secretase inhibitor; M2 antagonist; donezepil; CYP2C9; CYP2C19;
KW drug metabolizing enzyme; NAT1; CYP1A2; CYP2D6; CYP2A6; CYP2E1; CYP3A4;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200299422-A2.
XX
PD 12-DEC-2002.
XX
PF 06-JUN-2002; 2002WO-CA000838.
XX
PR 06-JUN-2001; 2001US-0295860P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-148687/14.
XX
PT Characterizing multi-determinant metabolic phenotype for Alzheimer's
PT disease agent, involves administering probe substrate specific to
PT metabolic pathway of agent and detecting metabolites in response to
PT substrate.
XX
PS Disclosure; Page 91; 251pp; English.
XX
CC PCR primers ABZ23145-47 were used to amplify a 175 bp fragment of the
CC human N-acetyltransferase-1 (NAT1) gene. Restriction analysis of the
CC amplified fragment allowed the identification of the mutant and wild type
CC alleles. Drugs which are affected by the NAT1 pathway are used to treat
CC Alzheimer's disease. The specification describes a method for
CC characterizing the multi-determinant metabolic phenotype for at least one
CC Alzheimer's disease agent. The method comprises administering a probe
CC substrate specific to metabolic pathway(s) for the Alzheimer's disease
CC agent, detecting metabolites of the pathway(s) in a sample in response to
CC the substrate and characterizing phenotypic determinants of the metabolic
CC phenotype based on detected metabolites. The method is useful for
CC characterizing a multi-determinant metabolic phenotype for at least one
CC Alzheimer's disease agent such as acetylcholinesterase inhibitor,
CC nicotinic compound, gamma secretase inhibitor and M2 antagonist,
CC especially donezepil. The multi-determinant metabolic phenotype is
CC comprised of at least one determinant indicative of an individual's
CC metabolic capacity for at least one drug metabolizing enzyme, such as N-
CC acetyltransferase-1 (NAT1), NAT2, CYP1A2, CYP2D6, CYP2A6, CYP2E1, CYP2C9,
CC CYP2C19, UGTs, GSTs, and STs, preferably CYP3A4. The method is useful to
CC individualize a treatment regimen for at least one Alzheimer's disease
CC agent
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
||||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3937
ABV72580
ID ABV72580 standard; DNA; 22 BP.
XX
AC ABV72580;
XX
DT 12-FEB-2003 (first entry)
XX
DE Primer used to determine N-acetyltransferase 1 A560G mutation.
XX
KW Metabolic phenotype; antidepressant; metabolic pathway;
KW tricyclic antidepressant; serotonin reuptake inhibitor;
KW monoamine oxidase inhibitor; psychostimulant; N-acetyltransferase 1;
KW NAT1; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200273197-A2.
XX
PD 19-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-CA000361.
XX
PR 14-MAR-2001; 2001US-0275490P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-058322/05.
XX
PT Characterizing a metabolic phenotype for an antidepressant agent,

PT comprises administering a probe substrate specific to a metabolic pathway
PT of a determinant and detecting metabolites of the pathway.
XX
PS Disclosure; Page 82; 225pp; English.
XX
CC The specification describes a method for characterizing a multi-
CC determinant metabolic phenotype for an antidepressant agent. The method
CC comprises administering to an individual a probe substrate specific to a
CC metabolic pathway for an antidepressant agent; detecting metabolites of
CC the metabolic pathway in a sample from the individual in response to the
CC probe substrate; and characterizing respective phenotypic determinants of
CC the phenotype based on detected metabolites. The method is useful for
CC characterizing a multi-determinant metabolic phenotype for an
CC antidepressant agent such as tricyclic antidepressants, selective
CC serotonin reuptake inhibitors, monoamine oxidase inhibitors,
CC psychostimulants and atypical (or nontricyclic) antidepressants. The
CC present PCR primer (ABV72578) was used to determine the presence of the N
CC -acetyltransferase 1 (NAT1) allele NAT1*14, comprising the A560G
CC mutation. The primers were used in the method of the invention for
CC indirect phenotyping (genotyping) of NAT1
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTAAATACATT 1843
|||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3938
AAL53876
ID AAL53876 standard; DNA; 22 BP.
XX
AC AAL53876;
XX
DT 18-FEB-2003 (first entry)
XX
DE Gastroesophageal reflux disease agent therapy related PCR primer #5.
XX
KW H2-receptor antagonist; proton pump inhibitor; N-acetyltransferase-1;
KW gastroesophageal reflux disease; multi-determinant metabolic phenotype;
KW GERD agent; metabolic pathway; NAT-1; drug metabolising enzyme; PCR;
KW primer; ss.
XX
OS Unidentified.
XX
PN WO200286504-A2.
XX
PD 31-OCT-2002.
XX
PF 24-APR-2002; 2002WO-CA000607.
XX
PR 24-APR-2001; 2001US-0285687P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-075640/07.
XX
PT Characterizing multi-determinant metabolic phenotype for gastroesophageal
PT reflux disease agent, by administering probe substrate specific to
PT metabolic pathway of agent and detecting metabolites in response to
PT substrate.
XX
PS Disclosure; Page 89; 241pp; English.
XX
CC The invention relates to characterising method for a multi-determinant
CC metabolic phenotype for a gastroesophageal reflux disease (GERD) agent.
CC The method involves administering to a subject a probe substrate specific
CC to metabolic pathway(s) for a GERD agent and detecting metabolites of the
CC pathway(s) in a sample from the subject in response to the substrate. The
CC method is useful for characterising a multi-determinant metabolic
CC phenotype for at least one GERD agent such as H_2-receptor antagonists,
CC promotility agents and proton pump inhibitors. The multi-determinant
CC metabolic phenotype is comprised of at least one determinant indicative
CC of an individual's metabolic capacity for at least one drug metabolising
CC enzyme, such as N-acetyltransferase-1 (NAT-1), NAT-2, CYP1A2, CYP2D6,
CC CYP2A6, CYP2E1, CYP2C9, CYP2C19, UGTs, GSTs, and STs, preferably CYP3A4.
CC The characterising method is useful to individualise a treatment regimen
CC for at least one GERD agent for an individual. This polynucleotide
CC sequence represents a PCR primer used in the characterising method of the
CC invention
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTAAATACATT 1843
|||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3939
AAD51919
ID AAD51919 standard; DNA; 22 BP.
XX
AC AAD51919;
XX
DT 02-MAY-2003 (first entry)
XX
DE N-acetyl transferase (NAT)1 allele specific PCR primer #3.
XX
KW Antineoplastic agent; PCR; primer; N-acetyl transferase; NAT; ss.
XX
OS Unidentified.
XX
PN WO200288714-A2.
XX
PD 07-NOV-2002.
XX
PF 29-APR-2002; 2002WO-CA000642.
XX
PR 30-APR-2001; 2001US-0287014P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-140176/13.
XX
PT Characterizing metabolic phenotype for antineoplastic agent, based on
PT phenotypic determinants, by administering probe substrate specific to
PT metabolic pathway of determinant and detecting metabolites of pathway.
XX
PS Disclosure; Page 247; 251pp; English.
XX
CC The invention relates to a method of characterizing a multi-determinant
CC metabolic phenotype for an antineoplastic agent. The method involves
CC administering to an individual a probe substrate specific to a metabolic
CC pathway for an antineoplastic agent, detecting metabolites of metabolic
CC pathway in a biological sample from the individual in response to probe
CC substrate, and characterising respective phenotypic determinants of
CC metabolic phenotype based on detected metabolites. The method is useful
CC for characterising a multi-determinant metabolic phenotype for an
CC antineoplastic agent such as taxanes, estrogen antagonists, camptothecin
CC derivatives, anthracyclines, alkylating agents, podophyllotoxins, vinca
CC alkaloids, receptor tyrosine kinase inhibitors, nitrosureas, platinum
CC analogues and antimetabolites. The present sequence is N-acetyl
CC transferase (NAT)1 allele specific PCR primer used to illustrate the
CC method of the invention

```
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3940
ABZ23435
ID   ABZ23435 standard; DNA; 22 BP.
XX
AC   ABZ23435;
XX
DT   07-APR-2003  (first entry)
XX
DE   Primer used to amplify a fragment of N-acetyltransferase-1 DNA.
XX
KW   Metabolic phenotype; erectile dysfunction; phosphodiesterase 5 inhibitor;
KW   sildenafil Viagra; drug metabolizing enzyme; N-acetyltransferase-1;
KW   NAT-1; NAT-2; cytochrome P450; CYP1A2; CYP2D6; CYP2A6; CYP2E1; CYP2C9;
KW   CYP2C19; UDP-glucuronosyltransferase; glutathione-S-transferase;
KW   stromelysin; CYP3A4; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200288753-A1.
XX
PD   07-NOV-2002.
XX
PF   25-APR-2002; 2002WO-CA000586.
XX
PR   26-APR-2001; 2001US-0286336P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Leyland-Jones B;
XX
DR   WPI; 2003-175049/17.
XX
PT   Characterizing a multi-determinant metabolic phenotype for an erectile
PT   dysfunction agent, comprises administering a probe substrate to the
PT   metabolic pathway of the agent and detecting metabolites in response to
PT   the substrate.
XX
PS   Disclosure; Page 89; 247pp; English.
XX
CC   The specification describes a method for characterizing a multi-
CC   determinant metabolic phenotype for a erectile dysfunction (ED) agent.
CC   The method comprises administering to a subject a probe substrate
CC   specific to the metabolic pathway(s) for an ED agent; detecting
CC   metabolites of the pathway(s) in a sample from the subject in response to
CC   the substrate; and characterizing respective phenotypic determinants of
CC   the multi-determinant metabolic phenotype. The method is useful for
CC   characterizing a multi-determinant metabolic phenotype for an ED agent
CC   such as a phosphodiesterase 5 (PDE5) inhibitor, in particular sildenafil
CC   Viagra (RTM). The multi-determinant metabolic phenotype is comprised of a
CC   determinant indicative of an individual's metabolic capacity for a drug
CC   metabolizing enzyme, such as N-acetyltransferase-1 (NAT-1), NAT-2,
CC   cytochrome P450 (CYP)1A2, CYP2D6, CYP2A6, CYP2E1, CYP2C9, CYP2C19, UDP-
CC   glucuronosyltransferase (UGT)s, glutathione-S-transferase (GST)s, and
CC   stromelysin (ST)s, preferably CYP3A4. PCR primers ABZ23433-35 were used
CC   to amplify fragments of the NAT-1 gene. The amplified fragment was
CC   analysed by restriction analysis to identify the wild type and mutant
CC   alleles. The primers were used for indirect phenotyping (genotyping) of
CC   NAT-1, in the course of the invention
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
              |||||| |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3941
AAD54568
ID   AAD54568 standard; DNA; 22 BP.
XX
AC   AAD54568;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human M2-PK gene amplifying reverse PCR primer, MPKB5.
XX
KW   Chronic liver disease; pyruvate kinase; diagnosis; cancer; primer; PCR;
KW   L-PK; M2-PK; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO2002103035-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-AU000785.
XX
PR   14-JUN-2001; 2001AU-00005684.
XX
PA   (UYWA-) UNIV WESTERN AUSTRALIA.
XX
PI   Benson DM,  Lowes KN,  Olynyk JK,  Yeoh GCT;
XX
DR   WPI; 2003-167533/16.
XX
PT   Diagnosing, monitoring or assessing chronic liver disease, involves
PT   measuring the ratio of pyruvate kinase isoforms such as M2-PK to L-PK in
PT   a sample obtained from a subject, and comparing the ratio with a
PT   standard.
XX
PS   Claim 19; Page 11; 53pp; English.
XX
CC   The invention relates to a method of diagnosing, monitoring or assessing
CC   chronic liver disease. The method involves measuring the ratio of
CC   pyruvate kinase (PK) isoforms such as M2-PK to L-PK in a sample obtained
CC   from a subject and comparing the ratio with a standard. The method is
CC   useful for diagnosing and monitoring the severity of precancerous changes
CC   in liver disease, for assessing the risk of developing cancer in an
CC   individual subject having chronic liver disease, or for monitoring the
CC   onset of metastatic cancer in the liver. The present sequence is a PCR
CC   primer used to amplify human M2-PK gene
XX
SQ   Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2724 GTTCCCCAAATAATTG 2739
              ||||| ||||||||||
Db          7 GTTCCTCAAATAATTG 22


RESULT 3942
AAD47697
ID   AAD47697 standard; DNA; 22 BP.
XX
AC   AAD47697;
XX
DT   24-FEB-2003  (first entry)
```

XX
DE N-acetyltransfersse gene (NAT) 1 allele specific PCR primer #3.
XX
KW Therapy; antipsychotic; phenothiazine; dibenzodiazepine; dihydroindole;
KW piperazine; thioxanthene; benzisoxazole; phenylindole; butyrophenone;
KW N-acetyltransfersse; NAT; PCR; primer; ss.
XX
OS Unidentified.
XX
PN WO200273206-A2.
XX
PD 19-SEP-2002.
XX
PF 14-MAR-2002; 2002WO-CA000362.
XX
PR 14-MAR-2001; 2001US-0275493P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-018748/01.
XX
PT Characterizing a metabolic phenotype for an antipsychotic agent,
PT comprises administering a probe substrate specific to a metabolic pathway
PT of a determinant and detecting metabolites of the pathway.
XX
PS Disclosure; Page 87; 233pp; English.
XX
CC The invention relates to the individualisation of therapy on the basis of
CC a phenotypic profile of an individual. The method is useful for
CC characterising a multi-determinant metabolic phenotype for an
CC antipsychotic agent such as phenothiazines/piperazines, thioxanthene,
CC dibenzodiazepines, dibenzoxazepines, dihydroindoles, benzisoxazoles,
CC phenylindoles or butyrophenones. It is useful to individualise a
CC treatment regimen for an antipsychotic agent for an individual. It is
CC useful for identifying those individuals at high risk for serious adverse
CC events. The present sequence is a PCR primer specific for N-
CC acetyltransfersse gene (NAT) 1 allele. This sequence is used to
CC illustrate the method of the invention
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
|||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3943
ABV76236
ID ABV76236 standard; DNA; 22 BP.
XX
AC ABV76236;
XX
DT 28-MAR-2003 (first entry)
XX
DE N-acetyltransferase NAT1 PCR primer used for genotyping.
XX
KW N-acetyltransferase; enzyme; NAT1; human; genotyping; phenotyping;
KW analgesic; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200290994-A2.
XX
PD 14-NOV-2002.
XX
PF 07-MAY-2002; 2002WO-CA000687.
XX
PR 07-MAY-2001; 2001US-0288786P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-129192/12.
XX
PT Characterizing metabolic phenotype for analgesic, based on phenotypic
PT determinants, by administering probe substrate specific to metabolic
PT pathway of determinant and detecting metabolites of pathway.
XX
PS Disclosure; Page 96; 246pp; English.
XX
CC The present sequence is a primer used with the primer given in ABV76234
CC in an allele-specific PCR to confirm the NAT1*14 allele of an N-
CC acetyltransferase (NAT1) gene. Studies have demonstrated the presence of
CC one wild-type allele and 6 mutant alleles of NAT1. NAT1 metabolizes
CC several drugs (including the antimalarial dapsone) and dietary
CC constituents, and activates some environmental procarcinogens. It has 2
CC phenotypes: slow and rapid acetylators. The present invention relates to
CC the individualization of therapy, especially of treatment with
CC analgesics, on the basis of a phenotyping profile of an individual. In
CC the case of NAT1, an example of indirect phenotyping (genotyping)
CC involves the PCR amplification of a 175 bp fragment which includes an
CC A560G mutation, using the present primer and the primer given in
CC ABV76235. The 175 bp fragment is incubated with BsaI. The wild-type
CC allele produces fragments of 155 and 20 bp, whereas mutant allele NAT1*14
CC is uncleaved
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
|||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3944
ACF05573
ID ACF05573 standard; DNA; 22 BP.
XX
AC ACF05573;
XX
DT 06-NOV-2003 (first entry)
XX
DE N-acetyltransferase-1 PCR primer.
XX
KW N-acetyltransferase-1; NAT1; drug metabolism; metabolic phenotype; human;
KW enzyme; genotyping; antihistamine; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003052123-A1.
XX
PD 26-JUN-2003.
XX
PF 18-DEC-2002; 2002WO-CA001962.
XX
PR 19-DEC-2001; 2001US-0340827P.
XX
PA (XANT-) XANTHUS LIFE SCI INC.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-618024/58.
XX
PT Characterizing multi-determinant metabolic phenotype for an
PT antihistamine, by administering a probe substrate specific to metabolic
PT pathway of the antihistamine and detecting metabolites in response to

PT substrate.
XX
PS Disclosure; Page 84; 237pp; English.
XX
CC The present sequence is a primer for the PCR amplification of the N-
CC acetyltransferase (NAT1) gene. NAT1 activity varies broadly in a given
CC population. The NAT1*4 genotype is associated with slow drug metabolizers
CC and is found at a frequency of 50%, 30% and 35% in Indian, Malaysian and
CC Chinese populations, respectively. The NAT1*4 (wild-type) and the mutant
CC NAT1*14 alleles can be determined by PCR-RFLP of a fragment of the gene
CC containing an A560G mutation. PCR is performed with the primers fiven in
CC ACF05571 and ACF05572. The 175 bp product is incubated with BsaI. The
CC Nat1*1 allele produces 155 and 20 bp fragments, while the mutant NAT1*14
CC is uncleaved. The NAT1*14 allele is confirmed using the present primer
CC with the primer given in ACF05571. The present invention provides a
CC method for using multi-determinant phenotyping for the individualization
CC of treatment with an antihistamine, especially where the multi-
CC determinant phenotype is comprised of a determinant indicative of an
CC individual's metabolic capacity for a drug metabolizing enzyme such as
CC NAT1. The method involves administering a probe substrate specific to the
CC metabolic pathway of the antihistamine and detecting metabolites in
CC response to the substrate
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
|||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3945
ACC79724
ID ACC79724 standard; DNA; 22 BP.
XX
AC ACC79724;
XX
DT 28-AUG-2003 (first entry)
XX
DE N-acetyltransferase 1 mutation related PCR primer SEQ ID NO:5.
XX
KW Characterisation; multi-determinant metabolic phenotype; antiviral;
KW metabolic pathway; metabolite; detection; virucide; NAT1;
KW N-acetyltransferase 1; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003046559-A2.
XX
PD 05-JUN-2003.
XX
PF 27-NOV-2002; 2002WO-CA001824.
XX
PR 28-NOV-2001; 2001US-0333500P.
XX
PA (XANT-) XANTHUS LIFE SCI INC.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-493450/46.
XX
PT Characterizing multi-determinant metabolic phenotype for an antiviral
PT agent, by administering a probe substrate specific to metabolic pathway
PT of the antiviral agent and detecting metabolites in response to
PT substrate.
XX
PS Disclosure; Page 88; 256pp; English.
XX
CC The present invention describes a method (M1) for characterising the
CC multi-determinant metabolic phenotype (MP) for at least one antiviral
CC agent (I), which involves administering to a subject, a probe substrate
CC specific to metabolic pathway(s) for (I), detecting metabolites of the
CC pathway(s) in a sample from the subject in response to the substrate, and
CC characterising respective phenotypic determinants of MP based on detected
CC metabolites. (I) has virucide activity. (M1) is useful for characterising
CC a multi-determinant metabolic phenotype for at least one antiviral agent
CC such as nucleoside analogue reverse transcriptase inhibitor (NRT1), non-
CC nucleoside reverse transcriptase inhibitor (NNRT1), a protease inhibitor
CC (PI), an immune response modifier, preferably ritonavir. The multi-
CC determinant metabolic phenotype is comprised of at least one determinant
CC indicative of an individual's metabolic capacity for at least one drug
CC metabolising enzyme, such as CYP3A4, or chosen from N-acetyltransferase-1
CC (NAT-1), NAT-2, CYP1A2, CYP2D6, CYP2A6, CYP3A4, CYP2C9, CYP2C19, UGTs,
CC GSTs and STs. (M1) is useful to individualise a treatment regimen for at
CC least one antiviral agent compound for an individual. The method quickly
CC and accurately determines phenotypic determinants for the metabolic
CC pathways of drug metabolising enzymes, and avoids the severe side effects
CC and frustration that accompany trial and error treatment. The present
CC sequence represents a PCR primer for amplifying a NAT-1 mutant, which is
CC used in the exemplification of the present invention
XX
SQ Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1828 ATCTTTTAAATACATT 1843
|||||| |||||||||
Db 5 ATCTTTAAAATACATT 20

RESULT 3946
ACC83560
ID ACC83560 standard; DNA; 22 BP.
XX
AC ACC83560;
XX
DT 08-SEP-2003 (first entry)
XX
DE N-acetyltransferase-1 PCR primer.
XX
KW N-acetyltransferase; NAT1; drug metabolism; metabolic phenotype; human;
KW anaesthetic; genotyping; enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003046583-A2.
XX
PD 05-JUN-2003.
XX
PF 27-NOV-2002; 2002WO-CA001823.
XX
PR 28-NOV-2001; 2001US-0333486P.
XX
PA (XANT-) XANTHUS LIFE SCI INC.
XX
PI Leyland-Jones B;
XX
DR WPI; 2003-482556/45.
XX
PT Characterizing multi-determinant metabolic phenotype for an anesthetic,
PT by administering a probe substrate specific to metabolic pathway of the
PT anesthetic and detecting metabolites in response to substrate.
XX
PS Disclosure; Page 90; 239pp; English.
XX
CC The present sequence is a primer for the PCR amplification of the N-
CC acetyltransferase (NAT1) gene. NAT1 activity varies broadly in a given
CC population. The NAT1*4 genotype is associated with slow drug metabolizers
CC and is found at a frequency of 50%, 30% and 35% in Indian, Malaysian and
CC Chinese populations, respectively. The NAT1*4 (wild-type) and the mutant

```
CC   NAT1*14 alleles can be determined by PCR-RFLP of a fragment of the gene
CC   containing an A560G mutation. PCR is performed with the primers given in
CC   ACC83558 and ACC83559. The 175 bp product is incubated with BsaI. The
CC   Nat1*1 allele produces 155 and 20 bp fragments, while the mutant NAT1*14
CC   is uncleaved. The NAT1*14 allele is confirmed using the present primer
CC   with the primer given in ACC83558. The present invention provides a
CC   method for using multi-determinant phenotyping for the individualization
CC   of treatment with an anaesthetic, especially where the multi-determinant
CC   phenotype is comprised of a determinant indicative of an individual's
CC   metabolic capacity for a drug metabolizing enzyme such as NAT1. The
CC   method involves administering a probe substrate specific to the metabolic
CC   pathway of the anaesthetic and detecting metabolites in response to the
CC   substrate
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||||  |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3947
ACF04612
ID   ACF04612 standard; DNA; 22 BP.
XX
AC   ACF04612;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human NAT1 NAT1*14 allele coding sequence PCR primer #1.
XX
KW   Individualisation of therapy; phenotype; metabolic phenotyping;
KW   anxiolytic agent; metabolism; therapy; PCR; primer; anxiolytic; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003067257-A1.
XX
PD   14-AUG-2003.
XX
PF   08-OCT-2002; 2002WO-CA001512.
XX
PR   08-FEB-2002; 2002US-00072611.
PR   14-MAR-2002; 2002US-00100272.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Leyland-Jones B;
XX
DR   WPI; 2003-767277/72.
XX
PT   Characterization of a multi-determinant metabolic phenotype for at least
PT   one anxiolytic compound for treating an individual having a condition
PT   treatable with at least one anxiolytic compound.
XX
PS   Disclosure; Page 225; 117pp; English.
XX
CC   The present invention relates to a method of characterising a multi-
CC   determinant metabolic phenotype for at least one anxiolytic compound,
CC   which involves administering to an individual a probe substrate specific
CC   to metabolic pathway(s) for anxiolytic compound(s), detecting metabolites
CC   of the metabolic pathway(s) in response to the probe substrate and
CC   characterising respective phenotypic determinants of multi-determinant
CC   metabolic phenotype based on the detected metabolites. The method can be
CC   used for the characterization of a multi-determinant metabolic phenotype
CC   for at least one anxiolytic compound, useful for treating an individual
CC   having a condition treatable with at least one anxiolytic compound with
CC   individualisation of the treatment and for selecting an individual
CC   treatment regime. The present sequence is a PCR primer used in the
CC   exemplification of the invention
XX
SQ   Sequence 22 BP; 7 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 22;
  Best Local Similarity   93.8%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1828 ATCTTTTAAATACATT 1843
                ||||||  |||||||||
Db          5 ATCTTTAAAATACATT 20


RESULT 3948
ABA05517/c
ID   ABA05517 standard; DNA; 24 BP.
XX
AC   ABA05517;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Human Tre carcinogenic gene protein 10.56 PCR primer 2.
XX
KW   Human; Tre carcinogenic gene protein 10.56; cytostatic; haemostatic;
KW   virucide; immunomodulatory; antiinflammatory; gene therapy; cancer;
KW   haemopathy; human immunodeficiency virus; HIV; infection;
KW   immunological disease; inflammatory disorder; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200190131-A1.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-CN000833.
XX
PR   24-MAY-2000; 2000CN-00115824.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-083078/11.
XX
PT   Human tre carcinogenic gene protein 10.56 and encoding polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 2; Page 17; 36pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of human tre
CC   carcinogenic gene protein 10.56 comprising a 96 residue amino acid
CC   sequence, fully defined in the specification, or its fragment, analogue
CC   or derivative. The polypeptide is useful in the diagnosis and treatment
CC   of malignant tumours, haemopathy, human immunodeficiency virus (HIV)
CC   infection, immunological diseases and various inflammatory disorders. The
CC   present sequence is a primer used to amplify a polynucleotide encoding
CC   the polypeptide of the invention
XX
SQ   Sequence 24 BP; 0 A; 3 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 24;
  Best Local Similarity   75.0%;  Pred. No. 4.5e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                 ||   ||| ||| ||| |||||||
Db         24 AAAAAAAAGAAAGAAAGAAAAAAA 1


RESULT 3949
ABA99264/c
```

```
ID   ABA99264 standard; DNA; 24 BP.
XX
AC   ABA99264;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human tra oncogene 10-56 RT-PCR primer 2.
XX
KW   Oncogene; tra oncogene 10.56; human; treatment; gene therapy; cytostatic;
KW   haemostatic; virucide; immunomodulatory; antiinflammatory; diagnosis;
KW   malignant tumour; haemopathy; human immunodeficiency virus;
KW   HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200200824-A2.
XX
PD   03-JAN-2002.
XX
PF   11-JUN-2001; 2001WO-CN000936.
XX
PR   12-JUN-2000; 2000CN-00116436.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-075668/10.
XX
PT   human tre oncogene 10.56 and encoding polynucleotide, used in diagnosis
PT   and treatment of malignant tumors, hemopathy, human immunodeficiency
PT   virus infection, immunological diseases and inflammation.
XX
PS   Example 2; Page 12; 32pp; Chinese.
XX
CC   This invention describes a novel human tre oncogene 10.56 which has
CC   cytostatic, haemostatic, virucide, immunomodulatory and antiinflammatory
CC   activity and can be used for gene therapy. The polypeptide of the
CC   invention and its encoding polynucleotide are used in diagnosis and
CC   treatment of malignant tumours, haemopathy, human immunodeficiency virus
CC   (HIV) infection, immunological diseases and various inflammations. This
CC   sequence represents an RT-PCR primer used in the amplification of the
CC   human tre oncogene 10.56 gene which is described in the disclosure of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 3 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 24;
  Best Local Similarity   75.0%;  Pred. No. 4.5e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||| ||| ||| |||||||
Db         24 AAAAAAAAGAAAGAAAGAAAAAAA 1


RESULT 3950
ABZ57032
ID   ABZ57032 standard; DNA; 24 BP.
XX
AC   ABZ57032;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Human kinesin light chain 14.74 RT-PCR primer, SEQ ID NO:3.
XX
KW   Human; kinesin light chain 14.74; recombinant production; gene therapy;
KW   diabetes; hyperthyroidism; arrhythmia; tumour; cancer; infection;
KW   cardiant; cytostatic; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1364772-A.
XX
PD   21-AUG-2002.
XX
PF   10-JAN-2001; 2001CN-00105134.
XX
PR   10-JAN-2001; 2001CN-00105134.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-000484/01.
XX
PT   New human kinesin light chain 14.74 polypeptide and its encoding
PT   polynucleotide, useful in the treatment of cancer and diabetes.
XX
PS   Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to human kinesin light chain 14.74 (ABP58652) and
CC   nucleic acids encoding it (ABZ57031). The protein has a molecular weight
CC   of 15 kD. The invention also relates to a method for the recombinant
CC   production of the protein, an antagonist of the protein, and the use of
CC   the protein, gene and antagonist in therapeutic applications. Kinesin
CC   light chain 14.74 can be used in the treatment of a variety of diseases
CC   such as diabetes, hyperthyroidism, arrhythmia, tumours and infections.
CC   Sequences ABZ57032-ABZ57033 represent reverse transcription-PCR (RT-PCR)
CC   primers used in an exemplification of the invention to isolate human
CC   kinesin light chain 14.74 cDNA
XX
SQ   Sequence 24 BP; 1 A; 5 C; 17 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 24;
  Best Local Similarity   75.0%;  Pred. No. 4.5e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         49 GCGCGGCGGGGGCGGCGGCAGACG 72
              | | ||||  |||||||||| || |
Db          1 GGGGGGCGCTGGCGGCGGCGGAGG 24


RESULT 3951
ADE86193/c
ID   ADE86193 standard; DNA; 24 BP.
XX
AC   ADE86193;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Ret gene chair quadruplex DNA.
XX
KW   quadruplex DNA; gene therapy; cancer; cytostatic; RET; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003087317-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010658.
XX
PR   05-APR-2002; 2002US-0370358P.
PR   20-AUG-2002; 2002US-0404966P.
PR   20-MAR-2003; 2003US-0456637P.
XX
PA   (CYTE-) CYTERNEX INC.
PA   (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI   Siddiqui-Jain A,  Grand CL,  Bearss DJ,  Hurley LH,  Farrell TJ;
XX
DR   WPI; 2003-853947/79.
XX
PT   Identifying a compound that modulates the biological activity of a native
PT   quadruplex DNA for treating colorectal cancer comprises determining the
```

PT presence or absence of interaction between the candidate compound and the
PT test quadruplex DNA.
XX
PS Disclosure; Fig 8A; 69pp; English.
XX
CC The present sequence is that of a quadruplex structure-forming DNA
CC sequence from the nuclease hypersensitivity element (NHE) in the
CC regulatory regions of the human RET gene. Certain mutations in quadruplex
CC forming nucleotides sequences have been shown to destabilise quadruplex
CC structure and are associated with cancer. Methods are provided for
CC identifying quadruplex nucleotide sequences having destabilising guanine
CC substitutions, for determining whether a subject is at risk of developing
CC or having cancer, pharmacogenomic methods for targeting appropriate
CC prevention or therapeutic regiments, methods for screening molecules that
CC interact with stabilised and destabilised quadruplexes, and therapeutic
CC methods for treating cancers, such as antisense nucleic acid cancer
CC therapy that specifically targets DNA in subjects having a quadruplex-
CC destabilising mutation.
XX
SQ Sequence 24 BP; 1 A; 4 C; 19 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 280 CCTCTACAGCCCCGCGCCACCCCT 303
|| | | ||||||| || |||||
Db 24 CCGCCCCCGCCCCGCCCCGCCCCT 1

RESULT 3952
AAC95684/c
ID AAC95684 standard; DNA; 25 BP.
XX
AC AAC95684;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #19.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 38; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 3 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
||| | || ||||||||||||
Db 24 TGTACCAGTTACAAAAAAAAAAAA 1

RESULT 3953
AAC96504/c
ID AAC96504 standard; DNA; 25 BP.
XX
AC AAC96504;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #56.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 52; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 4 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 4.6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
||| | | ||||||||||||||
Db 24 TGTCTGGTTACAAAAAAAAAAAAA 1

RESULT 3954
AAC96321/c
ID AAC96321 standard; DNA; 25 BP.
XX

```
AC   AAC96321;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #53.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 49; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 3 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
                ||||   | ||  ||||||||||||
Db         24 TGTACCAGTTACAAAAAAAAAAAA 1


RESULT 3955
AAC95753/c
ID   AAC95753 standard; DNA; 25 BP.
XX
AC   AAC95753;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQB1 gene PCR primer #24.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 39; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 5 A; 4 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 25;
  Best Local Similarity   75.0%;  Pred. No. 4.6e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
                ||||   | ||  ||||||||||||
Db         24 TGTCTGGTTACAAAAAAAAAAAAA 1


RESULT 3956
ADD41445
ID   ADD41445 standard; DNA; 28 BP.
XX
AC   ADD41445;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Hepatitis C virus NS3 protease/helicase related PCR primer Seq ID26.
XX
KW   NS3 protease; NS3 helicase; hepatitis C virus; HCV; hepatitis C; ss; PCR;
KW   primer.
XX
OS   Unidentified.
XX
PN   JP2002345475-A.
XX
PD   03-DEC-2002.
XX
PF   25-MAY-2001; 2001JP-00156957.
XX
PR   25-MAY-2001; 2001JP-00156957.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
PA   (MITN ) MITSUBISHI GAS CHEM CO INC.
XX
DR   WPI; 2003-460881/44.
XX
PT   Functional nucleic acids targeting NS3 protease and/or helicase of
PT   hepatitis C virus (HCV) for prevention, diagnosis and treatment of
PT   hepatitis C.
XX
PS   Example 1; SEQ ID NO 26; 22pp; Japanese.
XX
CC   This invention relates to novel nucleic acids targeting the NS3 protease
CC   and/or helicase of hepatitis C virus (HCV). The invention provides RNA
CC   molecules having a base sequence with a structure given in the
CC   specification and capable of inhibition of NS3 protease and/or helicase
```

```
CC   of HCV, and capable of forming a secondary structure also given in the
CC   specification. The invention is useful for the effective prevention,
CC   diagnosis and treatment of hepatitis C. The present sequence is that of a
CC   PCR primer which was used during the exemplification of the invention.
XX
SQ   Sequence 28 BP; 20 A; 0 C; 8 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.4;  DB 1;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 4.8e+03;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1514 AAATAAAATTGGAACGAAGAAAGG 1537
              ||| ||||  |||  || ||||||
Db          5 AAAAAAAAAAGGAGAGAGGAAAGG 28


RESULT 3957
AAA47676
ID   AAA47676 standard; cDNA; 15 BP.
XX
AC   AAA47676;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Oligo d(T) primer for human DDAH1.
XX
KW   Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
KW   arginine deaminase; hyperlipidemia; renal failure; hypertension;
KW   restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;
KW   ischemia reperfusion injury; septic shock; multi organ failure;
KW   arthritis; skin disorders; inflammatory cardiac disease; migraine;
KW   infection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200044888-A2.
XX
PD   03-AUG-2000.
XX
PF   26-JAN-2000; 2000WO-GB000226.
XX
PR   26-JAN-1999;   99GB-00001705.
PR   04-JUN-1999;   99GB-00013066.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Vallance PJT,  Leiper JM,  Whitley GSJ,  Charles IG;
XX
DR   WPI; 2000-543392/49.
XX
PT   Novel methylarginase polypeptides and polynucleotides, used to identify
PT   modulators of them, which are used in the treatment of e.g. cancer,
PT   hypertension, and bacterial infections.
XX
PS   Example 1; Page 33; 68pp; English.
XX
CC   Nucleotides encoding methylarginase polypeptides, vectors comprising
CC   these mucleotides and the polypeptides themselves can be used in
CC   medicaments for the treatment of hyperlipidemia, renal failure,
CC   hypertension, restenosis after angioplasty, atherosclerosis,
CC   complications of heart failure, schizophrenia, multiple sclerosis or
CC   cancer. Modulators of the enzyme can be used in medicaments for the
CC   treatment of ischemia-reperfusion injury of the brain or heart, cancer,
CC   lethal hypertension in severe inflammatory conditions such as septic
CC   shock or multi-organ failure, or local and systemic inflammatory
CC   disorders including arthritis, skin disorders, inflammatory cardiac
CC   disease, migraine, or microbial or bacterial infection. The sequence of
CC   human DDAH1 was obtained by data base searching. The EST's used in the
CC   process are given in GENESEQ records AAA47661-A47677
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
              |||||||||||||||:
Db          1 TTTTTTTTTTTTTTV 15


RESULT 3958
AAA47676/c
ID   AAA47676 standard; cDNA; 15 BP.
XX
AC   AAA47676;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Oligo d(T) primer for human DDAH1.
XX
KW   Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
KW   arginine deaminase; hyperlipidemia; renal failure; hypertension;
KW   restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;
KW   ischemia reperfusion injury; septic shock; multi organ failure;
KW   arthritis; skin disorders; inflammatory cardiac disease; migraine;
KW   infection; ss.
XX
OS   Homo sapiens.
XX
PN   WO200044888-A2.
XX
PD   03-AUG-2000.
XX
PF   26-JAN-2000; 2000WO-GB000226.
XX
PR   26-JAN-1999;   99GB-00001705.
PR   04-JUN-1999;   99GB-00013066.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Vallance PJT,  Leiper JM,  Whitley GSJ,  Charles IG;
XX
DR   WPI; 2000-543392/49.
XX
PT   Novel methylarginase polypeptides and polynucleotides, used to identify
PT   modulators of them, which are used in the treatment of e.g. cancer,
PT   hypertension, and bacterial infections.
XX
PS   Example 1; Page 33; 68pp; English.
XX
CC   Nucleotides encoding methylarginase polypeptides, vectors comprising
CC   these mucleotides and the polypeptides themselves can be used in
CC   medicaments for the treatment of hyperlipidemia, renal failure,
CC   hypertension, restenosis after angioplasty, atherosclerosis,
CC   complications of heart failure, schizophrenia, multiple sclerosis or
CC   cancer. Modulators of the enzyme can be used in medicaments for the
CC   treatment of ischemia-reperfusion injury of the brain or heart, cancer,
CC   lethal hypertension in severe inflammatory conditions such as septic
CC   shock or multi-organ failure, or local and systemic inflammatory
CC   disorders including arthritis, skin disorders, inflammatory cardiac
CC   disease, migraine, or microbial or bacterial infection. The sequence of
CC   human DDAH1 was obtained by data base searching. The EST's used in the
CC   process are given in GENESEQ records AAA47661-A47677
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              :|||||||||||||||
Db         15 BAAAAAAAAAAAAAA 1
```

```
RESULT 3959
AAD44150
ID   AAD44150 standard; DNA; 15 BP.
XX
AC   AAD44150;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-AT PCR primer #1 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1D; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo AT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              |:|||||||||||||
Db          1 AVAAAAAAAAAAAAA 15


RESULT 3960
AAD44150/c
ID   AAD44150 standard; DNA; 15 BP.
XX
AC   AAD44150;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-AT PCR primer #1 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1D; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo AT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.1e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              |||||||||||||:|
Db         15 TTTTTTTTTTTTTBT 1


RESULT 3961
AAX18387
ID   AAX18387 standard; DNA; 16 BP.
XX
AC   AAX18387;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 28.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
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CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTA 2187
              |||||||||||||:
Db          1 TTTTTTTTTTTTTTV 15


RESULT 3962
AAX18387/c
ID   AAX18387 standard; DNA; 16 BP.
XX
AC   AAX18387;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 28.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Example 1; Page 12; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAA 2799
              :|||||||||||||||
Db         15 BAAAAAAAAAAAAAA 1


RESULT 3963
AAD44147
ID   AAD44147 standard; DNA; 16 BP.
XX
AC   AAD44147;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #7 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 2.5e+03;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTT 2179
              :|||||||||||||||
Db          2 VTTTTTTTTTTTTTT 16


RESULT 3964
AAD44149
ID   AAD44149 standard; DNA; 16 BP.
XX
AC   AAD44149;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #9 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
```

OS Unidentified.
XX
PN US6277571-B1.
XX
PD 21-AUG-2001.
XX
PF 30-SEP-1998; 98US-00163485.
XX
PR 03-OCT-1997; 97US-00943162.
PR 03-OCT-1997; 97US-0108152P.
XX
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI Fillmore H, Broaddus W, Gillies G;
XX
DR WPI; 2002-412824/44.
XX
PT Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT 2 samples, useful for disease diagnosis and gene analysis.
XX
PS Example; Fig 1C; 19pp; English.
XX
CC The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dT
CC PCR primer used to illustrate the method of the invention
XX
SQ Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTT 2179
:|||||||||||||
Db 2 VTTTTTTTTTTTTTT 16

RESULT 3965
AAT65892/c
ID AAT65892 standard; DNA; 19 BP.
XX
AC AAT65892;
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
DE Primer #1 to amplify repeat sequence marker Mfd48.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX
OS Synthetic.
XX
PN US5582979-A.
XX
PD 10-DEC-1996.
XX
PF 04-APR-1994; 94US-00222177.
XX
PR 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX
PA (MARS-) MARSHFIELD CLINIC.
XX
PI Weber JL;
XX
DR WPI; 1997-042299/04.
XX
PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
PT using novel nucleic acid mols. as primers.
XX
PS Disclosure; Col 11-12; 186pp; English.
XX
CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. Clones containing the
CC repeat sequences were isolated by hybridisation of chromosome-specific
CC phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100
CC repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR
CC amplify the inserts from the isolated clones containing the repeat
CC sequences. The primers AAT65892-3 were used to amplify the repeat
CC sequence marker clone Mfd48 (AAT65748). (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 19 BP; 4 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1727 CTATTATCAGAAGGTGACA 1745
||||| |||| ||| ||||
Db 19 CTATTCTCAGCAGGAGACA 1

RESULT 3966
AAZ00090
ID AAZ00090 standard; DNA; 19 BP.
XX
AC AAZ00090;
XX
DT 19-OCT-1999 (first entry)
XX
DE Primer LCF used for the analysis of transgene expression.
XX
KW Flavonoid biosynthesis gene; primer LCF; tomato flavour; anthocyanin; ss.
XX
OS Synthetic.
OS Lycopersicon esculentum.
XX
PN WO9937794-A1.
XX
PD 29-JUL-1999.
XX
PF 25-JAN-1999; 99WO-EP000419.
XX
PR 26-JAN-1998; 98GB-00001598.
XX
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
PA (HIND-) HINDUSTAN LEVER LTD.
XX
PI Bovy AG, Van Der Hijden HTWM, Hughes SG, Muir SR, Van Tunen AJ;
PI Verhoeyen ME, De Vos CH;
XX
DR WPI; 1999-479053/40.
XX
PT DNA construct comprising genes encoding transcription factor for
PT flavonoid biosynthesis.
XX
PS Example 8; Page 55; 101pp; English.
XX
CC Primers AAZ00087-Z00095 are used in the analysis of transgene expression
CC in a process to overexpress the flavonoid biosynthesis genes in tomato
CC fruits. This process results in the enhanced production of flavonoids
CC other than anthocyanins in plants or specific plant parts. Tomatoes and

```
CC   other plant seeds, fruits, progeny and hybrids that are transformed to
CC   have enhanced flavonol levels are useful in the preparation of food
CC   products, especially tomatoes for sauces, pastes, dressings, ketchup or
CC   soup. The food product has an improved flavour and/or increased thickness
XX
SQ   Sequence 19 BP; 7 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        226 CGGGAGCAGCAATGGGAAT 244
              ||||||||||| || |||
Db          1 CGGGAGCAGCACAGGAAAT 19


RESULT 3967
AAZ87035/c
ID   AAZ87035 standard; DNA; 19 BP.
XX
AC   AAZ87035;
XX
DT   16-MAY-2000  (first entry)
XX
DE   RBP-7 microsequencing primer for marker 5-124-273.
XX
KW   RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
KW   diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
KW   benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
KW   lymphoma; biallelic marker; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200000607-A1.
XX
PD   06-JAN-2000.
XX
PF   30-JUN-1999;   99WO-IB001242.
XX
PR   30-JUN-1998;   98US-0091315P.
PR   10-DEC-1998;   98US-0111909P.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L;
XX
DR   WPI; 2000-117170/10.
XX
PT   Novel nucleic acid and polymorphic markers used for diagnosis of
PT   diseases, especially those involving abnormal cell proliferation and
PT   differentiation.
XX
PS   Claim 15; Page 212; 223pp; English.
XX
CC   This sequence represents a microsequencing primer for a biallelic marker
CC   from the retinoblastoma binding protein-7 (RBP-7) genomic sequence
CC   (AAZ86967) of the invention. The RBP-7 coding sequence and regulatory
CC   sequences are useful for the recombinant production of the protein and
CC   for expressing heterologous nucleic acids. Primers and probes derived
CC   from the RBP-7 nucleotide sequence (such as this sequence) are useful for
CC   DNA amplification and detection methods. RBP-7 biallelic markers (see
CC   AAZ86993-Z87034) are useful for diagnosis of disease related to
CC   alteration in the regulation or in the coding regions of the RBP-7 gene
CC   and for prognosis/diagnosis of an eventual treatment with therapeutic
CC   agents, especially agents acting on pathologies involving abnormal cell
CC   proliferation and/or differentiation, these include thyroid hyperplasia,
CC   psoriasis, benign prostate hypertrophy, cancers, including breast cancer,
CC   sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer,
CC   prostate cancer, various leukaemias, and lymphomas. RBP-7 antibodies are
CC   useful as diagnostic agents
XX
SQ   Sequence 19 BP; 6 A; 5 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2533 ATACAGGGTATTAAGAATT 2551
              ||  |||||||||||||  |
Db         19 ATCTAGGGTATTAAGAAGT 1


RESULT 3968
AAA86471/c
ID   AAA86471 standard; DNA; 19 BP.
XX
AC   AAA86471;
XX
DT   04-DEC-2000  (first entry)
XX
DE   PCBA HH ribozyme binding site #203.
XX
KW   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS   Mammalia.
XX
PN   WO200032765-A2.
XX
PD   08-JUN-2000.
XX
PF   06-DEC-1999;   99WO-US028772.
XX
PR   04-DEC-1998;   98US-0110954P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Welch PJ,  Barber JR,  Robbins JM;
XX
DR   WPI; 2000-412314/35.
XX
PT   New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT   RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT   PCNA and Cyclin B1.
XX
PS   Disclosure; Page 108; 109pp; English.
XX
CC   The present invention relates to a hairpin or hammerhead ribozyme,
CC   designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC   other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC   Representative examples of ribozyme recognition sites are given in
CC   AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC   inhibiting restenosis by introduction of the ribozyme into cells. The
CC   ribozyme is resistant to endonuclease activity and hence is efficient in
CC   restenosis treatment
XX
SQ   Sequence 19 BP; 2 A; 6 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1491 TGGAGAAAATGGAGAAACA 1509
              |||||| ||| ||||||  |
Db         19 TGGAGAGAATAGAGAAAAA 1


RESULT 3969
AAA85728/c
ID   AAA85728 standard; DNA; 19 BP.
XX
AC   AAA85728;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Cyclin B1 ribozyme binding site #57.
XX
```

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 97; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 3 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1409 TACATCAAAGAAGCCCTGA 1427
              ||||||| ||||  |||||
Db         19 TACATCAGAGAAAGCCTGA 1

```

RESULT 3970
AAA84722/c
ID AAA84722 standard; DNA; 19 BP.
XX
AC AAA84722;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cyclin E ribozyme binding site #255.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 81; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 1 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        208 CTGCGAGGATCGCCACGAC 226
              |||||||||  |||||| |
Db         19 CTGCGAGGAGAGCCACGCC 1

```

RESULT 3971
AAA86468/c
ID AAA86468 standard; DNA; 19 BP.
XX
AC AAA86468;
XX
DT 04-DEC-2000 (first entry)
XX
DE PCBA HH ribozyme binding site #200.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 108; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 2 A; 3 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||||| || |||||||| |
Db         19 AGAATAGAGAAAAAAAATA 1
```

RESULT 3972
AAC60721
ID AAC60721 standard; DNA; 19 BP.
XX
AC AAC60721;
XX
DT 30-JAN-2001 (first entry)
XX
DE CYP2D1 gene partial sequence antisense strand.
XX
KW CYP2D1; cytochrome P450; drug metabolism; analgesia; sedation;
KW antussive effect; CYP2D6 inhibitor; antisense strand; ss.
XX
OS Unidentified.
XX
PN US6124282-A.
XX
PD 26-SEP-2000.
XX
PF 22-MAY-1998; 98US-00083027.
XX
PR 22-MAY-1997; 97US-0041500P.
XX
PA (SELL/) SELLERS E M.
PA (TYND/) TYNDALE R F.
XX
PI Tyndale RF, Sellers EM;
XX
DR WPI; 2000-627923/60.
XX
PT Drug formulations for treating cough and cold comprise a drug which is
PT metabolized by CYP2D6 enzyme and a CYP2D6 enzyme inhibitor.
XX
PS Example 2; Col 17-18; 29pp; English.
XX
CC The present invention is concerned with compounds which inhibit the
CC CYP2D6 enzyme of the cytochrome P450 system. This system is involved in
CC drug metabolism and inhibitors of the enzyme can be used to increase the
CC effectiveness and decrease the abuse liability of certain drugs,
CC particularly those with analgesic, sedative and antussive effects, and
CC including dextromethorphan and codeine. The present sequence is an
CC antisense strand to part of the CYP2D1 gene, and was used to demonstrate
CC the activity of the compounds of the invention
XX
SQ Sequence 19 BP; 1 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        603 CCGACCTGCTGCTGCCCCA 621
              | | | ||||||||||||||
Db          1 CTGCCTTGCTGCTGCCCCA 19
```

RESULT 3973
AAZ71872/c
ID AAZ71872 standard; DNA; 19 BP.
XX
AC AAZ71872;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:6228.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 1558; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 19 BP; 4 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1231 CCAGCAACTGTGTAAAGAA 1249
              |||| || |||| ||||||
Db         19 CCAGTAATTGTGCAAAGAA 1
```

RESULT 3974
AAC67521
ID AAC67521 standard; DNA; 19 BP.
XX
AC AAC67521;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alzheimer's disease-linked mitochondrial SNP PCR primer #221.
XX
KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200063441-A2.
XX
PD 26-OCT-2000.
XX
PF 19-APR-2000; 2000WO-US010906.

```
XX
PR   20-APR-1999;   99US-0130447P.
PR   22-OCT-1999;   99US-0160901P.
XX
PA   (MITO-) MITOKOR.
XX
PI   Herrnstadt C,  Davis RE;
XX
DR   WPI; 2000-672748/65.
XX
PT   Diagnosing a subject at the risk for or having Alzheimer's disease
PT   comprises determining at least one single nucleotide polymorphism in
PT   mitochondrial DNA associated with the disease in the sample from the
PT   subject.
XX
PS   Example 9; Page 52; 89pp; English.
XX
CC   The present invention describes a novel method for determining the risk
CC   of or diagnosing Alzheimer's disease using single nucleotide
CC   polymorphisms (SNPs) present in an individual's mitochondrial DNA
CC   (mtDNA). In additon, the SNPs identified can be used to identify agents
CC   suitable for use in treating Alzheimer's disease. Sequences AAC67301-
CC   C67610 are PCR primers used to demonstrate the method of the invention
XX
SQ   Sequence 19 BP; 2 A; 9 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        384 CCGACCCCTACTCGCATCT 402
              || || ||| |||||||||
Db          1 CCTACTCCTGCTCGCATCT 19


RESULT 3975
AAC83562
ID   AAC83562 standard; DNA; 19 BP.
XX
AC   AAC83562;
XX
DT   28-FEB-2001  (first entry)
XX
DE   DNA synthesis method linker/primer sequence SEQ ID NO: 1.
XX
KW   DNA synthesis; directional complementary DNA library; linker; PCR primer;
KW   ss.
XX
OS   Synthetic.
XX
PN   US6143531-A.
XX
PD   07-NOV-2000.
XX
PF   22-JUL-1997;   97US-00899029.
XX
PR   19-SEP-1988;   88US-00246567.
PR   02-MAY-1991;   91US-00700066.
PR   23-NOV-1992;   92US-00981931.
PR   02-SEP-1993;   93US-00116049.
XX
PA   (STRA-) STRATAGENE.
XX
PI   Hansen CJ,  Huse WD;
XX
DR   WPI; 2001-006435/01.
XX
PT   Double stranded DNA synthesis with specific orientation comprises
PT   synthesizing a first strand of DNA complementary to a selected DNA or RNA
PT   template and synthesizing second strand complementary to first one.
XX
PS   Example 1; Fig 1; 14pp; English.
XX
CC   The present invention describes an improved method of DNA synthesis which
CC   provides double stranded DNA where the predetermined orientation of the
CC   sequence is preserved. This can be used in the construction of
CC   complementary DNA and directional DNA libraries
XX
SQ   Sequence 19 BP; 1 A; 2 C; 2 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2180
              |||   ||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTT 19


RESULT 3976
AAH88897/c
ID   AAH88897 standard; DNA; 19 BP.
XX
AC   AAH88897;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human polymorphic oligonucleotide M33494 fragment #12.
XX
KW   Human; single nucleotide polymorphic; SNP; forensic science;
KW   paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW   plant breeding; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,c)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200134840-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US030766.
XX
PR   10-NOV-1999;   99US-0164596P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Au K,  Chen J,  Patil N,  Thomas D;
XX
DR   WPI; 2001-335945/35.
XX
PT   New polymorphic sites derived from the human genome are useful to
PT   determine sites correlating with phenotypic traits, particularly disease,
PT   and also in forensics and paternity testing.
XX
PS   Claim 37; Page 9; 43pp; English.
XX
CC   The present invention relates to human oligonucleotides comprising a
CC   single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC   sequence is one such oligonucleotide. The oligonucleotides can be used in
CC   forensics, paternity testing, correlation of polymorphisms with
CC   phenotypic traits, genetic mapping of phenotypic traits and marker
CC   assisted breeding of animals and crop plants
XX
SQ   Sequence 19 BP; 3 A; 1 C; 13 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        286 CAGCCCCGCGCCACCCCTC 304
              ||||||  | |||||||||
```

```
Db         19 CAGCCCTTCCCCACCCCTC 1

RESULT 3977
AAH61633/c
ID   AAH61633 standard; DNA; 19 BP.
XX
AC   AAH61633;
XX
DT   10-SEP-2001  (first entry)
XX
DE   PCNA HH ribozyme binding site SEQ ID NO:4057.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 367; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 2 A; 6 C; 0 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1491 TGGAGAAAATGGAGAAACA 1509
              |||||| ||| |||||| |
Db         19 TGGAGAGAATAGAGAAAAA 1

RESULT 3978
AAH59884/c
ID   AAH59884 standard; DNA; 19 BP.
XX
AC   AAH59884;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cyclin E ribozyme binding site SEQ ID NO:2308.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 239; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 1 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
```

```
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        208 CTGCGAGGATCGCCACGAC 226
              ||||||||  ||||||  |
Db         19 CTGCGAGGAGAGCCACGCC 1


RESULT 3979
AAH61630/c
ID   AAH61630 standard; DNA; 19 BP.
XX
AC   AAH61630;
XX
DT   10-SEP-2001  (first entry)
XX
DE   PCNA HH ribozyme binding site SEQ ID NO:4054.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 366; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 2 A; 3 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match           0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||||| || ||||||| |
Db         19 AGAATAGAGAAAAAAAATA 1


RESULT 3980
AAH60890/c
ID   AAH60890 standard; DNA; 19 BP.
XX
AC   AAH60890;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cyclin B1 ribozyme binding site SEQ ID NO:3314.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 313; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
```

```
SQ   Sequence 19 BP; 3 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1409 TACATCAAAGAAGCCCTGA 1427
              ||||||| ||||  |||||
Db         19 TACATCAGAGAAAGCCTGA 1


RESULT 3981
ABA91528
ID   ABA91528 standard; DNA; 19 BP.
XX
AC   ABA91528;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA-RNA-DNA oligonucleotide AGT02012 used to test RNase H cleavage.
XX
KW   DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        8. .10
FT                   /*tag=  a
FT                   /label= RNA
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 4; Page 49; 72pp; English.
XX
CC   The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC   AGT02012. This is one of a set of oligonucleotides (see ABA91527-30) used
CC   to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC   oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC   the set had a different number of ribonucleotides, 3 in the present case.
CC   The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC   (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC   minutes. The results showed that 4 ribonucleotides were the minimum
CC   number for RNA cleavage. The invention provides probes for nucleic acid
CC   hybridisation. The probes form a hairpin structure comprising a double-
CC   stranded stem and a single-stranded loop, and are capable of both
CC   intramolecular and intermolecular hybridisation. The double-stranded stem
CC   may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC   RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC   strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC   can be removed. Arrays and methods for nucleic acid hybridisation using
CC   the probes are provided
XX
SQ   Sequence 19 BP; 3 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||   |||||||||
Db          1 TTTTTTTAAATTTTTTTTT 19


RESULT 3982
ABA91528/c
ID   ABA91528 standard; DNA; 19 BP.
XX
AC   ABA91528;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA-RNA-DNA oligonucleotide AGT02012 used to test RNase H cleavage.
XX
KW   DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        8. .10
FT                   /*tag=  a
FT                   /label= RNA
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 4; Page 49; 72pp; English.
XX
CC   The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC   AGT02012. This is one of a set of oligonucleotides (see ABA91527-30) used
CC   to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC   oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC   the set had a different number of ribonucleotides, 3 in the present case.
CC   The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC   (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC   minutes. The results showed that 4 ribonucleotides were the minimum
CC   number for RNA cleavage. The invention provides probes for nucleic acid
CC   hybridisation. The probes form a hairpin structure comprising a double-
CC   stranded stem and a single-stranded loop, and are capable of both
CC   intramolecular and intermolecular hybridisation. The double-stranded stem
CC   may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC   RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC   strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC   can be removed. Arrays and methods for nucleic acid hybridisation using
CC   the probes are provided
XX
SQ   Sequence 19 BP; 3 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||   |||||||
Db         19 AAAAAAAAATTTAAAAAAA 1
```

RESULT 3983
ABX13088
ID ABX13088 standard; DNA; 19 BP.
XX
AC ABX13088;
XX
DT 29-MAY-2003 (first entry)
XX
DE Hantavirus gene rearrangement RT-PCR primer #11.
XX
KW Hantavirus; gene rearrangement; hantaan virus; seoul virus; primer; ss;
KW RT-PCR; reverse transcriptase.
XX
OS Hantavirus.
XX
PN KR2002009755-A.
XX
PD 02-FEB-2002.
XX
PF 26-JUL-2000; 2000KR-00043169.
XX
PR 26-JUL-2000; 2000KR-00043169.
XX
PA (KOCH-) KOREA CHUNGANG EDUCATIONAL FOUND.
XX
PI Choi JW, Jung DH, Lee PU, Park MS;
XX
DR WPI; 2002-747864/81.
XX
PT Hanta virus prepared by gene rearrangement.
XX
PS Disclosure; Page 5; 15pp; Korean.
XX
CC The invention relates to a mutant hantavirus prepared by gene
CC rearrangement through the super infection of different hantavirus serum
CC types such as hantaan virus and seoul virus, therefore the mutant
CC hantavirus has different virus serum types of gene fragment. This
CC sequence represents a reverse transcriptase PCR (RT-PCR) primer used in
CC the scope of the invention
XX
SQ Sequence 19 BP; 7 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 3.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1198 GATGGCAGCTAGGAAGAAC 1216
              |||  |||||  ||||||||
Db          1 GATTGCAGCAGGGAAGAAC 19
```

RESULT 3984
AAD34425/c
ID AAD34425 standard; DNA; 19 BP.
XX
AC AAD34425;
XX
DT 16-JUL-2002 (first entry)
XX
DE Barley chymotrypsin inhibitor CI-2A gene amplifying pep39 PCR primer.
XX
KW Protease; screening; barley; chymotrypsin inhibitor; CI-2A; laundry;
KW detergent industry; dishwash; fabric softener; PCR; primer; ss.
XX
OS Hordeum sp.
XX
PN WO200218588-A1.
XX
PD 07-MAR-2002.
XX
PF 17-JUL-2001; 2001WO-DK000503.
XX
PR 29-AUG-2000; 2000DK-00001273.
PR 05-SEP-2000; 2000US-0230017P.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Pedersen PE, Norregaard-Madsen M;
XX
DR WPI; 2002-329776/36.
XX
PT Screening protease/protease inhibitor gene library for gene encoding the
PT same, by constructing host cell having the gene, cultivating cell,
PT dissociating complex formed between them, selecting protein and isolating
PT gene.
XX
PS Example 1; Page 46; 54pp; English.
XX
CC The invention relates to a method for screening a protease/protease
CC inhibitor gene library for a gene encoding a protease of interest. The
CC method comprises introducing a first gene of the protease gene library
CC and a second gene encoding a protease inhibitor into a host cell;
CC cultivating the host cell, wherein the cell expresses the first and the
CC second genes to produce a complex of a protease and the inhibitor;
CC dissociating the inhibitor from the complex and selecting the protease of
CC interest and isolating the encoding gene. A complex may be used for a
CC number of industrial applications, in particular within the detergent
CC industry, thus, relates to a cleaning or detergent composition,
CC preferably a laundry or dishwash composition comprising the complex,
CC where hand or machine laundry detergent composition including a laundry
CC additive composition suitable for pre-treatment of stained fabrics and a
CC rinse added composition, or be formulated as a detergent composition for
CC use in general household hard surface cleaning operations or be
CC formulated for hand or machine dish washing operations. The present
CC sequence is a PCR primer used for amplifying barley chymotrypsin
CC inhibitor CI-2A gene used in the exemplification of the invention
XX
SQ Sequence 19 BP; 1 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 3.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        434 CTGCACCAGCCGGCGCCCA 452
              ||||| |||||||||| | |
Db         19 CTGCAGCAGCCGGCGGCAA 1
```

RESULT 3985
ABL40490/c
ID ABL40490 standard; DNA; 19 BP.
XX
AC ABL40490;
XX
DT 17-JUN-2002 (first entry)
XX
DE Nucleotide sequence of PCR primer pep39.
XX
KW Protease; allergenicity; detergent; subtilase; Sl1; Sl2; additive;
KW protease inhibitor; barley; chymotrypsin; CI-2A; subtilisin; savinase;
KW apr; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200216619-A1.
XX
PD 28-FEB-2002.
XX
PF 09-JUL-2001; 2001WO-DK000479.
XX
PR 21-AUG-2000; 2000DK-00001233.

PR 24-AUG-2000; 2000US-0227501P.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Pedersen PE;
XX
DR WPI; 2002-242031/29.
XX
PT Producing protease-inhibitor compositions with reduced allergenicity,
PT stability and activity for use in detergent compositions.
XX
PS Example 1; Page 44; 52pp; English.
XX
CC The invention provides a method for producing a protease-inhibitor
CC complex with reduced allergenicity for use in detergents. The method
CC involves (a) constructing a fusion polynucleotide sequence in frame, the
CC sequence comprising a first gene encoding a protease (preferably a
CC subtilase S11 or S12) and a second gene encoding a protease inhibitor;
CC (b) introducing the sequence into a host cell; and (c) cultivating the
CC host cell (the host cell expresses the sequence an produces a non-
CC covalently linked complex of the protease and the inhibitor). The
CC protease-inhibitor complex produced by the method may be used as an
CC additive in detergent compositions. Sequences ABL40485-497 represent PCR
CC primers used in the construction of expression cassettes for simultanoeus
CC expression of the apr gene encoding subtilisin 309 or savinase from
CC Bacillus lentus and the chymotrypsin inhibitor, CI-2A from barley
XX
SQ Sequence 19 BP; 1 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 434 CTGCACCAGCCGGCGCCCA 452
||||| |||||||||| | |
Db 19 CTGCAGCAGCCGGCGGCAA 1

RESULT 3986
ABA97625/c
ID ABA97625 standard; DNA; 19 BP.
XX
AC ABA97625;
XX
DT 11-APR-2002 (first entry)
XX
DE Probe d.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 19 BP; 15 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTA 2187
||||||||||||| | | ||
Db 19 TTTTTTTTTTTTATATATA 1

RESULT 3987
ABT13058/c
ID ABT13058 standard; DNA; 19 BP.
XX
AC ABT13058;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human apolipoprotein A-IV PCR primer (SNP specific) #24.
XX
KW Human; PCR; primer; ss; gene therapy; single nucleotide polymorphism;
KW cytochrome C oxidase subunit VIb; COX6B; high serum cholesterol; GPI-1;
KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
KW glycosylphosphatidylinositol-1; SNP; low serum high density lipoprotein.
XX
OS Homo sapiens.
XX
PN WO200272604-A2.
XX
PD 19-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US006728.
XX
PR 09-MAR-2001; 2001US-00802640.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Braun A, Bansal A, Kleyn PW;
XX
DR WPI; 2002-750478/81.
XX
PT Detecting the presence or absence of an allelic variant of a polymorphic
PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
PT to high serum cholesterol, low serum HDL and cardiovascular disease.
XX
PS Disclosure; Page 33; 199pp; English.
XX
CC The invention comprises methods of detecting the presence or absence of
CC at least one allelic variant of a polymorphic region of a gene associated
CC with cardiovascular disease. The invention specifically relates to
CC detecting the region of a cytochrome C oxidase subunit VIb (COX6B) gene
CC that is associated with high serum cholesterol, or the region of the N-
CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
CC (GPI-1) gene that is associated with low serum high density lipoprotein
CC (HDL). The methods of the invention are useful for detecting a
CC predisposition to high serum cholesterol, low serum HDL and
CC cardiovascular disease. The methods are also useful for elucidating
CC pathological pathways, developing diagnostic assays and new drug
CC therapies for such disorders. The present DNA sequence represents a PCR
CC primer used to amplify a human gene that is associated with high serum
CC cholesterol, low serum HDL and/or cardiovascular disease
XX
SQ Sequence 19 BP; 3 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        643 GGGCCTGGCCGAGAACCTG 661
              ||  |||||||||| ||||
Db         19 GGCACTGGCCGAGATCCTG 1
```

RESULT 3988
ADD43444
ID ADD43444 standard; DNA; 19 BP.
XX
AC ADD43444;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mitochondrial DNA (mtDNA) PCR primer SEQ ID NO:618.
XX
KW mitochondrial haplogroup; mitochondrial DNA; mtDNA;
KW single nucleotide polymorphism; SNP; genetic relationship; antidiabetic;
KW nootropic; neuroprotective; cytostatic; gene therapy; genealogy;
KW forensic; Alzheimer's disease; cancer; type 2 diabetes mellitus; human;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003046225-A1.
XX
PD 05-JUN-2003.
XX
PF 25-NOV-2002; 2002WO-US038276.
XX
PR 26-NOV-2001; 2001US-0333622P.
PR 28-MAR-2002; 2002US-0369131P.
PR 01-APR-2002; 2002US-0369539P.
XX
PA (MITO-) MITOKOR.
XX
PI Herrnstadt C;
XX
DR WPI; 2003-505214/47.
XX
PT Determining single nucleotide polymorphisms in mDNA or homoplasmic mDNA
PT mutations, useful for diagnosing and treating diseases, such as
PT Alzheimer's disease, cancer and type 2 diabetes mellitus.
XX
PS Example 2; SEQ ID NO 618; 193pp; English.
XX
CC The present invention describes a method (M1) for determining the
CC mitochondrial haplogroup of a subject, comprising determining in a
CC biological sample with mitochondrial DNA (mtDNA) from a subject, the
CC presence or absence of at least one mitochondrial single nucleotide
CC polymorphism (SNP) that is associated with a mitochondrial haplogroup.
CC Also described: (1) determining a genetic relationship between two
CC subjects; (2) determining a genetic relationship between an unknown
CC source or biological subject from which an unidentified sample is
CC obtained, and a known source or biological subject from an identified
CC sample is obtained; and (3) determining the presence of or the risk of
CC having a disease associated with a mtDNA SNP. Mitochondrial DNA can have
CC antidiabetic, nootropic, neuroprotective and cytostatic activities, and
CC can be used in gene therapy. M1 and compositions of the present invention
CC are useful for detecting the presence or risk of diseases, treating such
CC diseases, determining the haplogroup of an individual, and establishing
CC genetic relationships between individuals for genealogical and forensic
CC purposes. The diseases include Alzheimer's disease, cancer and type 2
CC diabetes mellitus. The present sequence represents a PCR primer used in
CC the amplification of human mtDNA in an example from the present
CC invention.
XX
SQ Sequence 19 BP; 2 A; 9 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        384 CCGACCCCTACTCGCATCT 402
              || || ||| |||||||||
Db          1 CCTACTCCTGCTCGCATCT 19
```

RESULT 3989
ADE65656
ID ADE65656 standard; RNA; 19 BP.
XX
AC ADE65656;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human c-fos transcript target sequence/siNA upper strand, SEQ ID NO:111.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping;
KW central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; epilepsy; dementia;
KW amyotrophic lateral sclerosis; cancer; proliferative disease; restenosis;
KW polycystic kidney disease; inflammatory disease; allergic disease;
KW viral infection; HIV infection; autoimmune disease; transplant rejection;
KW vasotropic; nootropic; antiparkinsonian; neuroprotective; cytostatic;
KW antiinflammatory; antiallergic; virucide; anti-HIV; immunosuppressive;
KW anticonvulsant; nephrotropic; human; c-fos; target sequence; ss.
XX
OS Homo sapiens.
XX
PN WO2003070914-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005162.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L;
XX
DR WPI; 2003-679877/64.
XX
PT New short interfering nucleic acid downregulates expression of the c-fos
PT gene useful for treatment and diagnosis of diseases, e.g. cancer and
PT inflammation.
XX
PS Example 3; SEQ ID NO 111; 145pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human c-fos gene by RNA interference. The
CC siNAs may or may not comprise ribonucleotides and may be double or single
CC stranded. They further comprise sense and antisense regions, or
CC alternatively are assembled from a sense oligonucleotide and an antisense
CC oligonucleotide. Specifically, the siNAs include short interfering RNA
CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the c-fos gene in cells, tissue explants or organisms

CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC central nervous system lesions and injuries (e.g., Alzheimer's disease,
CC Parkinson's disease, Huntington's disease, epilepsy, dementia or
CC amyotrophic lateral sclerosis); various cancers; other proliferative
CC diseases (e.g., restenosis and polycystic kidney disease); inflammatory
CC and/or allergic diseases; viral infections (including HIV infection);
CC autoimmune diseases; and transplant rejection. The siNAs are also useful
CC for drug screening, diagnosis, therapeutic target identification and
CC validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the upper strand of a human c-fos-
CC targeted double-stranded siNA, which is identical to the c-fos transcript
CC target sequence.
XX
SQ Sequence 19 BP; 2 A; 3 C; 0 G; 0 T; 14 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 10.5%; Pred. No. 3.5e+03;
Matches 2; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAACTT 2191
:::: :::::::: :| |::
Db 1 UUUUAUUUUUUUCUACCUU 19

RESULT 3990
ADE65772/c
ID ADE65772 standard; RNA; 19 BP.
XX
AC ADE65772;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human c-fos siNA lower strand, SEQ ID NO:227.
XX
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping;
KW central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; epilepsy; dementia;
KW amyotrophic lateral sclerosis; cancer; proliferative disease; restenosis;
KW polycystic kidney disease; inflammatory disease; allergic disease;
KW viral infection; HIV infection; autoimmune disease; transplant rejection;
KW vasotropic; nootropic; antiparkinsonian; neuroprotective; cytostatic;
KW antiinflammatory; antiallergic; virucide; anti-HIV; immunosuppressive;
KW anticonvulsant; nephrotropic; human; c-fos; ss.
XX
OS Homo sapiens.
XX
PN WO2003070914-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005162.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L;
XX
DR WPI; 2003-679877/64.
XX
PT New short interfering nucleic acid downregulates expression of the c-fos
PT gene useful for treatment and diagnosis of diseases, e.g. cancer and
PT inflammation.
XX
PS Example 3; SEQ ID NO 227; 145pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human c-fos gene by RNA interference. The
CC siNAs may or may not comprise ribonucleotides and may be double or single
CC stranded. They further comprise sense and antisense regions, or
CC alternatively are assembled from a sense oligonucleotide and an antisense
CC oligonucleotide. Specifically, the siNAs include short interfering RNA
CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the c-fos gene in cells, tissue explants or organisms
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC central nervous system lesions and injuries (e.g., Alzheimer's disease,
CC Parkinson's disease, Huntington's disease, epilepsy, dementia or
CC amyotrophic lateral sclerosis); various cancers; other proliferative
CC diseases (e.g., restenosis and polycystic kidney disease); inflammatory
CC and/or allergic diseases; viral infections (including HIV infection);
CC autoimmune diseases; and transplant rejection. The siNAs are also useful
CC for drug screening, diagnosis, therapeutic target identification and
CC validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the lower strand of a human c-fos-
CC targeted double-stranded siNA.
XX
SQ Sequence 19 BP; 14 A; 0 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2173 TTTTTTTTTTTTTTAACTT 2191
|||| ||||||| || |||
Db 19 TTTTATTTTTTTCTACCTT 1

RESULT 3991
ADE27175
ID ADE27175 standard; RNA; 19 BP.
XX
AC ADE27175;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:119.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 119; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 3 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 5.3%; Pred. No. 3.5e+03;
Matches 1; Conservative 15; Mismatches 3; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTA 2187
: :::: :::::::: :::|
Db 1 UCUUUUCUUUUUUUCUUUA 19

RESULT 3992
ADE27465/c
ID ADE27465 standard; RNA; 19 BP.
XX
AC ADE27465;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:409.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 409; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 15 A; 0 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTA 2187
| |||| ||||||| ||||
Db 19 TCTTTTCTTTTTTTCTTTA 1

RESULT 3993
ADE27307
ID ADE27307 standard; RNA; 19 BP.
XX
AC ADE27307;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:251.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.

```
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 251; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 1 A; 0 C; 3 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   5.3%;  Pred. No. 3.5e+03;
  Matches    1;  Conservative   15;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ::::::::::::::   ::|
Db          1 UUUUUUUUUUUUUGGGUUA 19


RESULT 3994
ADE27597/c
ID   ADE27597 standard; RNA; 19 BP.
XX
AC   ADE27597;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:541.
XX
KW   short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW   stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW   antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW   atherosclerosis; cancer; viral infection; drug screening;
KW   genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS   Synthetic.
XX
PN   WO2003070885-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004317.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   20-SEP-2002; 2002US-0412304P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L,  Thompson J;
XX
DR   WPI; 2003-721687/68.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of obesity or diabetes, downregulates expression of the
PT   stearoyl-CoA desaturase gene.
XX
PS   Example 3; SEQ ID NO 541; 139pp; English.
XX
CC   The present invention describes a short interfering nucleic acid (siNA)
CC   that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC   by RNA interference. Also described: (1) modulating expression of SCD
CC   genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC   kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC   complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC   siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC   virucide activities. The siNAs can be used to modulate expression of SCD
CC   genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC   diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC   They can also be used for drug screening; diagnosis; target
CC   identification and validation; genetic engineering; pharmacogenomics;
CC   studying gene function and gene mapping (e.g. of single-nucleotide
CC   polymorphisms). The present sequence represents an SCD siNA, which is
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 19 BP; 15 A; 3 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 3.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||   |||
Db         19 TTTTTTTTTTTTTGGGTTA 1


RESULT 3995
ABZ89873
ID   ABZ89873 standard; DNA; 20 BP.
XX
AC   ABZ89873;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
```

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5115; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAAA 2804
||||||||||||| || |
Db 1 AAAAAAAAAAAAAGGAAGA 19

RESULT 3996
AAT10129
ID AAT10129 standard; DNA; 20 BP.
XX
AC AAT10129;
XX
DT 21-AUG-1996 (first entry)
XX
DE Sequence #1 used in the method of the invention.
XX
KW Vascular endothelial growth factor; VEGF; antisense oligonucleotide;
KW therapy; abnormal angiogenesis; cancer; rheumatoid arthritis; diabetes;
KW ss.
XX
OS Synthetic.
XX
PN WO9600286-A1.
XX
PD 04-JAN-1996.
XX
PF 07-JUN-1995; 95WO-JP001121.
XX
PR 27-JUN-1994; 94JP-00145146.
PR 21-NOV-1994; 94JP-00311130.
XX
PA (TOAG) TOA GOSEI KK.
XX
PI Uchida K, Uchida T, Tanaka Y, Matsuda Y, Kondo S;
XX
DR WPI; 1996-068870/07.
XX
PT Anti-sense polynucleotide complementary to VEGF sequence - inhibit growth
PT factor expression and are used for diagnosis and treatment of cancer and
PT other diseases.
XX
PS Example 1; Page 45; 66pp; Japanese.
XX
CC AAT10129 and AAT10130 represent oligonucleotides used within the
CC invention. These sequences were used to determine the antisense
CC oligonucleotides of the invention (see AAT10121-T10128). These sequences
CC are antisense oligonucleotides complementary to at least 8 consecutive
CC nucleotides of the vascular endothelial growth factor (VEGF) gene (see
CC AAT10120). These antisense sequences inhibit the expression of VEGF to
CC below 30% of normal expression. The antisense oligonucleotides may be
CC used in diagnosis and treatment of diseases involving VEGF expression and
CC associated abnormal angiogenesis, such as cancer, rheumatoid arthritis
CC and diabetes
XX
SQ Sequence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAAA 2804
||||||| ||||| || ||
Db 1 AAAAAAACAAAAACAACAA 19

RESULT 3997
AAF99949/c
ID AAF99949 standard; DNA; 20 BP.
XX
AC AAF99949;
XX
DT 12-JUL-2001 (first entry)
XX
DE Synthetic oligonucleotide #15.
XX
KW Oligonucleotide purification; liquid chromatography;
KW hydrophobic protective group; deprotection; ds.
XX
OS Synthetic.
XX
PN JP2000342265-A.
XX
PD 12-DEC-2000.
XX
PF 02-JUN-1999; 99JP-00154974.
XX
PR 02-JUN-1999; 99JP-00154974.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 2001-268251/28.
XX
PT A process for purification of oligonucleotides using liquid
PT chromatography.
XX
PS Example 1; Page 4; 13pp; Japanese.
XX
CC The present sequence is an oligonucleotide provided in a specification
CC relating to the simplified purification of oligonucleotides by liquid
CC chromatography. The process comprises: (a) pouring oligonucleotides
CC protected with a hydrophobic group and oligonucleotide with no protective
CC group into a liquid chromatography column packed with an acid and alkali
CC resistant packing agent, such as polystyrene resin; (b) pouring a mixed
CC developing solvent composed of a buffer made from a volatile salt and a
CC water soluble organic solvent at a suitable concentration gradient into
CC the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into
CC the column to deprotect the oligonucleotides protected with the
CC hydrophobic group; (d) pouring a mixed developing solvent composed of a
CC buffer made from a volatile salt, particularly 0.05-0.5 N aqueous
CC ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water
CC soluble organic solvent at a suitable concentration gradient to elute the
CC deprotected oligonucleotides; and (e) removal of the solvent and the salt
CC from the eluted oligonucleotides

```
XX
SQ   Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| |||| ||||
Db         20 AAAATAAAACAAAAGAAAA 2

RESULT 3998
ABA91537
ID   ABA91537 standard; DNA; 20 BP.
XX
AC   ABA91537;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA oligonucleotide AGT02025 used to test RNase H cleavage.
XX
KW   Nucleic acid detection; probe; mismatch; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    12
FT                   /*tag=  a
FT                   /note= "mismatch to target DNA"
XX
PN   WO200206531-A2.
XX
PD   24-JAN-2002.
XX
PF   12-JUL-2001; 2001WO-US022166.
XX
PR   14-JUL-2000; 2000US-00616761.
PR   30-MAR-2001; 2001US-00823647.
XX
PA   (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI   Dattagupta N;
XX
DR   WPI; 2002-171819/22.
XX
PT   Probes for detecting target nucleotide sequence in sample, has sequence
PT   that forms hairpin structure having a double-stranded segment and single-
PT   stranded loop collectively forming region complementary to target
PT   sequence.
XX
PS   Example 5; Page 50; 72pp; English.
XX
CC   The present sequence is that of oligonucleotide AGT02025, which contains
CC   a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
CC   one of a set of oligonucleotides (see ABA91532-37) containing
CC   mismatch(es) to the target DNA that were tested in a hybridisation/RNase
CC   H cleavage assay. The results showed that 2 mismatches between the target
CC   and the probe ablated RNase H cleavage. The effect of one mismatch site
CC   was less than that of two mismatch sites, and showed a polarity effect,
CC   with weaker inhibition shown in assays with AGT02021 than in assays using
CC   an oligonucleotide in which the mismatch was at an adjacent position.
CC   Oligonucleotides in which the mismatch was G or C rather than A showed
CC   similar inhibition of RNase H cleavage. The invention provides probes for
CC   nucleic acid hybridisation. The probes form a hairpin structure
CC   comprising a double-stranded stem and a single-stranded loop, and are
CC   capable of both intramolecular and intermolecular hybridisation. The
CC   double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
CC   is resistant to RNase H cleavage. When the probe hybridises with a target
CC   DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
CC   treatment and can be removed. Arrays and methods for nucleic acid
CC   hybridisation using the probes are provided
XX
SQ   Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||| || |||||||
Db          2 AAAAAAAATTATAAAAAAA 20

RESULT 3999
ABX04655/c
ID   ABX04655 standard; DNA; 20 BP.
XX
AC   ABX04655;
XX
DT   14-JAN-2003  (first entry)
XX
DE   Human endogenous retrovirus k (herv-k) associated probe #27.
XX
KW   Human; endogenous retrovirus; herv; prostate cancer; testicular cancer;
KW   multiple sclerosis; insulin-dependent diabetes mellitus; HML-2 protease;
KW   cancer; transgenic animal; probe; ss.
XX
OS   Human endogenous retrovirus.
XX
PN   WO200246477-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US047824.
XX
PR   07-DEC-2000; 2000US-0251830P.
PR   07-DEC-2001; 2001US-00016604.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Garcia P,  Hardy SF,  Williams LT,  Escobedo J;
XX
DR   WPI; 2002-691475/74.
XX
PT   Novel isolated polypeptides useful for diagnosis of prostate cancer.
XX
PS   Claim 18; Page 146; 152pp; English.
XX
CC   The invention describes novel isolated polypeptides (I, Ib) useful for
CC   diagnosing prostate cancer comprising obtaining a patient sample
CC   containing prostate cells and detecting the presence or absence of an
CC   expression product of a HML-2 endogenous retrovirus in a patient sample.
CC   Polynucleotides associated with (I) are useful for diagnosis or treatment
CC   of testicular cancer, multiple sclerosis or insulin-dependent diabetes
CC   mellitus. An inhibitor of a HML-2 protease and a transdominant negative
CC   mutant of HML-2 cORF are also useful in the manufacture of a medicament
CC   for treating prostate cancer. (I) and (Ib) are useful for generating
CC   antibodies specific to the polypeptides associated with cancer, as
CC   targets for therapeutic intervention, and in immunising a transgenic
CC   animal. This sequence represents a probe used for detecting the presence
CC   of human endogenous retrovirus (herv) of the HML-2 sub-group in prostate
CC   tissue
XX
SQ   Sequence 20 BP; 16 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              | |||||||| |||||||
Db         20 TTCTTTTTTTGATTTTTTT 2

RESULT 4000
```

```
ABZ90374
ID   ABZ90374 standard; DNA; 20 BP.
XX
AC   ABZ90374;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5616; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| |||||| ||
Db          1 AAAACAAAACAAAAAACAA 19


RESULT 4001
```

```
ABZ85670/c
ID   ABZ85670 standard; DNA; 20 BP.
XX
AC   ABZ85670;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 912; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| | ||||||| |||
Db         20 AAAAATAGAAAAAAAGAAA 2


RESULT 4002
```

ABZ88438/c
ID ABZ88438 standard; DNA; 20 BP.
XX
AC ABZ88438;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3680; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1771 TTTTTTTTTTTGAACCCCA 1789
||||||||||||| | |
Db 19 TTTTTTTTTTGAAGTCAA 1

RESULT 4003

ABZ91225/c
ID ABZ91225 standard; DNA; 20 BP.
XX
AC ABZ91225;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6467; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTT 2184
|| |||||| |||||| ||
Db 20 TTGTTTTTTGTTTTTTCTT 2

RESULT 4004

```
AAL53968
ID   AAL53968 standard; DNA; 20 BP.
XX
AC   AAL53968;
XX
DT   18-FEB-2003  (first entry)
XX
DE   DNA mutation detection related ribonucleotide, SEQ ID No 18.
XX
KW   Detecting; point mutation; hybridising; target DNA; duplex; RNase H;
KW   single nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   US2002142308-A1.
XX
PD   03-OCT-2002.
XX
PF   30-MAR-2001; 2001US-00823634.
XX
PR   30-MAR-2001; 2001US-00823634.
XX
PA   (DATT/) DATTAGUPTA N.
PA   (TSEN/) TSENG T.
XX
PI   Dattagupta N,  Tseng T;
XX
DR   WPI; 2003-102506/09.
XX
PT   Detecting point mutation in DNA strand, by hybridizing target DNA strand
PT   having mutation with test DNA strand to form duplex, contacting the
PT   duplex with RNase H and determining the cleavage of test strand by RNase
PT   H.
XX
PS   Example 5; Fig 4; 26pp; English.
XX
CC   The invention relates to a novel method for detecting a point mutation in
CC   a DNA strand. The novel method comprises hybridising a target DNA strand
CC   containing or suspected of containing a point mutation with a test
CC   nucleic acid strand complementary to the DNA strand to form a target DNA
CC   strand/test nucleic acid strand duplex, contacting the duplex with an
CC   RNase H, and determining whether the ribonucleotide residues within the
CC   nucleotide sequence are cleaved by RNase H. The method is useful for
CC   detecting a point mutation in a DNA strand, where the point mutation to
CC   be detected is a single nucleotide polymorphism, preferably a
CC   polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian
CC   or human genome. The method is useful to detect any nucleic acids from
CC   any species of organisms such as Acintobacter, Bacillus, Candida,
CC   Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
CC   This polynucleotide sequence represents a ribonucleotide relating to the
CC   mutation detecting method of the invention
XX
SQ   Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||| |  ||||||||
Db          1 AAAAAAATATTAAAAAAAA 19


RESULT 4005
ADC98404/c
ID   ADC98404 standard; DNA; 20 BP.
XX
AC   ADC98404;
XX
DT   01-JAN-2004  (first entry)
XX
DE   ITGA12 polymorphism marker PCR primer S primer seq.
XX
KW   low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;
KW   single nucleotide polymorphism; SNP; PCR primer; ss; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003054218-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US040948.
XX
PR   20-DEC-2001; 2001US-0342711P.
PR   04-NOV-2002; 2002US-0423559P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA,  Valdes A,  Townley DJ,  Mangion J,  Galwey N,  Bennett S;
PI   Mckay I,  Schafer A;
XX
DR   WPI; 2003-559156/52.
XX
PT   Determining whether an individual is predisposed to susceptibility to low
PT   bone mineral density (BMD) and/or bone damage, involves identifying
PT   polymorphisms in associated genes.
XX
PS   Example 8; Page 237; 246pp; English.
XX
CC   The present invention describes a method of determining whether an
CC   individual is predisposed to susceptibility to low bone mineral density
CC   (BMD) and/or bone damage comprising identifying whether the individual
CC   has at least one polymorphism in a polynucleotide encoding a protein,
CC   where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,
CC   see ADC98235 to ADC98315). An agent identified in an method from the
CC   present invention which can be used for the prevention or treatment of a
CC   disease resulting in susceptibility to low BMD and/or bone damage is
CC   useful in the manufacture of a medicament for use in modulating the
CC   susceptibility to low BMD and/or bone damage. The disease associated with
CC   low BMD and/or bone damage is osteoporosis. The present PCR primer
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||| |||| ||||| |
Db         19 AAAAAACAAAATAAAAACA 1


RESULT 4006
AAQ22135
ID   AAQ22135 standard; DNA; 20 BP.
XX
AC   AAQ22135;
XX
DT   25-MAR-2003  (revised)
DT   03-JUL-1992  (first entry)
XX
DE   Primer G corresp. to region conserved between EBV type A and B.
XX
KW   Epstein Barr Virus; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   JP04027399-A.
XX
PD   30-JAN-1992.
XX
PF   23-MAY-1990;   90JP-00133618.
XX
```

```
PR   23-MAY-1990;   90JP-00133618.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
DR   WPI; 1992-084781/11.
XX
PT   Simultaneous type detection of epstein-barr virus and DNA sequence - in
PT   which specimen is amplified using primer and PCR process, and then
PT   amplified DNA is detected.
XX
PS   Disclosure; Page 4; 6pp; Japanese.
XX
CC   PCR primer G is used with primer H (see AAQ21998) to amplify a fragment
CC   of the EBV genome. The Primer sequences are common to viral types A and B
CC   but the sequence which is amplified differs between types A and B. Thus,
CC   by determining the mol. wt. of the amplified intervening region (e.g. by
CC   electrophoresis), it is possible to distinguish which EBV type is present
CC   in the sample. See also AAQ21996-Q22000 and AAQ22132-Q22139. (Updated on
CC   25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 20 BP; 9 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2721 AATGTTCCCCAAATAATTG 2739
             |||||  ||||||||| ||
Db          2 AATGTATCCCAAATAAATG 20


RESULT 4007
AAQ51661/c
ID   AAQ51661 standard; DNA; 20 BP.
XX
AC   AAQ51661;
XX
DT   24-MAY-1994  (first entry)
XX
DE   ADV primer (II)a.
XX
KW   ADV; Aujeszky's disease virus; primer; PCR; amplification;
KW   polymerase chain reaction; detection; ss.
XX
OS   Synthetic.
XX
PN   JP05276998-A.
XX
PD   26-OCT-1993.
XX
PF   01-APR-1992;   92JP-00079881.
XX
PR   01-APR-1992;   92JP-00079881.
XX
PA   (NISS ) NISSHIN SEIFUN KK.
PA   (ZENK-) ZENKOKU NOGYO KYODO KUMIAI REN.
XX
DR   WPI; 1993-373607/47.
XX
PT   Detection of Aujeszky's disease virus - using specified oligo-nucleotide
PT   as primer for selective detection.
XX
PS   Claim 1; Page 1; 9pp; Japanese.
XX
CC   The detection method for Aujezsky's disease virus uses a primer pair
CC   selected from the ADV DNA-specific region, with PCR designed to suit the
CC   amplification of DNA, thereby permitting specific and highly sensitive
CC   detection of ADV. Claimed primers are given in AAQ51659-72; additional
CC   primers are given in AAQ51673-74
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        549 TCTCCGGGCTGGAGGCGGG 567
              ||||||||  ||  ||  ||||
Db         19 TCTCCGGGATGAAGACGGG 1


RESULT 4008
AAQ62025/c
ID   AAQ62025 standard; DNA; 20 BP.
XX
AC   AAQ62025;
XX
DT   25-MAR-2003  (revised)
DT   17-NOV-1994  (first entry)
XX
DE   Mutant Ki-ras 5'-UTR/5' cap antisense phosphorothioate oligo ref. 6958.
XX
KW   Antisense; phosphorothioate; H-ras; translation initiation codon;
KW   codon-12 point mutation; activated; inhibition; ras-luciferase; activity;
KW   detection; modulation; inhibition; expression; oncogene; proliferation;
KW   Ki-ras; cancer cell; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .20
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages"
XX
PN   WO9408003-A1.
XX
PD   14-APR-1994.
XX
PF   01-OCT-1993;   93WO-US009346.
XX
PR   05-OCT-1992;   92US-00958134.
PR   21-JAN-1993;   93US-00007996.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Freier SM,  Ecker DJ;
XX
DR   WPI; 1994-135570/16.
XX
PT   New oligo:nucleotides hybridisable with H-ras or Ki-ras gene nucleic acid
PT   - in normal or mutated form, for detecting or modulating gene expression,
PT   specifically inhibiting proliferation of cancer cells.
XX
PS   Claim 109 and 115; Page 36; 104pp; English.
XX
CC   The sequences given in AAQ62025-38 are antisense phosphorothioate
CC   oligonucleotides which are targetted to various regions of Ki-ras
CC   oncogene. These oligonuceotides gave significant and reproducible
CC   inhibition of the level of Ki-ras mRNA. These oligonucleotides may be
CC   used for detecting and modulating, esp. inhibiting,expression of the Ki-
CC   ras gene, esp.for inhibiting proliferation of cancer cells, and other
CC   conditions associated with Ki-ras oncogene activation. Activated (mutant)
CC   Ki-ras can be detected from its differential affinity for particular
CC   oligos. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||  ||||  |||||  |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1
```

```
RESULT 4009
AAT41033/c
ID   AAT41033 standard; DNA; 20 BP.
XX
AC   AAT41033;
XX
DT   03-DEC-1996  (first entry)
XX
DE   Human gene signature HUMGS01006-derived sense primer.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; primer; PCR; amplification;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP001916.
XX
PR   12-NOV-1993;   93JP-00355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT   directed human cDNA library that reflects relative abundance of corresp.
PT   mRNA in specific human tissues.
XX
PS   Example 7; Fig 6; 2245pp; Japanese.
XX
CC   Primers T41001-T41382 are derived from novel human gene signature (GS)
CC   sequences which did not match with sequences deposited in Genbank release
CC   76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC   libraries prepared from various human tissues; synthesis of cDNA was
CC   initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC   Each library is constructed so as to reflect accurately the relative
CC   abundance of different mRNAs in the particular tissue from which it was
CC   derived. The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS sequences)
CC   as a means of diagnosing abnormal cell function or for recognising
CC   different cell types. The primers T41033-4 amplify clone pm1730 which
CC   comprises the GS HUMGS001006 (T20006), located on chromosome 2
XX
SQ   Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1332 GCTTGTCTCATTTCAGCCT 1350
              || || | ||||||||||
Db         19 GCATGCCACATTTCAGCCT 1


RESULT 4010
AAT41311/c
ID   AAT41311 standard; DNA; 20 BP.
XX
AC   AAT41311;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Human gene signature HUMGS01057-derived sense primer.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; primer; PCR; amplification;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP001916.
XX
PR   12-NOV-1993;   93JP-00355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Single-stranded DNA for identifying gene signatures - isolated from 3'-
PT   directed human cDNA library that reflects relative abundance of corresp.
PT   mRNA in specific human tissues.
XX
PS   Example 7; Fig 10; 2245pp; Japanese.
XX
CC   Primers T41001-T41382 are derived from novel human gene signature (GS)
CC   sequences which did not match with sequences deposited in Genbank release
CC   76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
CC   libraries prepared from various human tissues; synthesis of cDNA was
CC   initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
CC   Each library is constructed so as to reflect accurately the relative
CC   abundance of different mRNAs in the particular tissue from which it was
CC   derived. The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS sequences)
CC   as a means of diagnosing abnormal cell function or for recognising
CC   different cell types. The primers T41311-2 amplify clone pm2049 which
CC   comprises the GS HUMGS001057 (T20057). This amplification reaction gave a
CC   prod. indistinguisable from the same PCR using Chinese hamster ovary DNA
CC   as a template
XX
SQ   Sequence 20 BP; 9 A; 6 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1943 ATGGTTGGTTTTTGTGTCC 1961
              || | |||| |||||||||
Db         20 ATAGCTGGTGTTTGTGTCC 2


RESULT 4011
AAQ79844/c
ID   AAQ79844 standard; DNA; 20 BP.
XX
AC   AAQ79844;
XX
DT   25-MAR-2003  (revised)
DT   04-SEP-1995  (first entry)
XX
DE   K-ras modulating sequence, targetted to 5' UTR/5' cap.
XX
KW   Peptide nucleic acid; PNA; ligand; peptide backbone; human; H-ras; K-ras;
KW   expression; ras gene; mutation; tumour; cancer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /note= "Each base is attached to a N-acetyl(2-amino-
```

```
FT                   ethyl)Gly residue through the N-acetyl group"
XX
PN   WO9428720-A1.
XX
PD   22-DEC-1994.
XX
PF   10-JUN-1994;   94WO-US006620.
XX
PR   11-JUN-1993;   93US-00076234.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Lima W,  Monia B,  Freier S,  Ecker D;
XX
DR   WPI; 1995-035955/05.
XX
PT   New peptide nucleic acid oligomers for ras oncogene modulation -
PT   including specific inhibition of the activated gene, for diagnosis and
PT   treatment esp. of tumours.
XX
PS   Claim 1; Page 133; 148pp; English.
XX
CC   The sequences given in AAQ79822-57 represent peptide nucleic acids (PNA)
CC   that bind to complementary ssDNA and RNA strands through their
CC   oligoribonucleotide ligands which are linked to a peptide backbone. These
CC   sequences are directed to the human H-ras and K-ras genes and they
CC   modulate the expression of the ras gene in cells or tissues and
CC   specifically modulate the expression of the activated ras in cells or
CC   tissues suspected of harbouring a mutated gene. These sequences are
CC   designed to hybridise with the mRNA from the H-ras and K-ras genes which
CC   interferes with the normal role of mRNA causing a loss of function in the
CC   cell. These sequences are used in the treatment of tumours. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 4012
AAT86501/c
ID   AAT86501 standard; DNA; 20 BP.
XX
AC   AAT86501;
XX
DT   12-MAR-1998  (first entry)
XX
DE   S-adenosylmethionine decarboxylase antisense oligonucleotide #2.
XX
KW   S-adenosylmethionine decarboxylase; SAMDC; antisense oligonucleotide;
KW   antitumour; diagnosis; phosphorothioate; psoriasis; spermine; spermidine;
KW   ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /note= "nucleotides are bonded via phosphorothioate
FT                   linkages"
XX
PN   WO9605298-A1.
XX
PD   22-FEB-1996.
XX
PF   27-JUL-1995;   95WO-EP002985.
XX
PR   09-AUG-1994;   94US-00287753.
XX
PA   (CIBA ) CIBA GEIGY AG.
XX
PI   Mett H,  Haner R,  Dean NM;
XX
DR   WPI; 1996-139694/14.
XX
PT   New oligo:nucleotide derivs. specific for S-adenosyl:methionine
PT   decarboxylase related nucleic acid - useful as anti:sense inhibitors of
PT   this enzyme, esp. for treatment of tumours but also as hybridisation
PT   probes for diagnosis.
XX
PS   Claim 11; Page 45; 81pp; English.
XX
CC   This sequence represents a phosphorothioate analogue of an antisense
CC   oligonucleotide which targets the 5' untranslated region of S-
CC   adenosylmethionine decarboxylase (SAMDC) around nucleotides at positions
CC   -80 to -61. Antisense oligonucleotide analogues (AAT86500-14) which
CC   target the SAMDC gene are used to diagnose conditions associated with
CC   expression of SAMDC by specifically hybridising to RNA or DNA derived
CC   from the SAMDC gene. These antisense molecules are useful for therapeutic
CC   modulation (especially inhibition) of SAMDC synthesis, particularly to
CC   treat tumours (e.g. leukaemia, prostatic carcinoma, colon or brain
CC   tumours, but especially bladder cancer), but also other hyper-
CC   proliferative diseases such as psoriasis. They cause tumour regression
CC   and prevent establishment/growth of (micro)metastases. Inhibition of
CC   SAMDC reduces the level of polyamines (spermine and spermidine in cells),
CC   resulting in cytostasis and possibly apoptosis
XX
SQ   Sequence 20 BP; 0 A; 13 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||||||| ||| ||||| |
Db         20 GCGGCGGCGGCAGCGGCGG 2


RESULT 4013
AAV37666
ID   AAV37666 standard; DNA; 20 BP.
XX
AC   AAV37666;
XX
DT   15-SEP-1998  (first entry)
XX
DE   Allelic variant M4 containing a human G6PD locus polymorphic site.
XX
KW   Polymorphic sequence; human; glucose-6-phosphate dehydrogenase locus;
KW   G6PD; allele-specific; disease diagnosis; forensic analysis;
KW   paternity testing; allelic variant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    10
FT                   /*tag=  a
FT                   /note= "base occupying the polymorphic site"
XX
PN   WO9818967-A1.
XX
PD   07-MAY-1998.
XX
PF   27-OCT-1997;   97WO-US019665.
XX
PR   28-OCT-1996;   96US-0029374P.
PR   07-MAR-1997;   97US-00813508.
XX
PA   (AFFY-) AFFYMETRIX INC.
```

```
XX
PI   Chee M,  Fan J;
XX
DR   WPI; 1998-272250/24.
XX
PT   New polymorphic nucleic acid sequences from the human glucose-6-phosphate
PT   dehydrogenase locus - and derived allele-specific probes and primers,
PT   useful in disease diagnosis, forensic analysis and paternity testing.
XX
PS   Claim 6; Page 28; 37pp; English.
XX
CC   This sequence represents one of the allelic variants containing a human
CC   glucose-6-phosphate dehydrogenase (G6PD) locus polymorphic site.
CC   Sequences shown in AAV37652 to AAV37661 represent the 10 polymorphisms at
CC   10 nucleic acid sequence tagged sites in the human G6PD locus. Sequences
CC   flanking each of these polymorphic sites (allelic variants M1 to M10 )
CC   are shown in Table 2 to 11 of the specification. The invention provides
CC   new nucleic acid segments of 10-100 bases having at least 10 contiguous
CC   bases that include a polymorphic site, within the 10 potential sequences
CC   of the G6PD locus or their complements. Allele-specific oligonucleotides
CC   that hybridise with the nucleic acid sequences which are allelic variants
CC   or their complements are useful as probes and primers for analysing
CC   nucleic acid to indicate polymorphisms in the specified regions.
CC   Polymorphisms may be linked to disease or they can be used in forensic
CC   analysis or paternity testing. Since the 10 sequences are within 50000
CC   base pairs of the human genome (on chromosome X), the probability of
CC   recombination is low and the entire haplotype should be inherited
CC   unchanged for at least several generations making it a good indicator of
CC   paternity
XX
SQ   Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2718 GTAAATGTTCCCCAAATAA 2736
              ||||||| ||  |||||||
Db          1 GTAAATGCTCTGCAAATAA 19


RESULT 4014
AAV69993
ID   AAV69993 standard; DNA; 20 BP.
XX
AC   AAV69993;
XX
DT   04-FEB-1999  (first entry)
XX
DE   Mouse c-jun protein antisense oligonucleotide #38.
XX
KW   Mouse; c-fos; c-jun; activating protein 1; AP-1; diagnosis; metastasis;
KW   antisense oligonucleotide; phosphorothioate; regulation;
KW   malignant tumour; cell cycle expression; hyperproliferative disease; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /note= "phosphorothioate linkages"
XX
PN   WO9846272-A1.
XX
PD   22-OCT-1998.
XX
PF   14-APR-1998;   98WO-US007386.
XX
PR   14-APR-1997;   97US-00837201.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dean NM,  Mckay R,  Miraglia L,  Baker B;
XX
DR   WPI; 1998-609906/51.
XX
PT   Antisense oligonucleotides regulating Activating Protein 1 subunits -
PT   hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell
PT   cycle expression and hyperproliferative disease.
XX
PS   Example 7; Page 52; 120pp; English.
XX
CC   AAV69993 to AAV70008 represent antisense oligonucleotides which are
CC   specifically hybridisable with a region of a nucleic acid encoding mouse
CC   c-Jun protein. The antisense compound regulates the expression of the c-
CC   Jun protein. The present invention also describes antisense
CC   oligonucleotides which regulate the c-Fos protein. The antisense
CC   oligonucleotides are used for the diagnosis and treatment of diseases or
CC   disorders associated with Activating Protein 1 expression, of which c-Fos
CC   and c-Jun are subunits. The antisense oligonucleotides are used in
CC   compositions as c-Fos and/or c-Jun together with a carrier and a
CC   chemotherapeutic agent. They are used to regulate the expression of c-Fos
CC   or c-Jun in cells or tissues, preferably by inhibiting metastasis. They
CC   also regulate cell cycle expression and can be used to treat an animal
CC   with, or being prone to, a hyperproliferative disease
XX
SQ   Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       318 TCGCCGAATATCAGCCGCC 336
             ||||| ||  |||||||||
Db         2 TCGCCCAACTTCAGCCGCC 20


RESULT 4015
AAV11765/c
ID   AAV11765 standard; DNA; 20 BP.
XX
AC   AAV11765;
XX
DT   07-AUG-1998  (first entry)
XX
DE   Nucleic acid-polymer conjugate phosphorothioate primer ODN1.
XX
KW   Water-soluble vinylic monomer; conjugate; cationic radical initiator;
KW   gene transfer; antisense; gene expression; primer; ss.
XX
OS   Synthetic.
XX
PN   DE19746362-A1.
XX
PD   30-APR-1998.
XX
PF   21-OCT-1997;   97DE-01046362.
XX
PR   23-OCT-1996;   96DE-01043738.
XX
PA   (SUDD ) SKW TROSTBERG AG.
XX
PI   Bayer E,  Fritz H,  Maier M;
XX
DR   WPI; 1998-252414/23.
XX
PT   Production of nucleic acid conjugates - with polymer nano-particles
PT   formed by emulsion polymerisation.
XX
PS   Example 1; Col 5; 5pp; German.
XX
CC   Primers AAV11765-V11768 are used in a method for producing conjugates of
CC   nucleic acids with polymer nano-particles. This method involves
CC   subjecting sparingly water-soluble vinylic monomers to emulsion
CC   polymerisation in an aqueous medium in the presence of a cationic radical
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CC   initiator and in the absence of an emulsifier and reacting the resulting
CC   polymer suspension with a nucleic acid. The conjugates are useful for
CC   gene transfer or for antisense control of gene expression. Conjugates
CC   with high nucleic acid loadings and adequate resistance to enzymatic
CC   degradation can be produced
XX
SQ   Sequence 20 BP; 0 A; 12 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGG 505
              |||||||| || ||| |||
Db         19 GAGCCAGGGGGCAGCAGGG 1


RESULT 4016
AAZ11062
ID   AAZ11062 standard; DNA; 20 BP.
XX
AC   AAZ11062;
XX
DT   01-NOV-1999  (first entry)
XX
DE   PCR primer for cloning of HIV gene.
XX
KW   PCR primer; HIV-1; gene cloning; ss.
XX
OS   Synthetic.
OS   Human immunodeficiency virus 1.
XX
PN   JP11221076-A.
XX
PD   17-AUG-1999.
XX
PF   03-FEB-1998;   98JP-00022269.
XX
PR   03-FEB-1998;   98JP-00022269.
XX
PA   (YAMA/) YAMAMOTO M.
PA   (YAMA/) YAMAMOTO N.
XX
DR   WPI; 1999-520715/44.
XX
PT   New method for cloning specific genes - useful for altering genetic
PT   characteristics of cells.
XX
PS   Example 1; Page 6; 13pp; Japanese.
XX
CC   This sequence represents a PCR primer for HIV-1 sequences, that was used
CC   to test the method of the invention. The method is for cloning of a
CC   specific gene, and comprises: (1) treating a sample cDNA with the
CC   restriction enzyme RsaI; (2) binding the treated cDNA to a linker X; (3)
CC   treatment with the restriction enzyme BsmFI; (4) binding to a linker Y,
CC   different from X, to give a cDNA minor fragment library composed of 5'-
CC   linker X-[having 16 bases at RsaI cleaved site (AC) at 5'-side]-linker Y-
CC   3' and (5) cloning of consecutive 14 bases at the RsaI cleaved site (AC)
CC   specific to the sample cDNA. The method is used to clone specific genes
CC   which may then be used to alter the characteristics of cells
XX
SQ   Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1272 ACCGGACACCCCATGGGAC 1290
              || ||| || |||||||||
Db          2 ACAGGATACGCCATGGGAC 20


RESULT 4017
AAZ00584
ID   AAZ00584 standard; DNA; 20 BP.
XX
AC   AAZ00584;
XX
DT   06-OCT-1999  (first entry)
XX
DE   Human glypican sequence tag STS MV2b.
XX
KW   Glypican; GPC1; GPC3; GPC4; GPC5; GPC6; human; glypican-related protein;
KW   glypican-6; glypican-4; glypican-1; glypican-3; glypican-5; diagnosis;
KW   treatment; abnormal; cell growth; cell behaviour; somatic overgrowth;
KW   tumour formation; sequence tag; STS; MV2b; ss.
XX
OS   Homo sapiens.
XX
PN   WO9937764-A2.
XX
PD   29-JUL-1999.
XX
PF   20-JAN-1999;   99WO-EP000329.
XX
PR   27-JAN-1998;   98EP-00200226.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Veugelers MPD,  David GJF;
XX
DR   WPI; 1999-469128/39.
XX
PT   New polynucleotides encoding glypican-related proteins, used to diagnose,
PT   e.g. tumor formation.
XX
PS   Example 2; Page 33; 79pp; English.
XX
CC   This invention describes the isolation of novel human polynucleotides
CC   encoding glypican-related proteins, glypican-6 (GPC6) and glypican-4
CC   (GPC4). The invention also describes the polynucleotide and encoded
CC   protein sequences of glypican-1 (GPC1), glypican-3 (GPC3) and glypican-5
CC   (GPC5). The products of the invention can be used to diagnose and treat
CC   disorders and diseases, particularly those involving abnormal cell growth
CC   and behaviour, such as somatic overgrowth and tumour formation. AAZ00581-
CC   Z00586 represent novel glypican sequence tags (STS's)
XX
SQ   Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2315 ATTTGTTGCTGCTTGTCAC 2333
              ||||  ||||||| |||||
Db          1 ATTTCCTGCTGCTGGTCAC 19


RESULT 4018
AAV84024/c
ID   AAV84024 standard; DNA; 20 BP.
XX
AC   AAV84024;
XX
DT   05-MAR-1999  (first entry)
XX
DE   Antisense oligonucleotide 6958 directed against Ki-ras 5' UTR/5' cap.
XX
KW   Antisense oligonucleotide; phosphorothioate; human H-ras;
KW   tumour formation; cancer cell proliferation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9849349-A1.
XX
```

```
PD   05-NOV-1998.
XX
PF   30-APR-1998;   98WO-US008800.
XX
PR   30-APR-1997;   97US-00848840.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ,  Cook PD,  Monia BP,  Freier SM,  Sanghvi YS;
XX
DR   WPI; 1999-024070/02.
XX
PT   New oligonucleotides for inhibiting ras gene in mutant and activated form
PT   - also used to detect ras genes.
XX
PS   Disclosure; Page 38; 118pp; English.
XX
CC   AAV84024-37 represent antisense phosphorothioate oligonucleotides
CC   directed against human Ki-ras. The oligonucleotides are representative of
CC   the invention, where each oligonucleotide has at least one portion
CC   comprising at least one CH2-NH-O-CH2, CH2-O-N(CH3)-CH2, CH2-N(CH3)-N(CH3)
CC   -CH2 or O-N(CH3)-CH2-CH2 linkage alternating with a phosphorothioate or
CC   phosphodiester linkage. The oligonucleotides are used for the inhibition
CC   of expression of the ras gene in both the normal and the activated form,
CC   the latter of which has been implicated in tumour formation. They are
CC   also used for the detection of the ras gene in cells and tissues and the
CC   treatment of conditions arising from the activation of the ras gene i.e.
CC   to inhibit the proliferation of cancer cells
XX
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 4019
AAX21620/c
ID   AAX21620 standard; DNA; 20 BP.
XX
AC   AAX21620;
XX
DT   14-MAY-1999  (first entry)
XX
DE   Human Ki-ras specific antisense oligo ISIS #6958.
XX
KW   Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
KW   diagnostic; therapeutic; tumour; Ki-ras; antisense; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9902732-A1.
XX
PD   21-JAN-1999.
XX
PF   06-JUL-1998;   98WO-US013966.
XX
PR   08-JUL-1997;   97US-00889296.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM,  Manoharan M;
XX
DR   WPI; 1999-120932/10.
XX
PT   New oligonucleotide targetting human N-ras nucleic acid - is capable of
PT   inhibiting human N-ras expression, useful for preventing or treating
PT   conditions arising from the activation of a human N-ras oncogene.
XX
PS   Disclosure; Page 35; 97pp; English.
XX
CC   The invention relates to oligonucleotides, which target a nucleic acid
CC   encoding human N-ras, and are capable of inhibiting human N-ras
CC   expression. The antisense oligonucleotides form a pharmaceutical
CC   composition, which is useful for modulating the expression of human N-
CC   ras, inhibiting the proliferation of cancer cells, and preventing or
CC   treating conditions arising from the activation of a human N-ras
CC   oncogene. The oligonucleotides are also useful in diagnostics,
CC   therapeutics, and as research reagents and kits. The oligonucleotides
CC   enable the specific modulation of activated human N-ras expression, which
CC   is associated with tumour formation. Sequences AAX21620-633 represent
CC   antisense oligonucleotides complementary to human Ki-ras
XX
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 4020
AAX56984/c
ID   AAX56984 standard; DNA; 20 BP.
XX
AC   AAX56984;
XX
DT   16-JUL-1999  (first entry)
XX
DE   Ras gene modulating liposomal entrapped oligonucleotide primer 28.
XX
KW   Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
KW   cell growth inhibitor; treatment; cancer; ras protein; ss.
XX
OS   Synthetic.
XX
PN   WO9922772-A1.
XX
PD   14-MAY-1999.
XX
PF   28-OCT-1998;   98WO-US022821.
XX
PR   31-OCT-1997;   97US-00961469.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Hardee GE,  Geary RS,  Levin A,  Templin MV,  Howard R,  Mehta RC;
XX
DR   WPI; 1999-313181/26.
XX
PT   Liposome-encapsulated oligonucleotides useful for treating or preventing
PT   cancers associated with ras gene activation.
XX
PS   Example 1; Page 111; 120pp; English.
XX
CC   This invention describes novel compositions comprising oligonucleotides
CC   (AAX56957-X57017), entrapped within liposomes, that hybridize
CC   specifically to a target DNA or mRNA which encodes a mutant or wild-type
CC   ras protein. The products of the invention have anticancer activity and
CC   specifically bring about the antisense inhibition of ras genes or mRNA.
CC   The products of the invention are used to modulate expression of a ras
CC   gene in cells, tissue, organs or organisms, particularly to inhibit cell
CC   growth and especially to treat or prevent cancers associated with
CC   activation of a ras gene. Encapsulating the oligonucleotide reduces the
CC   rate at which it is cleared from the blood when compared with non-
CC   encapsulated material, and the oligonucleotides become distributed to
CC   practically all parts of the body
XX
```

```
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 4021
AAZ01454
ID   AAZ01454 standard; DNA; 20 BP.
XX
AC   AAZ01454;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB001939.
XX
PR   28-NOV-1997;   97FR-00015041.
PR   17-DEC-1997;   97FR-00016034.
PR   04-NOV-1998;   98US-0107077P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-371125/31.
XX
PT   Genome sequence of Chlamydia trachomatis.
XX
PS   Disclosure; Page 1444; 1755pp; English.
XX
CC   PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC   (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC   encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC   against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC   be used to control growth of the microorganism. Chlamydia trachomatis is
CC   responsible for a large number of diseases, e.g. eye diseases such as
CC   conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC   conjunctivitis; genital diseases such as nongonococcal uretritis,
CC   epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC   pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC   The polypeptides of the invention may be of use in treating these
CC   diseases
XX
SQ   Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2651 CCCTAAGGTGAGTGTGCAG 2669
              || | ||||||||||| |||
Db          1 CCTTCAGGTGAGTGTACAG 19


RESULT 4022
AAZ05484/c
ID   AAZ05484 standard; DNA; 20 BP.
XX
AC   AAZ05484;
XX
DT   07-OCT-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW   Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW   paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW   nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW   bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   WO9928475-A2.
XX
PD   10-JUN-1999.
XX
PF   27-NOV-1998;   98WO-IB001939.
XX
PR   28-NOV-1997;   97FR-00015041.
PR   17-DEC-1997;   97FR-00016034.
PR   04-NOV-1998;   98US-0107077P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-371125/31.
XX
PT   Genome sequence of Chlamydia trachomatis.
XX
PS   Disclosure; Page 1774; 1755pp; English.
XX
CC   PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC   (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC   encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC   against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC   be used to control growth of the microorganism. Chlamydia trachomatis is
CC   responsible for a large number of diseases, e.g. eye diseases such as
CC   conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC   conjunctivitis; genital diseases such as nongonococcal uretritis,
CC   epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC   pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC   The polypeptides of the invention may be of use in treating these
CC   diseases
XX
SQ   Sequence 20 BP; 6 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1100 CATTTGGCTAGGGACTTTG 1118
              |||||||| | ||| ||||
Db         20 CATTTGGCGAAGGAGTTTG 2


RESULT 4023
AAX21925/c
ID   AAX21925 standard; DNA; 20 BP.
XX
AC   AAX21925;
XX
DT   18-MAY-1999  (first entry)
XX
DE   Human B-raf kinase antisense oligonucleotide Isis#13742.
XX
KW   Antisense oligonucleotide; B-raf; human; inhibitor; T-cell activation;
```

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KW   hyperproliferative disorder; cancer; restenosis; psoriasis;
KW   atherosclerosis; raf-associated tumour; diagnosis; therapy; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /note= "phosphorothioate bases"
XX
PN   WO9902167-A1.
XX
PD   21-JAN-1999.
XX
PF   06-JUL-1998;   98WO-US013961.
XX
PR   07-JUL-1997;   97US-00888982.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP;
XX
DR   WPI; 1999-120502/10.
XX
PT   New antisense oligonucleotides - for modulation of human B-raf gene
PT   expression.
XX
PS   Claim 7; Page 22; 72pp; English.
XX
CC   This sequence represents an example of an antisense oligonucleotide of
CC   the invention. The oligonucleotides are 8-50 nucleotides in length, and
CC   are targeted to a nucleic acid encoding human B-raf and which is capable
CC   of inhibiting human B-raf expression. The oligonucleotides is used to
CC   inhibit the (abnormal) expression of human B-raf, to inhibit
CC   hyperproliferation of cells, to treat or prevent an abnormal
CC   proliferative condition, e.g. hyperproliferative disorders such as cancer
CC   (e.g. of the brain or nervous system), restenosis, psoriasis or a
CC   disorder characterised by T-cell activation and growth. They may also be
CC   used to diagnose these diseases, as well as atherosclerosis. The
CC   oligonucleotides of the invention may be used to distinguish raf-
CC   associated tumours from tumours having other etiologies. The antisense
CC   oligonucleotides can also be used to quantify raf expression in assays
XX
SQ   Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1531 AGAAAGGTTAGGAGAGTAG 1549
              ||| || | ||||||||||
Db         20 AGAGAGTTCAGGAGAGTAG 2


RESULT 4024
AAX92436
ID   AAX92436 standard; DNA; 20 BP.
XX
AC   AAX92436;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1511; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 7 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        769 CAAGAACCCTCTGAACCTC 787
              ||| ||||||  |||||||
Db          1 CAACAACCCTTGGAACCTC 19


RESULT 4025
AAX95694/c
ID   AAX95694 standard; DNA; 20 BP.
XX
AC   AAX95694;
XX
DT   13-SEP-1999  (first entry)
XX
DE   PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW   neutralising epitope; PCR primer; ss.
XX
OS   Synthetic.
OS   Chlamydophila pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB001890.
XX
PR   21-NOV-1997;   97FR-00014673.
PR   04-NOV-1998;   98US-0107078P.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
```

```
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 1768; Disclosure; 1912pp; English.
XX
CC   AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC   and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC   (see AAX91990). C. pneumoniae causes respiratory disease such as
CC   pneumonia and bronchitis and is thought to be a contributing factor in
CC   heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC   in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae
XX
SQ   Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1585 CACAGACTGGGAACCCCTC 1603
              |||||| |||||| ||| |
Db         19 CACAGATTGGGAAGCCCCC 1


RESULT 4026
AAX29320
ID   AAX29320 standard; DNA; 20 BP.
XX
AC   AAX29320;
XX
DT   10-JUN-1999  (first entry)
XX
DE   JNK1-specific probe ISIS No: 12551.
XX
KW   Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW   JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW   hyperproliferative disease; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9909214-A1.
XX
PD   25-FEB-1999.
XX
PF   07-AUG-1998;   98WO-US016488.
XX
PR   13-AUG-1997;   97US-00910629.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Dean N,  Monia BP,  Nero PS,  Gaarde WA;
XX
DR   WPI; 1999-181060/15.
XX
PT   New antisense oligonucleotides that detect and modulate the expression of
PT   Jun N-terminal kinase proteins - useful for treating hyperproliferative
PT   diseases and inhibiting tumor growth in animals, and for modulating
PT   protein phosphorylation by these proteins.
XX
PS   Example 3; Page 66; 190pp; English.
XX
CC   The invention relates to antisense oligonucleotides that detect and
CC   modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC   oligonucleotides specifically hybridize to a nucleic acid encoding a
CC   JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC   proteins. The oligonucleotides are useful for modulating JNK protein
CC   expression and cell cycle progression in cultured cells or animal cells.
CC   The oligonucleotides are also useful for modulating the phosphorylation
CC   of a protein that has been phosphorylated by a JNK protein, and the
CC   expression of a cellular protein that promotes one or more metastatic
CC   events. The oligonucleotides also form pharmaceutical compositions for
CC   treating animals with a hyperproliferative disease, and for inhibiting
CC   tumor growth in an animal
XX
SQ   Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        813 CCGTAATGAACCCCACTGA 831
              || ||||| ||||||| ||
Db          2 CCATAATGCACCCCACAGA 20


RESULT 4027
AAZ57332
ID   AAZ57332 standard; DNA; 20 BP.
XX
AC   AAZ57332;
XX
DT   03-APR-2000  (first entry)
XX
DE   Human interferon alpha m preparation PCR primer #2.
XX
KW   Human; interferon alpha m; IFN alpha m; IFN alpha 1c; PCR primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   CN1231290-A.
XX
PD   13-OCT-1999.
XX
PF   23-APR-1999;   99CN-00105695.
XX
PR   23-APR-1999;   99CN-00105695.
XX
PA   (KEYV-) STATE KEY LAB VIRUS GENE ENG.
XX
PI   Ma X,  Hou Y,  Hu R;
XX
DR   WPI; 2000-087877/08.
XX
PT   High specific activity recombined human interferon alpha m and its
PT   preparation process.
XX
PS   Claim 2; Page 1; 7pp; Chinese.
XX
CC   On the basis of research on interferon (IFN) alpha Ic and the experiment
CC   of IFN alpha 1c/86D, the present invention applies the peptide pool
CC   constructed by using bacteriophage display technology to the research of
CC   alpha interferon receptor binding zone to develop a new-type mutant IFN
CC   alpha m, based on IFN alpha 1c/86D. Its specific activity can be up to
CC   1.1X10 to the power 8 IU/mg. The invented IFN alpha m possesses high
CC   specific activity to reduce the toxic side effects due to long-period
CC   application of interferon therapy, and can be used as a candidate
CC   production strain for producing a second generation interferon product.
CC   The present sequence represents a PCR primer used in the preparation of
CC   the novel human IFN alpha m
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        370 CTACTCCCAGTCGGCCGAC 388
              ||| || || |||||||||
Db          1 CTATTCTCACTCGGCCGAC 19
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RESULT 4028
AAA46210/c
ID   AAA46210 standard; DNA; 20 BP.
XX
AC   AAA46210;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Primer IPM18R for interphotoreceptor matrix proteoglycan IPM150 cDNA.
XX
KW   Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW   chromosome 6q13-q15; ocular disease; retinal detachment;
KW   chorioretinal degeneration; retinal degeneration; cone degeneration;
KW   age related macular degeneration; photoreceptor degeneration;
KW   retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW   rod- cone dystrophy; cone-rod dystrophy; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200026367-A2.
XX
PD   11-MAY-2000.
XX
PF   29-OCT-1999;   99WO-US025440.
XX
PR   29-OCT-1998;   98US-00183972.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Hageman GS,  Kuehn MH;
XX
DR   WPI; 2000-365616/31.
XX
PT   Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT   preventing, diagnosing and treating ocular disorders such as retinal
PT   detachment and chorioretinal degeneration.
XX
PS   Claim 43; Page 44; 183pp; English.
XX
CC   PCR primers AAA46209-42 were used to amplify cDNA encoding an
CC   interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The
CC   protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and
CC   IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15,
CC   between markers CHLC.GATA11F10 and D6S284. The IPM proteins may be used
CC   to supplement a patients own production of the protein or to rectify
CC   alterations in their nucleic acids that result in expression of an
CC   inactive protein. The IPM nucleic acids may be used in this way to treat
CC   ocular diseases such as retinal detachment, chorioretinal degeneration,
CC   retinal degeneration, age related macular degeneration, photoreceptor
CC   degeneration, RPE (retinal pigment epithelium) degeneration, cone
CC   degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod
CC   dystrophy. The nucleic acids and proteins may also be used to assay for
CC   other modulators of IPM proteoglycan expression and activity that may be
CC   used to treat ocular diseases. The nucleic acids and proteins may also be
CC   used as diagnostic reagents to detect the presence of IPM nucleic acids
CC   and their products in samples from patients according to standard
CC   methodologies
XX
SQ   Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2078 GACACACTCTAAACCCCGT 2096
                ||||  |||  |||  ||||||
Db         19 GACAGACTTTAACCCCCGT 1


RESULT 4029
AAA95858/c
ID   AAA95858 standard; DNA; 20 BP.
XX
AC   AAA95858;
XX
DT   18-JAN-2001  (first entry)
XX
DE   Human Ki-ras antisense oligonucleotide ISIS #6958.
XX
KW   Human; antisense oligonucleotide; ras; H-ras; Ki-ras; N-ras; cytostatic;
KW   phosphorothioate; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US6117848-A.
XX
PD   12-SEP-2000.
XX
PF   03-AUG-1998;   98US-00128494.
XX
PR   05-OCT-1992;   92US-00958134.
PR   21-JAN-1993;   93US-00007996.
PR   01-OCT-1993;   93WO-US009346.
PR   03-APR-1995;   95US-00411734.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Cowsert LM,  Monia BP;
XX
DR   WPI; 2000-610851/58.
XX
PT   Oligonucleotides targeted to human H-ras or human Ki-ras coding
PT   sequences, useful for treating and preventing cancer.
XX
PS   Claim 9; Col 19; 41pp; English.
XX
CC   The present sequence was used in methods for the modulation of ras
CC   expression. Antisense oligonucleotides were designed to specifically
CC   target mRNA encoding human H-ras, Ki-ras and N-ras. The oligonucleotides
CC   can be used to inhibit the proliferation of cancer cells and to prevent
CC   or treat a condition arising from the activation of a ras oncogene. They
CC   may also be used to modulate the expression of human H-ras or human Ki-
CC   ras. The antisense oligonucleotides may contain modified backbones,
CC   substituted sugar moieties and modified bases. The sequences preferably
CC   have a phosphorothioate backbone. They are preferably
CC   oligodeoxynucleotides or chimeric oligonucleotides containing 2'-O-methyl
CC   ends and a central deoxy gap
XX
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              ||  ||||  |||||  |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 4030
AAZ47296
ID   AAZ47296 standard; DNA; 20 BP.
XX
AC   AAZ47296;
XX
DT   11-APR-2000  (first entry)
XX
DE   Enterohaemorrhagic E. coli detection oligonucleotide #6.
XX
KW   Detection; pathogen; enterohaemorrhagic Escherichia coli; EHEC;
KW   verotoxin; clinical examination; food poisoning; diarrhoea; ss.
XX
OS   Escherichia coli.
XX
PN   JP11332599-A.
XX
```

PD 07-DEC-1999.
XX
PF 29-MAY-1998; 98JP-00149749.
XX
PR 29-MAY-1998; 98JP-00149749.
XX
PA (SHMA) SHIMADZU CORP.
XX
DR WPI; 2000-091366/08.
XX
PT Oligonucleotides for detection of enterohemorrhagic Escherichia coli.
XX
PS Claim 3; Page 3; 8pp; Japanese.
XX
CC Oligonucleotides AAZ47291-Z47299 are used in various combinations for
CC detecting pathogenic enterohaemorrhagic Escherichia coli (EHEC), such as
CC E. coli strain 0157. The oligonucleotides are synthesised based on the
CC nucleotide sequences of the verotoxin type 1 (VT1) gene, verotoxin type 2
CC (VT2) gene, variants of VT2 (VT2vha, VT2vhb, VT2vp1 and Vt2vp2) and a
CC pathogen synthetic region gene of pathogenic Escherichia coli O157. The
CC oligonucleotides are used for the detection of enterohemorrhagic
CC Escherichia coli (EHEC) or verotoxin producing Escherichia coli (VTEC)
CC for clinical examination and rapid treatment of food poisoning and
CC diarrhoea
XX
SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2445 TTTTTTGAGACATGGGATC 2463
| ||| |||||||||||
Db 2 TATTTGGAGACATGGGAGC 20

RESULT 4031
AAZ70845/c
ID AAZ70845 standard; DNA; 20 BP.
XX
AC AAZ70845;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:5201.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1340; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 1 A; 8 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1518 AAAATTGGAACGAAGAAAG 1536
||||| |||| |||| |||
Db 19 AAAATAGGAAGGAAGGAAG 1

RESULT 4032
AAZ71898
ID AAZ71898 standard; DNA; 20 BP.
XX
AC AAZ71898;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:6254.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 1564; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.

```
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        794 CAGAAGGAGCTGGTGGGGG 812
              ||||| ||| ||||||  ||
Db          2 CAGAATGAGGTGGTGGTGG 20


RESULT 4033
AAZ76242
ID   AAZ76242 standard; DNA; 20 BP.
XX
AC   AAZ76242;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:10598.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 9; Page 2490; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 20 BP; 1 A; 4 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2558 ATGCTGGGCTCTGTTCTTG 2576
              ||||||| ||||||| | |
Db          2 ATGCTGGTCTCTGTTTTGG 20


RESULT 4034
AAA09679/c
ID   AAA09679 standard; DNA; 20 BP.
XX
AC   AAA09679;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Human SHP-1 antisense oligonucleotide SEQ ID 43.
XX
KW   Human; SHP-1; Src homology region 2-domain phosphatase; phosphorothioate;
KW   cytosolic tyrosine phosphatase; antisense oligonucleotide; cancer;
KW   leukaemia; inflammation; infection; ss.
XX
OS   Homo sapiens.
XX
PN   US6121047-A.
XX
PD   19-SEP-2000.
XX
PF   21-JUL-1999;   99US-00358685.
XX
PR   21-JUL-1999;   99US-00358685.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Cowsert LM;
XX
DR   WPI; 2000-593714/56.
XX
PT   Novel antisense oligonucleotides for modulating the expression of human
PT   SHP-1, especially for treating a disease or condition associated with SHP
PT   -1 expression, e.g. cancer.
XX
PS   Claim 3; Col 41; 33pp; English.
XX
CC   The invention relates to antisense oligonucleotides which modulate the
CC   expression of human SHP-1 (Src homology region 2-domain phosphatase) a
CC   cytosolic tyrosine phosphatase. The invention includes antisense
CC   molecules AAA09644-A09683 which have modified phosphorothioate
CC   internucleoside linkages which target various regions of the SHP-1 gene.
CC   The oligonucleotides inhibit the expression of human SHP-1 in cells or
CC   tissues, and may be used to treat diseases or conditions associated with
CC   SHP-1 expression e.g. cancers, specifically leukaemia
XX
SQ   Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        495 AGGGAGCGGGGCTGCCCTC 513
              || |||||| |||| ||||
Db         19 AGTGAGCGGTGCTGTCCTC 1


RESULT 4035
AAA11880
ID   AAA11880 standard; DNA; 20 BP.
XX
AC   AAA11880;
```

```
XX
DT   16-AUG-2000  (first entry)
XX
DE   Human MDMX antisense oligonucleotide #31040.
XX
KW   MDMX; human; antisense; inhibitor; anticarcinogen; antiinflammatory;
KW   antiinfectious; modulation; treatment; disease; diagnosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6046320-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1999;   99US-00289267.
XX
PR   09-APR-1999;   99US-00289267.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-282710/24.
XX
PT   New antisense oligonucleotides targeting nucleic acids encoding human
PT   MDMX useful for inhibiting MDMX expression and for treating diseases
PT   associated with MDMX expression e.g. tumor formation, inflammation.
XX
PS   Claim 3; Col 79-80; 51pp; English.
XX
CC   This invention describes a novel antisense compound (I), 8-30 nucleobases
CC   in length, targeted to a nucleic acid encoding a human MDMX. (I)
CC   specifically hybridizes with and inhibits the expression of human MDMX.
CC   The products of the invention have anticarcinogen, antiinflammatory and
CC   antiinfectious activity. Synthesized chimeric oligonucleotides targeted
CC   to human MDMX, 20 nucleotides in length, composed of a central gap region
CC   consisting of ten 2'-deoxynucleotides flanked on both sides by 5-
CC   nucleotide wings were tested for antisense inhibition of MDMX expression.
CC   Results of real-time quantitative polymerase chain reaction (PCR) showed
CC   71 out of the 159, 20 base pair sequences, all fully defined in the
CC   specification, demonstrated at least 30% inhibition of MDMX expression.
CC   The antisense oligonucleotides are useful for effective and specific
CC   modulation, particularly inhibition of MDMX expression, and may be used
CC   in treating humans or animals suspected of having or being prone to a
CC   disease or condition associated with expression of MDMX. The antisense
CC   oligonucleotides may also be used as research reagents or kits, and as
CC   diagnostics, e.g. to elucidate the function of a particular gene or to
CC   distinguish between functions of various members of a biological pathway,
CC   and as prophylaxis, e.g. to prevent or delay infection, inflammation or
CC   tumor formation. AAA11781-A11945 represent antisense oligonucleotides
CC   described in the method of the invention
XX
SQ   Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        222 ACGACGGGAGCAGCAATGG 240
              ||||| ||||| | |||||
Db          2 ACGACAGGAGCCGAAATGG 20


RESULT 4036
AAZ59002
ID   AAZ59002 standard; DNA; 20 BP.
XX
AC   AAZ59002;
XX
DT   11-APR-2000  (first entry)
XX
DE   Escherichia coli strain O-157 detection oligonucleotide #2.
XX
KW   O-antigen; Escherichia coli O-157; pathogen; enterohaemorrhagic colitis;
KW   detection; food poisoning; diarrhoea; ss.
XX
OS   Escherichia coli.
XX
PN   JP11332600-A.
XX
PD   07-DEC-1999.
XX
PF   29-MAY-1998;   98JP-00149750.
XX
PR   29-MAY-1998;   98JP-00149750.
XX
PA   (SHMA ) SHIMADZU CORP.
XX
DR   WPI; 2000-091367/08.
XX
PT   Oligonucleotides for detection of pathogenic Escherichia coli O-157.
XX
PS   Claim 1; Page 2; 11pp; Japanese.
XX
CC   Oligonucleotides AAZ59001-Z59004 are targeted to the O-antigen synthesis
CC   genes of Escherichia coli O-157 which is a major pathogenic bacterium of
CC   enterohaemorrhagic colitis. The oligonucleotides are used as probes
CC   and/or primers for detecting Escherichia coli O-157 in food poisoning and
CC   diarrhoea
XX
SQ   Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2445 TTTTTTGAGACATGGGATC 2463
              | ||| ||||||||||| |
Db          2 TATTTGGAGACATGGGAGC 20


RESULT 4037
AAC60557/c
ID   AAC60557 standard; DNA; 20 BP.
XX
AC   AAC60557;
XX
DT   31-JAN-2001  (first entry)
XX
DE   Human fra-1 mRNA antisense oligonucleotide ISIS 109048.
XX
KW   Human; fra-1; antisense oligonucleotide; phosphorothioate; cytostatic;
KW   antiinflammatory; 2'-methoxyethyl wing; 2'-MOE wing; infection; cancer;
KW   ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6124133-A.
XX
PD   26-SEP-2000.
XX
PF   15-OCT-1999;   99US-00418641.
XX
PR   15-OCT-1999;   99US-00418641.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Taylor JK,  Cowsert LM;
XX
DR   WPI; 2000-601552/57.
XX
PT   Novel antisense compound 8-30 nucleobases in length targeted to human fra
PT   -1 and which specifically hybridizes with and inhibits the expression of
PT   human fra-1, useful for modulating the expression of fra-1 in cells.
XX
```

PS Claim 3; Col 41; 38pp; English.
XX
CC The present sequence is one of a large number of antisense
CC oligonucleotides which are targeted to nucleic acids encoding fra-1. The
CC sequences may be oligodeoxyribonucleotides or chimeric oligonucleotides
CC containing a central gap region consisting of ten 2'-deoxynucleotides,
CC which is flanked on both sides by 2'-methoxyethyl (2'-MOE) wings. The
CC oligonucleotides have a phosphorothioate backbone and the cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines. The fra-1 antisense
CC oligonucleotides are useful for inhibiting the expression of fra-1 in
CC human cells or tissues. They can be used for diagnostics, therapeutics,
CC prophylaxis and as research reagents and in kits. Use of the antisense
CC compounds may also be useful prophylactically, e.g. to prevent or delay
CC infection, inflammation or tumour formation
XX
SQ Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 684 AGATGGACGAGGTGCAGAA 702
|||| || ||| |||||||
Db 19 AGATTGAGGAGCTGCAGAA 1

RESULT 4038
AAC62863
ID AAC62863 standard; DNA; 20 BP.
XX
AC AAC62863;
XX
DT 06-FEB-2001 (first entry)
XX
DE JNK antisense oligonucleotide ISIS #12551.
XX
KW Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
KW cellular hyperproliferation; Alzheimer's; Parkinson's disease;
KW amylotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
KW myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
KW diabetes; Jun N-terminal kinase; ss.
XX
OS Homo sapiens.
XX
PN WO200059549-A1.
XX
PD 12-OCT-2000.
XX
PF 04-APR-2000; 2000WO-US008880.
XX
PR 07-APR-1999; 99US-00287796.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Mckay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
XX
DR WPI; 2000-638427/61.
XX
PT Novel methods for reducing apoptosis comprising contacting cells with
PT antisense oligonucleotides, useful for treating apoptotic disorders, e.g.
PT cancer.
XX
PS Example 3; Page 131; 160pp; English.
XX
CC The present invention relates to antisense oligonucleotides (AAC62844-
CC C63000, AAA96093-A96099 and AAA07993) that hybridise specifically to a
CC nucleotide encoding a Jun N-terminal kinase (JNK2) protein, resulting in
CC decrease of JNK2 expression and leading to induction of apoptosis. The
CC present sequence is one such antisense oligonucleotide. The
CC oligonucleotides of the present invention are useful for treating
CC diseases or conditions with reduced apoptosis, e.g. cancer and cellular
CC hyperproliferation. The oligonucleotides may also be used to increase the
CC stimulation of apoptotic proteins, e.g. for treating Alzheimer's or
CC Parkinson's disease, amylotrophic lateral sclerosis, retinitis,
CC pigmentosa, epilepsy, myocardial infarction, stroke, obstructive
CC jaundice, polycystic kidney and diabetes. The present sequence may have a
CC phosphorothioate backbone
XX
SQ Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 813 CCGTAATGAACCCCACTGA 831
|| ||||| ||||||| ||
Db 2 CCATAATGCACCCCACAGA 20

RESULT 4039
AAC65597/c
ID AAC65597 standard; DNA; 20 BP.
XX
AC AAC65597;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human uteroglobin SNP PCR primer hUG-3100GR.
XX
KW Mouse; uteroglobin; immunoglobulin A mediated disease; IgA nephropathy;
KW autoimmune disorder; pulmonary inflammation; Wegener's granulomatosus;
KW Goodpasture's disease; diabetic glomerulosclerosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200062795-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009979.
XX
PR 21-APR-1999; 99US-0130434P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Mukherjee AB, Zheng F, Zhang Z;
XX
DR WPI; 2000-687100/67.
XX
PT Use of a composition comprising uteroglobin (or a fragment, derivative,
PT mimetic or variant), for inhibiting or treating an immunoglobulin-A
PT mediated autoimmune disorders, e.g. diabetic glomerulosclerosis and
PT pulmonary inflammation.
XX
PS Example 12; Page 43; 60pp; English.
XX
CC The present invention describes the use of uteroglobin in the diagnosis
CC and prevention of IgA mediated diseases, such as IgA nephropathy,
CC Wegener's granulomatosus, Goodpasture's disease and diabetic
CC glomerulosclerosis. This is possible as uteroglobin binds to fibronectin,
CC preventing the complexing of fibronectin with IgA and the deposition of
CC immune complexes in the kidney
XX
SQ Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2255 TTTATTTGCATATTTATTT 2273
||| |||| |||||||||
Db 19 TTTGTTTGTTTATTTATTT 1

RESULT 4040
AAC66295

```
ID   AAC66295 standard; DNA; 20 BP.
XX
AC   AAC66295;
XX
DT   20-FEB-2001  (first entry)
XX
DE   Primer P13 used in EIAV DNA isolation.
XX
KW   Equine infectious anemia virus; EIAV; donkey leukocyte strain; vaccine;
KW   gene therapy; human immunodeficiency virus; HIV; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200063387-A1.
XX
PD   26-OCT-2000.
XX
PF   21-APR-2000; 2000WO-CN000096.
XX
PR   21-APR-1999;   99CN-00105852.
XX
PA   (NAAI-) NAT CENT AIDS PREVENTION & CONTROL.
PA   (HARB-) HARBIN VETERINARY RES INST CHINESE ACAD.
XX
PI   Shao Y,  Shen R,  Chen G,  Yu K,  Pan P,  Jia B,  Feng Y,  Xue F;
PI   Xiang W,  Fan X,  Lue X,  Zhao L;
XX
DR   WPI; 2000-672738/65.
XX
PT   Full-length DNA sequence of provirus genomes, sequences of various
PT   functional genes and protein of donkey leukocyte strain of equine
PT   infectious anemia virus, used for preparing vaccines and studying HIV.
XX
PS   Example 1; Page 6; 26pp; Chinese.
XX
CC   This invention relates to a full length provirus genomic DNA sequence
CC   AAC66281 of equine infectious anemia virus (EIAV) from the donkey
CC   leukocyte strain. Included in the invention are the gag, pol, env, rev,
CC   tat, and S2 gene sequences AAC66314 - AAC66319 and their encoded proteins
CC   AAB35754 - AAB35759. The invention also relates to PCR primers AAC66282 -
CC   AAC66288 which are used to isolate the EIAV DNA sequences. Other primers
CC   represented in AAC66289 - AAC66313 are also used in the course of the
CC   invention for the isolation and characterisation of the DNA sequences
CC   identified in the invention. The genes and proteins can be used for
CC   preparing gene mutation and deletion vaccines, DNA vaccines and
CC   diagnostics and in producing an equine infectious anemia virus gene
CC   transfer system for gene therapy. The proteins and polynucleotides may
CC   also be used in the study of HIV
XX
SQ   Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2206 TCAAATGGGAGACTCTTTG 2224
              | | |||||||||| |||||
Db          2 TAAGATGGGAGACCCTTTG 20


RESULT 4041
AAC60958
ID   AAC60958 standard; DNA; 20 BP.
XX
AC   AAC60958;
XX
DT   13-FEB-2001  (first entry)
XX
DE   Interleukin 2 short tandem repeat primer SEQ ID NO:18.
XX
KW   Short tandem repeat; primer; STR; susceptibility; HIV; infection; AIDS;
KW   detection; polymorphism; interleukin 10 promoter; IL-10;
KW   chromosome position 4q26-q27; interleukin 2; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061811-A2.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US009355.
XX
PR   09-APR-1999;   99US-0128521P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Smith MW,  Shin HD,  O'brien SJ;
XX
DR   WPI; 2000-687051/67.
XX
PT   Predicting susceptibility to HIV infection or progression useful for
PT   selection of therapeutic treatment for persons infected with HIV virus,
PT   comprises detecting polymorphism in human interleukin-10 promoter.
XX
PS   Example 1; Page 11; 40pp; English.
XX
CC   The present invention describes a method for predicting susceptibility to
CC   HIV infection or HIV progression in a subject. The method involves
CC   detecting a polymorphism in a human interleukin-10 (IL-10) promoter,
CC   where the presence of the polymorphism indicates susceptibility to HIV
CC   infection or HIV progression. The method provides prognostic information
CC   to persons infected with HIV virus and is useful to help select
CC   treatments (such as administration of IL-10 or gene therapy with IL-10).
CC   The presence of polymorphism is useful as predictor that very aggressive
CC   treatment could substantially eradicate the virus from the infected
CC   person. The method is useful for the generation of normograms or other
CC   predictive algorithms that can be used, in association with allele
CC   status, to prognose probable survival or years to development of AIDS
CC   following HIV seroconversion. It indicates that increased expression of
CC   the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression
CC   and enables a variety of new therapeutic interventions in the treatment
CC   of HIV disease. The present sequence represents a short tandem repeat
CC   (STR) primer which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 4 A; 3 C; 3 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAAC 1785
              | ||||| |||| ||||||
Db          2 ATGCTTTATTTTCTTGAAC 20


RESULT 4042
AAS02211
ID   AAS02211 standard; DNA; 20 BP.
XX
AC   AAS02211;
XX
DT   04-JUL-2001  (first entry)
XX
DE   A. thaliana phosphoenolpyruvate carboxylase (PEPc) kinase PCR primer #5.
XX
KW   Phosphoenolpyruvate carboxylase kinase; PEPc kinase; CAM; C_3 plant;
KW   Crassulacean acid metabolism; C_4 plant; reversible phosphorylation; ss;
KW   transgenic plant; sugar; storage; carbohydrate; lipid; leaf; fruit; seed;
KW   tuber; carbon; nitrogen; Brassicaceae; Musaceae; Solanaceae; Poaceae;
KW   Malvaceae; PCR primer.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200118191-A2.
XX
PD   15-MAR-2001.
```

```
XX
PF   04-SEP-2000; 2000WO-GB003392.
XX
PR   04-SEP-1999;   99GB-00020816.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Nimmo HG,  Jenkins GI,  Hartwell J;
XX
DR   WPI; 2001-244569/25.
XX
PT   New isolated phosphoenolpyruvate carboxylase kinase (PEPc kinase) enzyme
PT   useful for production of transgenic plants such as Brassicaceae, Musaceae
PT   and Solanaceae.
XX
PS   Disclosure; Page 29; 76pp; English.
XX
CC   The sequence represents a PCR primer used in expression studies of
CC   phosphoenolpyruvate carboxylate (PEPc) kinase enzyme. PEPc kinase
CC   regulates PEPc activity in C_3 and C_4 plants and in plants that exhibit
CC   Crassulacean acid metabolism (CAM), by reversible phosphorylation.
CC   Antibodies can be raised to plant PEPc kinase for detecting the presence
CC   of the enzyme in a sample. PEPc kinase DNA is useful for the production
CC   of transgenic plants, such as CAM plants, C_3 plants or C_4 plants, from
CC   the family Brassicaceae, Musaceae, Solanaceae, Poaceae or Malvaceae. The
CC   DNA may also be used in the production of eukaryotic cells, particularly
CC   plant cells having a modified PEPc kinase activity, as a probe to amplify
CC   and/or analyse PEPc kinase coding sequence from a chosen organism and in
CC   diagnostic assays to determine the presence of a PEPc kinase coding
CC   sequence in an organism. PEPc kinase can be used to supply and manipulate
CC   PEPc kinase enzymatic activity in vitro in order to alter levels of
CC   sugar, storage, carbohydrate, lipid and/or protein content of leaves,
CC   fruits, seeds, tubers and other organs in a wider range of species as a
CC   result of altered partitioning of carbon/nitrogen
XX
SQ   Sequence 20 BP; 7 A; 2 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2640 GTTGGGCTGAACCCTAAGG 2658
              |||||| ||||||  ||||
Db          1 GTTGGGATGAACCAGAAGG 19


RESULT 4043
AAD14811/c
ID   AAD14811 standard; DNA; 20 BP.
XX
AC   AAD14811;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116652.
XX
KW   Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;
KW   antisense therapy; diabetes; hyperproliferative disorder; inflammation;
KW   neurological disorder; tumour; haematopoietic disorder; infection;
KW   hyperproliferative disorder; developmental disorder; antisense;
KW   phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Methoxyethyl residues"
FT   modified_base   6
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   14
FT                   /*tag=  e
FT                   /mod_base= m5c
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Methoxyethyl residues"
XX
PN   WO200152865-A1.
XX
PD   26-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US001411.
XX
PR   21-JAN-2000; 2000US-00488856.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Mckay R,  Butler MM,  Wyatt JR;
XX
DR   WPI; 2001-442247/47.
XX
PT   Antisense compound 8 to 30 nucleobases in length comprising a compound
PT   that is targeted to a nucleic acid molecule encoding glycogen synthase
PT   kinase 3 alpha, useful for the treatment of e.g. diabetes and
PT   hyperproliferative disorders.
XX
PS   Example 15; Page 83; 115pp; English.
XX
CC   The invention relates to an antisense compound 8 to 30 nucleobases in
CC   length targetted to a nucleic acid encoding glycogen synthase kinase 3
CC   alpha. The antisense compound specifically hybridises with and inhibits
CC   the expression of glycogen synthase kinase 3 alpha. The antisense
CC   compound is useful for the treatment of a diseases associated with
CC   glycogen synthase kinase 3 alpha such as diabetes, a neurological
CC   disorder, a haematopoietic disorder, a hyperproliferative disorder or a
CC   developmental disorder. The antisense compounds may also be used
CC   prophylactically to prevent or delay infection, inflammation or tumour
CC   formation. The present sequence is a phosphorothioate antisense
CC   oligonucleotide targetted to human glycogen synthase kinase 3 alpha
CC   genomic DNA
XX
SQ   Sequence 20 BP; 5 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        758 ATTTCCATGACCAAGAACC 776
              |||||  | ||||||||||
Db         20 ATTTCTGTCACCAAGAACC 2


RESULT 4044
AAS45779
ID   AAS45779 standard; DNA; 20 BP.
XX
AC   AAS45779;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Mouse PARP-2 antisense inhibitor ISIS #110245.
XX
KW   Mouse; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
KW   cytostatic; nootropic; neuroprotective; antiinflammatory; antidiabetic;
KW   immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
KW   oxidative stress; neurological disorder; parkinsonism; apoptosis;
KW   meningitis-associated intracranial complication; ischaemia; probe;
KW   inflammatory disorder; autoimmune disorder; arthritis; diabetes.
```

```
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "All cytidine residues are 5-methyl cytidine"
FT   modified_base   1. .5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2' methoxyethyl nucleotides"
XX
PN   WO200164955-A1.
XX
PD   07-SEP-2001.
XX
PF   01-MAR-2001; 2001WO-US006572.
XX
PR   02-MAR-2000; 2000US-00517467.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Popoff I,  Cowsert LM;
XX
DR   WPI; 2001-602570/68.
XX
PT   Antisense compound useful for treating hyperproliferative, neurological,
PT   inflammatory and autoimmune disorders and diabetes inhibits human PARP.
XX
PS   Example 17; Page 88; 168pp; English.
XX
CC   The invention relates to antisense oligonucleotides targeted to human
CC   PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly
CC   (ADP-ribose) polymerase plays an important role in chromatin
CC   decondensation, DNA replication, DNA repair, gene expression, malignant
CC   transformation, cellular differentiation and apoptosis. The antisense
CC   oligonucleotide inhibitors are useful for inhibiting the expression of
CC   PARP in human cells or tissues. They are also useful for treating a human
CC   with a disease associated with PARP especially hyperproliferative
CC   disorders (e.g. cancer), cellular injury resulting from oxidative stress,
CC   neurological (e.g parkinsonism, meningitis-associated intracranial
CC   complications and ischaemia) , inflammatory and autoimmune disorders (e.g
CC   arthritis) and diabetes. The present sequence is an antisense
CC   oligonucleotide of the invention
XX
SQ   Sequence 20 BP; 4 A; 1 C; 7 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2679 TGTGGGTGAAATGGAGATT 2697
              ||| | |||| ||||||||
Db          1 TGTTGTTGAACTGGAGATT 19


RESULT 4045
AAH00614
ID   AAH00614 standard; DNA; 20 BP.
XX
AC   AAH00614;
XX
DT   24-JUL-2001  (first entry)
XX
DE   Staphylococcus detection nucleotide sequence SEQ ID NO:605.
XX
KW   Species specific; genus specific; family specific; probe; detection;
KW   identification; algal; archaeal; bacterial; fungal; parasitical;
KW   microorganism; diagnosis; translation elongation factor Tu; toxin;
KW   translation elongation factor G; RecA recombinase; resistance;
KW   catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW   primer; ss.
XX
OS   Staphylococcus sp.
XX
PN   WO200123604-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-CA001150.
XX
PR   28-SEP-1999;   99CA-02283458.
PR   19-MAY-2000; 2000CA-02307010.
XX
PA   (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI   Bergeron MG,  Boissinot M,  Huletsky A,  Menard C,  Ouellette M;
PI   Picard FJ,  Roy PH;
XX
DR   WPI; 2001-245006/25.
XX
PT   Nucleic acid sequences are used to generate universal probes and primers
PT   which can be used to identify and detect the presence of algal, archaeal,
PT   bacterial, fungal and parasitical species in a test sample.
XX
PS   Claim 11; Page 756; 1580pp; English.
XX
CC   The present invention describes a method for generating a repertory of
CC   nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC   and/or primers are derived. The method comprises amplifying the nucleic
CC   acids of determined algal, archaeal, bacterial, fungal and parasitical
CC   species with a combination of defined primer pairs. The method can be
CC   used for producing probes and/or primers for detecting one or more
CC   related microorganisms e.g. algae, archaea, bacteria, fungi and
CC   parasites, for universal detection and for specific and ubiquitous
CC   detection and identification of an algal, archaeal, bacterial, fungal and
CC   parasitical species, genus, family and group. A nucleic acid (I) obtained
CC   using the method of the invention can be used for the universal detection
CC   of any bacterium, fungus or parasite in a sample and for the detection of
CC   at least one antimicrobial agent resistance gene or at least one toxin
CC   gene. hexA nucleic acids are used for the specific and ubiquitous
CC   detection and for identification of Streptococcus pneumoniae. (I) can be
CC   used to design a therapeutic agent which is effective against
CC   microorganisms. Microbial species or genus or family or phylum or group
CC   which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC   Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC   Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC   gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC   results than substrate specificity tests as results can be determined in
CC   an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC   represent nucleotide sequences and primers/probes which are given in the
CC   exemplification of the present invention
XX
SQ   Sequence 20 BP; 7 A; 2 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2720 AAATGTTCCCCAAATAATT 2738
              |||||||| |||| |||
Db          2 AAATGTTCCGTAAATTATT 20


RESULT 4046
AAF62926/c
ID   AAF62926 standard; DNA; 20 BP.
```

XX
AC AAF62926;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human PEPCK-cytosolic antisense oligonucleotide ISIS 108096.
XX
KW Human; antiinflammatory; cytostatic; antisense gene therapy;
KW phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection;
KW inflammation; tumour formation; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN US6187545-B1.
XX
PD 13-FEB-2001.
XX
PF 21-JAN-2000; 2000US-00488671.
XX
PR 21-JAN-2000; 2000US-00488671.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Mckay R, Butler MM, Wyatt J, Cowsert LM;
XX
DR WPI; 2001-190979/19.
XX
PT Antisense compound capable of modulating the expression of phosphoenol
PT pyruvate carboxykinase-cytosolic, useful for preventing or delaying
PT infection, inflammation or tumor formation.
XX
PS Claim 1; Col 43; 64pp; English.
XX
CC The present sequence is one of a number of antisense compounds of up to
CC 30 nucleobases in length that are capable of inhibiting the expression of
CC phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). The
CC antisense compounds are useful for inhibiting the expression of PEPCK-
CC cytosolic in cells or tissues. They are commonly used as research
CC reagents and in diagnostics, e.g. to elucidate the function of particular
CC genes. They are also useful for distinguishing between functions of
CC various members of a biological pathway and for research use. The
CC antisense compounds are also useful prophylactically, e.g. to prevent or
CC delay infection, inflammation or tumour formation. The present sequence
CC is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
CC deoxy gap
XX
SQ Sequence 20 BP; 1 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 216 ATCGCCACGACGGGAGCAG 234
||| |||| |||||||||
Db 19 ATCACCACACCGGGAGCAG 1

RESULT 4047
AAS04459
ID AAS04459 standard; DNA; 20 BP.
XX
AC AAS04459;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human DAXX gene promoter region reverse PCR primer #4.
XX
KW Death-associated protein 6; DAXX; polymorphism; haplotype pair; human;
KW immune disorder; autoimmune disease; population diversity; ss;
KW paternity testing; anthropological lineage; forensic application;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN WO200125245-A2.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027487.
XX
PR 06-OCT-1999; 99US-0157909P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;
XX
DR WPI; 2001-308220/32.
XX
PT New human death-associated protein 6 (DAXX) gene variants comprising 19
PT polymorphic sites useful in studying the effect of variation on the
PT biological activity of DAXX and in developing drugs targeting the
PT protein.
XX
PS Example 1; Page 30; 97pp; English.
XX
CC Sequences AAS04452-AAS04485 represent PCR primers used to amplify regions
CC of a DNA encoding human death-associated protein 6 (DAXX). This DNA may
CC comprise one or more polymorphisms at specific nucleotide positions to
CC form one of nineteen possible polymorphic variants. Associations between
CC a trait and a genotype or a haplotype of the DAXX gene can be identified
CC by comparing the frequency of the genotype or haplotype in a population
CC exhibiting the trait with that of a reference population. A higher
CC frequency in the trait population indicates an association. Methods
CC involving genotyping or haplotyping of the DAXX gene of an individual can
CC lead to prediction of haplotype pairs for the DAXX gene of related
CC individuals, and may be useful in studying the expression and biological
CC function of DAXX, as well as in developing drugs targeting this protein.
CC Polymorphic variants of DAXX are useful in studying the effect of the
CC variation on the biological activity of DAXX as well as on the binding
CC affinity of candidate drugs targeting DAXX for the treatment of
CC autoimmune diseases and other immune disorders. Polymorphism is also
CC useful for studying population diversity, anthropological lineage,
CC paternity testing, forensic applications, and for identifying
CC associations between the DAXX genetic variation and a trait such as level
CC of drug response or susceptibility to disease. DAXX proteins may be used
CC to measure binding affinities of one or more candidate drugs targeting
CC the DAXX protein
XX
SQ Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 333 CGCCACCCTACTTTCCCCC 351
| |||||||| ||| ||||
Db 2 CCCCACCCTAATTTTCCCC 20

RESULT 4048
AAF28352
ID AAF28352 standard; DNA; 20 BP.
XX
AC AAF28352;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA oligomer #2.
XX
KW Deoxynucleic S-Methythiourea; DNmt; antisense therapy;
KW cardiovascular disease; inflammatory disease; neurocellular disease;
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW influenza; herpes; infection; ss.
XX
OS Unidentified.
XX

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PN   US6169176-B1.
XX
PD   02-JAN-2001.
XX
PF   28-SEP-1999;   99US-00407675.
XX
PR   02-JUL-1998;   98US-0091481P.
PR   11-DEC-1998;   98US-0111800P.
PR   02-JUL-1999;   99US-00347443.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Dev AP,  Bruice TC;
XX
DR   WPI; 2001-122276/13.
XX
PT   Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
PT   antisense therapy, by synthesizing oligonucleotides comprising backbone
PT   of alkyl or alkoxy thiourea linkages in solution or on solid phase.
XX
PS   Example 7; Fig 16; 48pp; English.
XX
CC   The present sequence was used to demonstrate the ability of deoxynucleic
CC   S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An
CC   increase in the C content of the oligos resulted in a large decrease in
CC   binding. This experiment was performed as an example of a method for
CC   preparing oligonucleotides comprising a backbone of alkyl or alkoxy
CC   thiourea linkages. The method is useful for preparing oligonucleotides
CC   for use in antisense or antigene therapy, to inhibit production of
CC   proteins associated with genetic diseases, cardiovascular, inflammatory
CC   and neurocellular diseases, and for antiviral therapy, e.g. to treat
CC   human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
CC   infections. The compounds are also useful as diagnostic reagents to
CC   detect the presence or absence of the target DNA or RNA sequences to
CC   which they specifically bind and by antagonising the normal biological
CC   activity of a target protein, they can be used in the manipulation of
CC   tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
CC   cultures. The method provides an efficient and rapid solid-phase method
CC   for the synthesis of thiourea and S-methylthiourea
XX
SQ   Sequence 20 BP; 16 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||| |||| |||| ||||
Db          2 AAAACAAAACAAAACAAAA 20


RESULT 4049
AAF28352/c
ID   AAF28352 standard; DNA; 20 BP.
XX
AC   AAF28352;
XX
DT   02-APR-2001  (first entry)
XX
DE   DNA oligomer #2.
XX
KW   Deoxynucleic S-Methythiourea; DNmt; antisense therapy;
KW   cardiovascular disease; inflammatory disease; neurocellular disease;
KW   antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW   influenza; herpes; infection; ss.
XX
OS   Unidentified.
XX
PN   US6169176-B1.
XX
PD   02-JAN-2001.
XX
PF   28-SEP-1999;   99US-00407675.
XX
PR   02-JUL-1998;   98US-0091481P.
PR   11-DEC-1998;   98US-0111800P.
PR   02-JUL-1999;   99US-00347443.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Dev AP,  Bruice TC;
XX
DR   WPI; 2001-122276/13.
XX
PT   Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
PT   antisense therapy, by synthesizing oligonucleotides comprising backbone
PT   of alkyl or alkoxy thiourea linkages in solution or on solid phase.
XX
PS   Example 7; Fig 16; 48pp; English.
XX
CC   The present sequence was used to demonstrate the ability of deoxynucleic
CC   S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An
CC   increase in the C content of the oligos resulted in a large decrease in
CC   binding. This experiment was performed as an example of a method for
CC   preparing oligonucleotides comprising a backbone of alkyl or alkoxy
CC   thiourea linkages. The method is useful for preparing oligonucleotides
CC   for use in antisense or antigene therapy, to inhibit production of
CC   proteins associated with genetic diseases, cardiovascular, inflammatory
CC   and neurocellular diseases, and for antiviral therapy, e.g. to treat
CC   human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
CC   infections. The compounds are also useful as diagnostic reagents to
CC   detect the presence or absence of the target DNA or RNA sequences to
CC   which they specifically bind and by antagonising the normal biological
CC   activity of a target protein, they can be used in the manipulation of
CC   tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
CC   cultures. The method provides an efficient and rapid solid-phase method
CC   for the synthesis of thiourea and S-methylthiourea
XX
SQ   Sequence 20 BP; 16 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||| |||| |||| ||||
Db         20 TTTTGTTTTGTTTTGTTTT 2


RESULT 4050
AAS03670
ID   AAS03670 standard; DNA; 20 BP.
XX
AC   AAS03670;
XX
DT   29-AUG-2001  (first entry)
XX
DE   PCR primer re012, used to detect RHD positive haplotypes.
XX
KW   Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; SMP1;
KW   RHCE; RHD negative; blood group typing; blood transfusion; antigen C;
KW   haemolytic disease of the newborn; chromosome 1 p34.1-p36; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200132702-A2.
XX
PD   10-MAY-2001.
XX
PF   31-OCT-2000; 2000WO-EP010745.
XX
PR   02-NOV-1999;   99EP-00121686.
PR   31-MAY-2000; 2000EP-00111696.
XX
PA   (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.
XX
```

PI Flegel WA, Wagner FF;
XX
DR WPI; 2001-291052/30.
XX
PT New nucleic acid molecular structure, useful for detection of common RHD
PT positive haplotypes in D-negative individuals, comprises RHD, SMP1 and
PT RHCE genes.
XX
PS Example 12; Page 66; 135pp; English.
XX
CC The sequence represents PCR primer re012, used to detect RHD positive
CC haplotypes in RHD negative individuals. The primer was used in DNA typing
CC using PCR-sequence length polymorphism (SSP) of the Rhesus genes locus
CC comprising the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus
CC box(es), preferably the hybrid Rhesus box, the upstream Rhesus box and/or
CC the downstream Rhesus box. The RHD and RHCE genes are located at
CC chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
CC RHD deletion in the common RHD negative haplotypes. The primers of the
CC invention are useful for: (1) the specific detection of the common RHD
CC positive haplotypes in D-negative individuals; (2) blood group typing;
CC (3) determining whether a patient can be transfused with RhD negative
CC blood and whether blood is suitable for transfusion to patients who
CC should not be exposed to antigen C; (4) assessing the risk of a RhD
CC negative mother of conceiving or carrying an RhD positive foetus. Anti-D
CC antibodies are useful for treating pregnant women who are Rhesus D
CC negative, where the foetus is not homozygous for the RHD gene to treat or
CC prevent haemolytic disease of the newborn
XX
SQ Sequence 20 BP; 2 A; 11 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 340 CTACTTTCCCCCTCCCTAC 358
|| ||||||| ||||||| |
Db 2 CCACTTTCCACCTCCCTGC 20

RESULT 4051
AAF27109/c
ID AAF27109 standard; DNA; 20 BP.
XX
AC AAF27109;
XX
DT 06-APR-2001 (first entry)
XX
DE Human MEKK1 phosphorothioate antisense oligonucleotide, SEQ ID NO:31.
XX
KW Human MEKK1; mitogen-activated protein kinase kinase kinase 1;
KW MEK kinase 1; MAP/ERK kinase kinase 1; pro-apoptotic;
KW apoptosis signal regulation; programmed cell death;
KW serine/threonine kinase; MAP kinase cascade; JNK/SAPK;
KW Jun N-terminal kinase/stress-activated protein kinase; Bcl-2 substrate;
KW NF-kappa-B-mediated transcription regulation; expression inhibition;
KW antisense; hyperproliferative disorder; cancer; inflammation;
KW phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN US6168950-B1.
XX
PD 02-JAN-2001.
XX
PF 23-JUL-1999; 99US-00359756.
XX
PR 23-JUL-1999; 99US-00359756.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM, Gaarde W, Ward DT;
XX
DR WPI; 2001-122264/13.
XX
PT New antisense compound targeting nucleic acid encoding human mitogen-
PT activated protein kinase kinase 1 (MEKK1), useful for treating diseases
PT or conditions associated with MEKK1 expression, or preventing
PT inflammation or tumor formation.
XX
PS Claim 14; Col 40; 35pp; English.
XX
CC Sequences AAF27086-AAF27125 represent phosphorothioate antisense
CC oligonucleotides targetted to the human MEKK1 gene, which inhibit its
CC expression. The antisense oligonucleotides were designed to target
CC different regions of the human MEKK1 RNA, and were analysed for their
CC effect on MEKK1 mRNA levels by quantitative real-time PCR. MEKK1 (also
CC known as mitogen-activated protein kinase kinase kinase 1, MEK kinase 1
CC and MAP/ERK kinase kinase 1) is a dual-specific serine/threonine kinase
CC which mediates cellular responses to mitogenic stimuli, being involved in
CC JNK/SAPK (Jun N-terminal kinase/stress- activated protein kinase) MAP
CC kinase cascades. MEKK1 regulates signalling events associated with
CC apoptosis (programmed cell death) and NF-kappa-B, both of which have been
CC associated with the development of hyperproliferative disorders such as
CC cancer. Specifically, MEKK1 lies directly downstream of Bcl-2 in an
CC apoptotic signalling cascade, and plays a critical role in the control of
CC NF-kappa-B-mediated transcription at multiple points in the apoptotic
CC cascade. The oligonucleotides of the invention are useful for diagnosis,
CC prevention and treatment of conditions associated with MEKK1 expression,
CC such as inflammation, and cancer and other hyperproliferative disorders
XX
SQ Sequence 20 BP; 3 A; 6 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2284 GAGTAAACTTGAAAAGGGT 2302
||| ||||| ||||||| |
Db 20 GAGAAAACTGGAAAAGGAT 2

RESULT 4052
AAH45579
ID AAH45579 standard; DNA; 20 BP.
XX
AC AAH45579;
XX
DT 13-SEP-2001 (first entry)
XX
DE Enterohaemorrhagic/verotoxin producing E. coli specific oligo #1.
XX
KW Enterohaemorrhagic Escherichia coli; EHEC; verotoxin-producing E. coli;
KW VTEC; bacterial gene; shiga toxin; ss.
XX
OS Synthetic.
XX
PN JP2001095576-A.
XX
PD 10-APR-2001.
XX
PF 28-SEP-1999; 99JP-00273560.
XX
PR 28-SEP-1999; 99JP-00273560.
XX
PA (SHMA) SHIMADZU CORP.
XX
DR WPI; 2001-341248/36.
XX
PT Detecting enterohemorrhagic Escherichia coli (EHEC) or verotoxin-
PT producing E. coli (VTEC) comprises polymerase chain reaction analysis
PT using specific oligonucleotides.
XX
PS Claim 1; Page 2; 5pp; Japanese.
XX
CC This invention relates to a method for the detection of
CC enterohaemorrhagic Escherichia coli (EHEC) or verotoxin-producing E. coli

```
CC   (VTEC). The method involves PCR analysis using specific oligonucleotides
CC   represented by sequences AAH45579 - AAH45584. The oligonucleotides are
CC   complementary to nucleotide sequences of bacterial genes, and can
CC   therefore be used for the selective detection of Escherichia coli having
CC   the vero (Shiga) toxin 1 or vero (Shiga) toxin 2 genes. The method is
CC   used for the detection and identification of EHEC or VTEC in the clinical
CC   examination of food poisoning or diarrhoea cases. The method is also used
CC   for the treatment of infectious diseases including E. coli 0-157
XX
SQ   Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2445 TTTTTTGAGACATGGGATC 2463
              | ||| ||||||||||| |
Db          2 TATTTGGAGACATGGGAGC 20


RESULT 4053
AAS23808
ID   AAS23808 standard; DNA; 20 BP.
XX
AC   AAS23808;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Primer B #61 used as probe for identifying C. albicans GRACE strain.
XX
KW   Gene identification; essential gene; GRACE; pathogenic fungus;
KW   gene replacement and conditional expression; fungal infection; probe; ss.
XX
OS   Candida albicans.
OS   Synthetic.
XX
PN   WO200160975-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005551.
XX
PR   18-FEB-2000; 2000US-0183534P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Roemer T,  Jiang B,  Boone C,  Bussey H;
XX
DR   WPI; 2001-489080/53.
XX
PT   Identifying genes essential to fungal metabolisms and identifying
PT   potential therapeutic agents that target these genes.
XX
PS   Disclosure; Page 324; 324pp; English.
XX
CC   The present invention relates to novel methods for constructing fungal
CC   strains useful for identification and validation of gene products as
CC   targets for therapeutic agents, for creating a collection of identified
CC   essential genes, and screening assays for the discovery of new drugs. The
CC   invention provides the GRACE (gene replacement and conditional
CC   expression) method for the construction of mutant organisms referred to
CC   as GRACE strains of the organism. The invention can be applied to any
CC   organism, particularly a pathogenic fungus e.g. Candida albicans,
CC   Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful
CC   to identify agents that may be used in the treatment of fungal
CC   infections. AAS23748-AAS23808 represent primers B #1-61 used as probes
CC   for identifying C. albicans GRACE strains
XX
SQ   Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         87 CCCCGATTTTGGATTTACC 105
              ||||||| || ||||| ||
Db          1 CCCCGATCTTCGATTTTCC 19


RESULT 4054
AAF91339
ID   AAF91339 standard; DNA; 20 BP.
XX
AC   AAF91339;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human E2F transcription factor 1 antisense oligonucleotide #45.
XX
KW   Antisense; E2F transcription factor 1; human; infection; inflammation;
KW   tumour; ss.
XX
OS   Homo sapiens.
XX
PN   US6187587-B1.
XX
PD   13-FEB-2001.
XX
PF   02-MAR-2000; 2000US-00517584.
XX
PR   02-MAR-2000; 2000US-00517584.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Popoff I,  Brown-Driver VL,  Cowsert LM;
XX
DR   WPI; 2001-190981/19.
XX
PT   Antisense compound capable of inhibiting the expression of E2F
PT   transcription factor 1, useful for preventing or delaying infection,
PT   inflammation or tumor formation.
XX
PS   Claim 1; Col 42; 40pp; English.
XX
CC   The present invention relates to antisense compounds up to 30 nucleobases
CC   in length targeted to a E2F transcription factor 1 The invention is
CC   useful for inhibiting the expression of E2F transcription factor 1 in
CC   cells or tissues. The antisense oligonucleotides may also be used as a
CC   research agent and to prevent infection, inflammation or tumours
XX
SQ   Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2017 AAGTCCTCTGGTAGGAGGC 2035
              || ||||| || |||||||
Db          2 AACTCCTCAGGGAGGAGGC 20


RESULT 4055
AAS08770/c
ID   AAS08770 standard; DNA; 20 BP.
XX
AC   AAS08770;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human PD-ABC form 1 DNA exon 26 3' splice site.
XX
KW   PD-ATP-binding cassette; PD-ABC; chromosome 19p13.3; spleen; thymus; ds;
KW   peripheral blood leukocyte; bone marrow; lymph node; dyslipidaemia;
KW   cardiovascular disorder; inflammatory disorder; abnormal calcium flux;
KW   epilepsy; coronary artery disease; Tangier's disease; atherosclerosis;
KW   familial high-density lipoprotein deficiency; fatty liver disease;
```

KW atherosclerosis; diabetes; insulin resistance; obesity; drug screening;
KW alcoholism; retinal degeneration; hypertension; vascular disease.
XX
OS Homo sapiens.
XX
PN WO200153490-A1.
XX
PD 26-JUL-2001.
XX
PF 23-JAN-2001; 2001WO-US002191.
XX
PR 24-JAN-2000; 2000US-0177889P.
PR 30-JUN-2000; 2000US-0215405P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Tafuri SR, Wang M;
XX
DR WPI; 2001-442259/47.
XX
PT New Human PD-ABC DNA molecules and proteins for diagnosis and treatment
PT of dyslipidemia, epilepsy and diseases related to abnormal calcium flux.
XX
PS Disclosure; Page 38; 77pp; English.
XX
CC The sequence represents a splice site within a DNA molecule encoding
CC human PD-ATP-binding cassette (PD-ABC) protein. PD-ABC maps to chromosome
CC 19p13.3 and is expressed in various tissues including spleen, thymus,
CC peripheral blood leukocytes, bone marrow and lymph nodes. The PD-ABC DNA
CC molecules and proteins are used to diagnose and treat cardiovascular
CC disorders, inflammatory disorders, dyslipidaemia, epilepsy, diseases
CC related to abnormal calcium flux, coronary artery disease, Tangier's
CC disease, familial high-density lipoprotein deficiency, atherosclerosis,
CC diabetes, fatty liver disease, insulin resistance, obesity, alcoholism,
CC retinal degeneration, hypertension and vascular disease. The sequences
CC are also used in drug screening assays
XX
SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1599 CCCTCCTGGCCTGGGGGAA 1617
||||||| |||||| |||
Db 20 CCCTCCTCACCTGGGCGAA 2

RESULT 4056
AAS08861/c
ID AAS08861 standard; DNA; 20 BP.
XX
AC AAS08861;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human PD-ABC form 2 DNA exon 26 3' splice site.
XX
KW PD-ATP-binding cassette; PD-ABC; chromosome 19p13.3; spleen; thymus; ds;
KW peripheral blood leukocyte; bone marrow; lymph node; dyslipidaemia;
KW cardiovascular disorder; inflammatory disorder; abnormal calcium flux;
KW epilepsy; coronary artery disease; Tangier's disease; atherosclerosis;
KW familial high-density lipoprotein deficiency; fatty liver disease;
KW atherosclerosis; diabetes; insulin resistance; obesity; drug screening;
KW alcoholism; retinal degeneration; hypertension; vascular disease.
XX
OS Homo sapiens.
XX
PN WO200153490-A1.
XX
PD 26-JUL-2001.
XX
PF 23-JAN-2001; 2001WO-US002191.
XX
PR 24-JAN-2000; 2000US-0177889P.
PR 30-JUN-2000; 2000US-0215405P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Tafuri SR, Wang M;
XX
DR WPI; 2001-442259/47.
XX
PT New Human PD-ABC DNA molecules and proteins for diagnosis and treatment
PT of dyslipidemia, epilepsy and diseases related to abnormal calcium flux.
XX
PS Disclosure; Page 40; 77pp; English.
XX
CC The sequence represents a splice site within a DNA molecule encoding
CC human PD-ATP-binding cassette (PD-ABC) protein. PD-ABC maps to chromosome
CC 19p13.3 and is expressed in various tissues including spleen, thymus,
CC peripheral blood leukocytes, bone marrow and lymph nodes. The PD-ABC DNA
CC molecules and proteins are used to diagnose and treat cardiovascular
CC disorders, inflammatory disorders, dyslipidaemia, epilepsy, diseases
CC related to abnormal calcium flux, coronary artery disease, Tangier's
CC disease, familial high-density lipoprotein deficiency, atherosclerosis,
CC diabetes, fatty liver disease, insulin resistance, obesity, alcoholism,
CC retinal degeneration, hypertension and vascular disease. The sequences
CC are also used in drug screening assays
XX
SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1599 CCCTCCTGGCCTGGGGGAA 1617
||||||| |||||| |||
Db 20 CCCTCCTCACCTGGGCGAA 2

RESULT 4057
ABL96288
ID ABL96288 standard; DNA; 20 BP.
XX
AC ABL96288;
XX
DT 21-AUG-2002 (first entry)
XX
DE Primer #1 related to human NHAD3.
XX
KW Human; alcohol dehydrogenase type III; NHAD3; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1292419-A.
XX
PD 25-APR-2001.
XX
PF 10-OCT-1999; 99CN-00116953.
XX
PR 10-OCT-1999; 99CN-00116953.
XX
PA (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-409819/44.
XX
PT Human III type ethanol dehydrogenase and its coding sequence.
XX
PS Example 3; Page 12 (Disclosure); 21pp; Chinese.
XX
CC The present invention discloses a new polypeptide-novel human alcohol
CC dehydrogenase type III, called NHAD3. The invention also discloses the
CC method for curing several diseases by using novel human alcohol

```
CC   dehydrogenase type III. The present sequence represents a primer related
CC   to novel human alcohol dehydrogenase type III, NHAD3
XX
SQ   Sequence 20 BP; 7 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1550 GGAAGGAACAGGACTGCAA 1568
              ||| |||| |||||| |||
Db          1 GGAGGGAAGAGGACTCCAA 19


RESULT 4058
AAH80595
ID   AAH80595 standard; cDNA; 20 BP.
XX
AC   AAH80595;
XX
DT   11-SEP-2003  (revised)
DT   19-SEP-2001  (first entry)
XX
DE   Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 559.
XX
KW   Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
KW   disease diagnosis; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   US6251588-B1.
XX
PD   26-JUN-2001.
XX
PF   10-FEB-1998;   98US-00021701.
XX
PR   10-FEB-1998;   98US-00021701.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Shannon KW,  Wolber PK,  Delenstarr GC,  Webb PG,  Kincaid RH;
XX
DR   WPI; 2001-424456/45.
XX
PT   Predicting the potential of an oligonucleotide to hybridize to a target
PT   nucleotide sequence, useful for evaluating oligonucleotide probe
PT   sequences, by identifying a oligonucleotides based on the evaluation of
PT   parameters.
XX
PS   Example 2; Col 65; 342pp; English.
XX
CC   The present invention describes a method for predicting the potential of
CC   an oligonucleotide to hybridise to a (complementary) target nucleotide
CC   sequence, involving identifying a subset of oligonucleotides within the
CC   predetermined number of unique oligonucleotides based on the evaluation
CC   of the parameter. Oligonucleotides in the subset are identified that are
CC   clustered along a region of the nucleotide sequence that is hybridisable
CC   to the target nucleotide sequence. This is useful for evaluating
CC   oligonucleotide probe sequences. The present sequence is an
CC   oligonucleotide described in the exemplification of the invention.
CC   (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 20 BP; 2 A; 5 C; 1 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTG 2193
              ||||| |||||||||  ||
Db          1 TTTTTCTTTTTTAACCCTG 19


RESULT 4059
ABA01567
ID   ABA01567 standard; DNA; 20 BP.
XX
AC   ABA01567;
XX
DT   30-JAN-2002  (first entry)
XX
DE   HLA class I microsatellite marker C1_4_3 PCR primer SEQ ID NO:8.
XX
KW   HLA class I; human leukocyte antigen class I; microsatellite;
KW   gene mapping; microsatellite genetic polymorphism marker; PCR primer;
KW   hereditary factor; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179482-A1.
XX
PD   25-OCT-2001.
XX
PF   30-OCT-2000; 2000WO-JP007621.
XX
PR   13-APR-2000; 2000JP-00112699.
XX
PA   (INOK/) INOKO H.
XX
PI   Inoko H;
XX
DR   WPI; 2002-017613/02.
XX
PT   Gene mapping method using microsatellite genetic polymorphism markers at
PT   about 1 to 100 kb for identification of disease associated genes.
XX
PS   Example 1; Page 38; 59pp; Japanese.
XX
CC   The present invention describes a method for gene mapping in which
CC   microsatellite genetic polymorphism markers are used at a spacing of 1 to
CC   50-150 kilo base pairs (kb) to locate the position of the gene of
CC   interest. The method can be used for the mapping and identification of
CC   genes associated with diseases and genes associated with hereditary
CC   factors in different phenotypes. The present sequence represents a PCR
CC   primer for a human leukocyte antigen (HLA) class I microsatellite marker,
CC   which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        126 CTGGATTTAACTGGCGACT 144
              ||||||| | |||| ||||
Db          1 CTGGATTAACCTGGAGACT 19


RESULT 4060
ABK96703/c
ID   ABK96703 standard; DNA; 20 BP.
XX
AC   ABK96703;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Interleukin-3 (IL-3) reverse sequencing primer #9.
XX
KW   Interleukin 3; colony-stimulating factor; IL3; transgenic animal;
KW   IL3 isogene; central nervous system disorder; multiple sclerosis;
KW   Alzheimer's disease; Parkinson's disease; CNS injury; immune disorder;
KW   inflammatory disorder; sequencing; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200244410-A1.
```

```
XX
PD   06-JUN-2002.
XX
PF   28-NOV-2000; 2000WO-US032381.
XX
PR   28-NOV-2000; 2000WO-US032381.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Denton RR,  Nandabalan K,  Stephens JC;
XX
DR   WPI; 2002-519590/55.
XX
PT   Novel isolated polynucleotide comprising a sequence which is a
PT   polymorphic variant for a reference sequence for interleukin 3 gene
PT   useful for studying the expression and biological function of the
PT   protein.
XX
PS   Example 1; Page 27; 62pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) comprising a
CC   sequence which is a polymorphic variant for a reference sequence for
CC   interleukin 3 (colony-stimulating factor) (IL3) gene or its fragment. (I)
CC   Is useful for studying the expression and biological function of IL3, as
CC   well as in developing drugs targeting the IL3 protein. A transgenic
CC   animal is useful for studying expression of IL3 isogenes in vivo, for in
CC   vivo screening and testing of drugs targeted against IL3 protein, and for
CC   testing the efficacy of therapeutic agents and compounds for diseases of
CC   the central nervous system e.g. multiple sclerosis, Alzheimer's disease,
CC   Parkinson's disease and CNS injury, and immune or inflammatory disorders.
CC   The method described in the invention is useful in developing diagnostic
CC   tests and therapeutic treatments for diseases of the central nervous
CC   system and immune or inflammatory disorders. This sequence represents a
CC   sequencing primer used to sequence regions of the IL-3 gene in order to
CC   study polymorphisms in the gene
XX
SQ   Sequence 20 BP; 5 A; 3 C; 10 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        603 CCGACCTGCTGCTGCCCCA 621
              ||| |||||| |||| |||
Db         20 CCGTCCTGCTCCTGCTCCA 2


RESULT 4061
ABQ78576/c
ID   ABQ78576 standard; DNA; 20 BP.
XX
AC   ABQ78576;
XX
DT   25-NOV-2002  (first entry)
XX
DE   RT-PCR primer used to amplify mucin 5B (MUC5B) cDNA.
XX
KW   Human; mucin 4; MUC4; peripheral blood monocyte; PBMC; tumour marker;
KW   pancreatic cancer; pancreatic adenocarcinoma; MUC5B; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200259368-A1.
XX
PD   01-AUG-2002.
XX
PF   07-DEC-2001; 2001WO-US046887.
XX
PR   08-DEC-2000; 2000US-00733444.
XX
PA   (UYNE-) UNIV NEBRASKA.
XX
PI   Batra SK,  Brand RE,  Ringel J,  Faulamnn G,  Lohr M,  Varsheny GC;
XX
DR   WPI; 2002-643346/69.
XX
PT   Diagnosing pancreatic adenocarcinoma, particularly for the early
PT   detection of the pancreatic cancer, comprises employing primers or
PT   antibodies that are specific for the MUC4-encoding nucleic acid or MUC4
PT   protein, respectively.
XX
PS   Example 1; Page 29; 63pp; English.
XX
CC   PCR primers ABQ78575-76 were used to amplify human mucin 5B (MUC5B) cDNA.
CC   Peripheral blood monocytes (PBMCs) isolated from pancreatic cancer
CC   patients are positive for MUC4, while MUC4 expression is not observed in
CC   PBMCs isolated from normal patients or from patients suffering from
CC   chronic pancreatitis or other types of cancers. Expression of MUC4 can
CC   therefore be used as an indication of pancreatic cancer. The
CC   specification describes a method for detecting a MUC4-encoding nucleic
CC   acid or a MUC4 protein in a biological sample as a tumour marker for
CC   pancreatic cancer. The method comprises contacting a nucleic acid
CC   extracted from the sample with oligonucleotide primers that specifically
CC   hybridise to the MUC4 nucleic acid; or contacting a biological sample
CC   with an antibody (or its fragment) that has specific binding affinity for
CC   MUC4. The method is useful for diagnosing pancreatic cancer or pancreatic
CC   adenocarcinoma, particularly for early detection of pancreatic cancer
XX
SQ   Sequence 20 BP; 5 A; 4 C; 10 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        601 CTCCGACCTGCTGCTGCCC 619
              |||||  || |||||||||
Db         20 CTCCGTGCTCCTGCTGCCC 2


RESULT 4062
AAD41796
ID   AAD41796 standard; DNA; 20 BP.
XX
AC   AAD41796;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Human RECQL2 antisense oligonucleotide, ISIS #137576.
XX
KW   Antisense; RECQL2; Bloom's disorder; prophylaxis; infection; tumour;
KW   inflammation; therapy; human; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl nucleotides"
FT   modified_base    4. .7
FT                    /*tag=  d
FT                    /mod_base= m5c
FT   modified_base    10
FT                    /*tag=  e
FT                    /mod_base= m5c
FT   modified_base    12
FT                    /*tag=  f
FT                    /mod_base= m5c
FT   modified_base    15. .16
FT                    /*tag=  g
FT                    /mod_base= m5c
```

```
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl nucleotides"
FT   modified_base   19
FT                   /*tag=  h
FT                   /mod_base= m5c
XX
PN   US6399378-B1.
XX
PD   04-JUN-2002.
XX
PF   01-MAR-2001; 2001US-00798096.
XX
PR   01-MAR-2001; 2001US-00798096.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ward DT,  Watt AT;
XX
DR   WPI; 2002-535979/57.
XX
PT   Antisense compounds targeted to nucleic acids encoding RECQL2 associated
PT   with Bloom's disorder, for modulating RECQL2 expression and treating
PT   diseases e.g. tumors associated with expression of the RECQL2 in humans.
XX
PS   Claim 3; Col 45; 86pp; English.
XX
CC   The invention relates to antisense compounds targetted to nucleic acid
CC   encoding RECQL2 (gene associated with Bloom's disorder) to inhibit the
CC   expression of RECQL2. Antisense compounds of the invention are useful for
CC   treating diseases associated with expression of RECQL2, in humans. They
CC   are useful for diagnostics, therapeutics and as research reagent, e.g.
CC   prophylactically to prevent or delay infection, inflammation or tumour
CC   formation. They are also useful in antisense therapy. The present
CC   sequence is an antisense oligonucleotide targetted to human RECQL2 DNA
XX
SQ   Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        344 TTTCCCCCTCCCTACCAGC 362
              ||||||| || || |||||
Db          1 TTTCCCCATCTCTTCCAGC 19


RESULT 4063
AAL43954
ID   AAL43954 standard; DNA; 20 BP.
XX
AC   AAL43954;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Polynucleotide separation method - related oligonucleotide SEQ ID #2.
XX
KW   Polynucleotide separation; ss; non-polar surface;
KW   multivalent cation free.
XX
OS   Unidentified.
XX
PN   WO200240130-A1.
XX
PD   23-MAY-2002.
XX
PF   05-SEP-2001; 2001WO-US027495.
XX
PR   16-NOV-2000; 2000US-00714579.
XX
PA   (TRAN-) TRANSGENOMIC INC.
XX
PI   Gjerde DT,  Haefele RM,  Hanna CP,  Hornby D,  Kuklin AI,  Taylor PD;
XX
DR   WPI; 2002-566535/60.
XX
PT   Separation of a mixture of single-stranded polynucleotides e.g. DNA, or
PT   RNA, comprises applying the mixture to a polymeric separation medium
PT   having non-polar surfaces, and then separating the mixture.
XX
PS   Example 16; Page 43; 91pp; English.
XX
CC   The invention comprises a method of separating a mixture which contains
CC   single-stranded polynucleotides. The method of the invention involves
CC   applying the mixture to a polymeric separation medium having non-polar
CC   surfaces. The non-polar surfaces are free from multivalent cations
CC   (preferably chromium, iron, nickel and/or copper) and are free to bind or
CC   interfere with the polynucleotides. The method of the invention is useful
CC   for separating a mixture that contains single-stranded polynucleotides
CC   (e.g. DNA and RNA) having lengths from 5 - 200 up to 2000 - 20000
CC   nucleotides from impurities (e.g. failure sequences, salts and/or
CC   proteins). The method of the invention allows separation to be achieved
CC   within 10 - 30 minutes, in contrast to conventional gel chromatography
CC   which can require hours or days. The present DNA sequence represents an
CC   oligonucleotide that was used in an example of the invention
XX
SQ   Sequence 20 BP; 5 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2516 AGGTTTTATTCATATATAT 2534
              ||||||||||  ||||| |
Db          2 AGGTTTTATTATTATATTT 20


RESULT 4064
ABK99983
ID   ABK99983 standard; DNA; 20 BP.
XX
AC   ABK99983;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human CADPKL DNA PCR primer #7.
XX
KW   Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ss;
KW   PCR; neuropsychiatric disorder; attention deficit disorder; ADD; primer;
KW   schizoaffective disorder; bipolar disorder; unipolar affective disorder;
KW   schizophrenia; adolescent conduct disorder; pharmacogenomics;
KW   fingerprinting; paternity testing; antidepressant; neuroleptic.
XX
OS   Homo sapiens.
XX
PN   WO200254939-A2.
XX
PD   18-JUL-2002.
XX
PF   07-JAN-2002; 2002WO-US000367.
XX
PR   09-JAN-2001; 2001US-00757300.
PR   23-AUG-2001; 2001US-00935464.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Meyer JM,  Barrington-Martin R,  Parker A;
XX
DR   WPI; 2002-590643/63.
XX
PT   New variants of calcium/calmodulin-dependent protein kinase-like nucleic
PT   acids and polypeptides, useful for diagnosing and treating
PT   neuropsychiatric disorders, e.g. schizophrenia, schizoaffective disorder,
PT   and bipolar disorder.
XX
```

PS Claim 17; Page 98; 223pp; English.
XX
CC The invention relates to a nucleic acid comprising a polymorphic region
CC of a Calcium/Calmodulin-dependent protein kinase-like gene (CADPKL)
CC allelic variant, and the polypeptide it encodes. CADPKL allelic variants
CC are useful in determining whether a subject has or is at risk of
CC developing a neuropsychiatric disorder, such as schizophrenia, attention
CC deficit disorder (ADD), schizoaffective disorder, bipolar disorder,
CC unipolar affective disorder and adolescent conduct disorder. The
CC polypeptides, polynucleotides, antibodies and modulators of the CADPKL
CC allelic variants are useful for diagnosing or treating these
CC neuropsychiatric disorders. The polypeptides may be used to raise
CC antibodies to a CADPKL polypeptide. The nucleic acids may be used as
CC probes or primers, in pharmacogenomics for designing therapies for the
CC disorders, and in fingerprinting for detection of different individuals
CC with the same species (e.g. paternity testing). This sequence represents
CC a PCR primer used to amplify human CADPKL DNA of the invention
XX
SQ Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 838 CTGCTCAGTCCCTGGAAGA 856
||||.||.||||||||.||
Db 2 CTGCCCACTCCCTGGATGA 20

RESULT 4065
ABL45623
ID ABL45623 standard; DNA; 20 BP.
XX
AC ABL45623;
XX
DT 11-APR-2002 (first entry)
XX
DE Human chromosome 21q22.1 PCR primer SEQ ID NO:2667.
XX
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2001321190-A.
XX
PD 20-NOV-2001.
XX
PF 12-MAR-2001; 2001JP-00068285.
XX
PR 10-MAR-2000; 2000JP-00066716.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
DR WPI; 2002-144136/19.
XX
PT Arraying genome clones.
XX
PS Claim 6; Page 57; 528pp; Japanese.
XX
CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1170 CCAGACCTCATCTTGGAGG 1188
||||||||||.|.||.|||
Db 2 CCAGACCTCAACCTGAAGG 20

RESULT 4066
AAL45626/c
ID AAL45626 standard; DNA; 20 BP.
XX
AC AAL45626;
XX
DT 11-JUN-2002 (first entry)
XX
DE Human serine/threonine protein kinase BioSTPK cDNA PCR primer #1.
XX
KW Human; serine/threonine protein kinase BioSTPK; enzyme; cancer;
KW immunological disorder; haemopathy; gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1326970-A.
XX
PD 19-DEC-2001.
XX
PF 06-JUN-2000; 2000CN-00116353.
XX
PR 06-JUN-2000; 2000CN-00116353.
XX
PA (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-217565/28.
XX
PT New human protein kinase and its coding sequence, useful for treating
PT various diseases, such as malignant tumors, immunological disorder,.
XX
PS Example 3; Page 12(Disclosure); 25pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC serine/threonine protein kinase BioSTPK. The sequences can be used in the
CC treatment of cancer, haemopathy and immunological disorders. The present
CC sequence is a PCR primer for the coding sequence of the invention
XX
SQ Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 745 TCGCAAAGGTCCCATTTCC 763
||.|||||||.|.|||||
Db 20 TCCCAAAGGTCCTCTTTCC 2

RESULT 4067
ABK94489/c

```
ID   ABK94489 standard; DNA; 20 BP.
XX
AC   ABK94489;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human BRCA1 gene forward PCR primer for exon fragment 11.15.
XX
KW   hMLH1; DNA mismatch repair; BRCA1; ss; PCR; primer; BRCA1;
KW   breast and ovarian cancer susceptibility gene; TGDS; human;
KW   two-dimensional DNA electrophoresis; tumour suppressor gene;
KW   breast cancer; ovarian cancer; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200236819-A1.
XX
PD   10-MAY-2002.
XX
PF   06-NOV-2000; 2000WO-IB001607.
XX
PR   06-NOV-2000; 2000WO-IB001607.
XX
PA   (SCSC-) ACAD APPLIED SCI.
XX
PI   Vijg J;
XX
DR   WPI; 2002-471507/50.
XX
PT   Detecting mutations in the BRCA1 and hMLH1 gene comprises subjecting
PT   amplification products to 2-dimensional gel electrophoresis to produce a
PT   characteristic spot pattern for a specific mutation in either the BRCA1
PT   or the hMLH1 gene.
XX
PS   Claim 1; Page 40; 57pp; English.
XX
CC   The invention relates to detecting mutations in the BRCA1 and hMLH1 gene
CC   comprising subjecting a set of amplification products to two-dimensional
CC   DNA electrophoresis (TGDS) to produce a characteristic spot pattern for a
CC   specific mutation in either the BRCA1 or the hMLH1 gene. Also included
CC   are test kits for enabling BRCA1 or hMLH1 gene testing comprising short
CC   PCR primers given in the specification, mixed in 20 mM of Tris-HCl, 50 mM
CC   KCl, 25 micro M of dNTP, and 5 % formamide. The method is useful for
CC   detecting mutations in the BRCA1 (breast and ovarian cancer
CC   susceptibility gene, a tumour suppressor gene) and hMLH1 gene (a DNA
CC   mismatch repair gene). The present sequence is a PCR primer specific to
CC   BRCA1 used in the method of the invention
XX
SQ   Sequence 20 BP; 5 A; 7 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2673 AGTGTGTGTGGGTGAAATG 2691
              | ||||| |||||||||| |
Db         19 AATGTGTATGGGTGAAAAG 1


RESULT 4068
ABA03194/c
ID   ABA03194 standard; DNA; 20 BP.
XX
AC   ABA03194;
XX
DT   08-FEB-2002  (first entry)
XX
DE   Human KRGF1 PCR primer #1.
XX
KW   Kidney repair factor; KRGF1; antiinflammatory; nephrotropic; PCR primer;
KW   gene therapy; vaccine; kidney damage; kidney failure; inflammation;
KW   human; ss.
XX
OS   Homo sapiens.
XX
PN   WO200168817-A1.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-JP002087.
XX
PR   16-MAR-2000; 2000JP-00073632.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Takeuchi K,  Kato Y,  Sekine S,  Kikuchi Y,  Sakurada K;
XX
DR   WPI; 2002-055101/07.
XX
PT   Kidney repair factor KRGF1 for the treatment and diagnosis of damage to
PT   kidney tissue comprises monitoring the increased expression in damaged
PT   kidney tissue of KRGF1 and antibodies recognizing it.
XX
PS   Example 6; Page 114; 121pp; Japanese.
XX
CC   The present invention relates to human kidney repair factor, KRGF1 (see
CC   AAM47451). KRGF1 was found to have increased expression in damaged kidney
CC   tissue. KRGF1 can be used for the diagnosis of kidney tissue damage and
CC   kidney failure; and for the treatment of damaged/inflamed kidney tissues.
CC   The present sequence is a PCR primer, which was used in an example from
CC   the present invention
XX
SQ   Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1576 TCTCCACCGCACAGACTGG 1594
              |||| ||| ||||| ||||
Db         19 TCTCAACCTCACAGCCTGG 1


RESULT 4069
ABK24613/c
ID   ABK24613 standard; DNA; 20 BP.
XX
AC   ABK24613;
XX
DT   09-APR-2002  (first entry)
XX
DE   EIF2AK3 gene sequencing primer #29.
XX
KW   Human; EIF2AK3; antidiabetic; osteopathic; antiarthritic; hepatotropic;
KW   nephrotropic; nootropic; diabetes; Wolcott-Rallison syndrome; WRS;
KW   osteoporosis; arthritis; hepatic dysfunction; nephropathy;
KW   renal dysfunction; mental retardation; primer; ss;
KW   eukaryotic initiation factor 2 alpha kinase 3.
XX
OS   Homo sapiens.
XX
PN   WO200190371-A1.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-IB001153.
XX
PR   23-MAY-2000; 2000EP-00401436.
PR   02-OCT-2000; 2000EP-00402707.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (NAGE-) CENT NAT GENOTYPAGE.
XX
PI   Julier C,  Delepine M,  Nicolino M;
XX
DR   WPI; 2002-122021/16.
```

XX
PT New mutated eukaryotic initiation factor 2 alpha kinase 3 genes and
PT polypeptides in patients with Wolcott-Rallison syndrome, useful for
PT preventing or treating e.g. diabetes, osteoporosis, arthritis or mental
PT retardation.
XX
PS Example 4; Page 31; 93pp; English.
XX
CC The invention relates to an isolated variant of a mammal genomic sequence
CC of the gene coding for the translation initiation factor 2 alpha kinase 3
CC (EIF2AK3). The EIF2AK3 nucleic acid variant is useful for the production
CC of a recombinant or synthetic polypeptide, and for screening compounds
CC capable of modulating EIF2AK3. The nucleic acid is also useful for
CC screening or diagnosing the diseases cited below. The nucleic acid of may
CC be used as sense or anti-sense oligonucleotide. The nucleic acid may also
CC be used as a primer or a probe, for detecting and/or amplifying a nucleic
CC acid sequence. The compound is useful as a medicament, particularly for
CC preventing and/or treating diabetes and/or pathology related to WRS, e.g.
CC type 1 diabetes, type 2 diabetes, the others forms of diabetes,
CC osteoporosis, arthritis, hepatic dysfunction, nephropathies or other
CC renal dysfunction, or mental retardation. The cell the mammal or the
CC polypeptide is useful for studying the expression or the activity of the
CC EIF2AK3 protein, and the direct or indirect interactions between the
CC EIF2AK3 protein and chemical or biochemical compounds, which may be
CC involved in the activity of the EIF2AK3 protein. The cell or polypeptide
CC is also useful for screening chemical or biochemical compounds capable of
CC interacting directly or indirectly with the EIF2AK3 protein, and/or
CC capable of modulating the expression or the activity of the EIF2AK3
CC protein. ABK24521-ABK24624 represent human EIF2AK3 coding sequences and
CC PCR primers of the invention
XX
SQ Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2668 AGTACAGTGTGTGTGGGTG 2686
||||||||| ||||| ||
Db 19 AGTACAGTGGGTGTGCATG 1

RESULT 4070
ABL58300
ID ABL58300 standard; DNA; 20 BP.
XX
AC ABL58300;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human GLUT 10 SSCP analysis primer GLUT10 ex2cF.
XX
KW Glucose transporter; GLUT10; insulin; chromosome 20Q12-13.3; human;
KW glucose metabolism; single strand conformational polymorphism; PCR;
KW type 2 diabetes; SSCP; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200218621-A2.
XX
PD 07-MAR-2002.
XX
PF 22-AUG-2001; 2001WO-US026184.
XX
PR 31-AUG-2000; 2000US-00652292.
XX
PA (UYWA-) UNIV WAKE FOREST.
XX
PI Bowden DW, Dawson PA, Fossey SC;
XX
DR WPI; 2002-371828/40.
XX
PT New glucose transporter gene and protein, designated GLUT10, useful for
PT studying and analyzing biological processes of glucose metabolism and
PT Type 2 diabetes, as well as for screening modulators of glucose
PT transporter activity.
XX
PS Example 4; Page 52; 85pp; English.
XX
CC The invention relates to a novel glucose transporter gene and protein,
CC designated GLUT10. GLUT 10 is an insulin-responsive glucose transporter
CC gene located in the type 2 diabetes linked region of chromosome 20Q12-
CC 13.3. The GLUT 10 polypeptide can be expressed by standard recombinant
CC methodology. The GLUt 10 glucose transporter gene and protein are useful
CC for studying and analysing biological processes of both glucose
CC metabolism and type 2 diabetes. These are also useful in drug screening
CC techniques, especially for screening modulators of glucose transporter
CC activity or compounds having the ability to be transported across the
CC cell membranes. Sequences ABL58290-315 represent primers specific for the
CC various regions of the human GLUT 10 glucose transporter gene, used in
CC single strand conformational polymorphism (SSCP) analysis of the gene
XX
SQ Sequence 20 BP; 3 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2309 GAAGCAATTTGTTGCTGCT 2327
| ||||| ||| |||||||
Db 1 GGAGCAACTTGGTGCTGCT 19

RESULT 4071
ABZ30568
ID ABZ30568 standard; DNA; 20 BP.
XX
AC ABZ30568;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans GRACE strain PCR primer SEQ ID NO 4719.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR WPI; 2002-566694/60.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 36; SEQ ID NO 4719; 167pp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous

CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 690 ACGAGGTGCAGAATGTCGA 708
||| ||||| |||||||| |
Db 1 ACGTGGTGCGAAATGTCGA 19

RESULT 4072
ABZ30869
ID ABZ30869 standard; DNA; 20 BP.
XX
AC ABZ30869;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans GRACE strain PCR primer SEQ ID NO 5088.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR WPI; 2002-566694/60.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 36; SEQ ID NO 5088; 167pp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 87 CCCCGATTTTGGATTTACC 105
||||||| || ||||| ||
Db 1 CCCCGATCTTCGATTTTCC 19

RESULT 4073
ABA97642/c
ID ABA97642 standard; DNA; 20 BP.
XX
AC ABA97642;
XX
DT 11-APR-2002 (first entry)
XX
DE probe m.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 6; Page 18; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid

```
XX
SQ   Sequence 20 BP; 12 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATATA 2535
              || ||| || |||||||||
Db         20 GGGTTTTTTTATATATATA 2


RESULT 4074
ABA97644/c
ID   ABA97644 standard; DNA; 20 BP.
XX
AC   ABA97644;
XX
DT   11-APR-2002  (first entry)
XX
DE   probe o.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 6; Page 18; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 20 BP; 14 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2517 GGTTTTATTCATATATATA 2535
              | |||| || |||||||||
Db         20 GTTTTTTTTTATATATATA 2


RESULT 4075
ABN80890
ID   ABN80890 standard; DNA; 20 BP.
XX
AC   ABN80890;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human caspase 7 phosphorothioate oligonucleotide SEQ ID NO:68.
XX
KW   Caspase 7; antisense modulation; antiinflammatory; cytostatic;
KW   antisense therapy; caspase 7 inhibitor; inflammatory condition;
KW   hyperproliferative disorder; cancer; bone metabolism; infection;
KW   cholesterol disorder; inflammation; tumour; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate linkages"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) wing"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) wing"
XX
PN   WO200222640-A1.
XX
PD   21-MAR-2002.
XX
PF   10-SEP-2001; 2001WO-US028232.
XX
PR   11-SEP-2000; 2000US-00659860.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Zhang H,  Watt AT;
XX
DR   WPI; 2002-404806/43.
XX
PT   Novel antisense compounds targeted to nucleic acids encoding caspase 7,
PT   for modulating gene expression and treating diseases associated with
PT   expression of caspase 7 in humans.
XX
PS   Claim 3; Page 86; 138pp; English.
XX
CC   The present invention describes a compound (I) 8-50 nucleobases in length
CC   targeted to a nucleic acid molecule encoding caspase 7, which
CC   specifically hybridises with and inhibits the expression of caspase 7.
CC   (I) has antiinflammatory and cytostatic activities, and can be used in
CC   antisense therapy and as an inhibitor of caspase 7 expression. (I) is
CC   useful for inhibiting the expression of caspase 7 in human cells or
CC   tissues, and for treating a human having a disease or condition
CC   associated with caspase 7 including inflammatory condition,
CC   hyperproliferative disorder (cancer), or bone metabolism or cholesterol
CC   disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as
CC   research reagent and kits. (I) is useful prophylactically to prevent or
CC   delay infection, inflammation or tumour formation. The present sequence
CC   represent a human caspase 7 inhibiting chimeric phosphorothioate
CC   oligonucleotide having 2'-MOE wings and a deoxy gap, which is used in an
CC   example from the present invention
XX
SQ   Sequence 20 BP; 1 A; 4 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2564 GGCTCTGTTCTTGGCTTGG 2582
              |||| |||||||| | |||
Db          1 GGCTTTGTTCTTGTCATGG 19


RESULT 4076
ABQ74654
ID   ABQ74654 standard; DNA; 20 BP.
```

```
XX
AC   ABQ74654;
XX
DT   24-OCT-2002  (first entry)
XX
DE   STEAP gene sense PCR primer SEQ ID NO:24.
XX
KW   Human; PCR primer; identification; tumour senescence; cytotoxic; ss;
KW   abnormal cell proliferation; neoplastic cell growth; growth-inhibitory.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200261134-A2.
XX
PD   08-AUG-2002.
XX
PF   21-DEC-2001; 2001WO-US050574.
XX
PR   21-DEC-2000; 2000US-0257907P.
PR   17-DEC-2001; 2001US-00257907.
XX
PA   (UNII ) UNIV ILLINOIS FOUND.
XX
PI   Roninson IB,  Chang B;
XX
DR   WPI; 2002-619266/66.
XX
PT   Identifying a compound that induces senescence in a mammalian p53
PT   deficient or tumor cell comprises assaying expression of cellular genes
PT   in the presence of the compound with expression of the genes in the
PT   absence of the compound.
XX
PS   Example 4; Page 51; 73pp; English.
XX
CC   The present invention describes a method for identifying a compound that
CC   induces senescence in a mammalian cell comprising culturing the cell in
CC   the presence and absence of the compound, assaying expression of at least
CC   one cellular gene (G1a) from 56 or a gene (G2) from 64 genes, with
CC   corresponding accession numbers given in the specification, and
CC   identifying compounds that induce senescence when expression of (G1a) or
CC   expression of (G2) is lower, in the presence of the compound. Also
CC   described: (1) a compound that induces senescence in a mammalian cell;
CC   (2) assessing efficacy of a treatment of a disease or condition relating
CC   to abnormal cell proliferation or neoplastic cell growth; (3) treating a
CC   disease or condition relating to abnormal cell proliferation or
CC   neoplastic cell growth; or (4) identifying a compound that inhibits
CC   senescence-associated induction of cellular gene expression. The compound
CC   is useful for treating or for assessing efficacy of treatment of a
CC   disease or condition relating to abnormal cell proliferation or
CC   neoplastic cell growth. The compound of the invention has a growth-
CC   inhibitory effect without producing systemic side effects found with
CC   other growth-inhibitory compounds. ABQ74611 to ABQ74734 represent PCR
CC   primers which are used in an example from the present invention
XX
SQ   Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1397 GCCCTGCAGAACTACATCA 1415
             ||||| ||||||| || ||
Db          1 GCCCTTCAGAACTTCAGCA 19


RESULT 4077
AAD44809/c
ID   AAD44809 standard; DNA; 20 BP.
XX
AC   AAD44809;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Human B-raf kinase antisense oligonucleotide ISIS #13742.
XX
KW   Human; raf; hyperproliferation; neovascularisation; ocular angiogenesis;
KW   therapy; cancer; cytostatic; anti-angiogenic; vascular; ophthalmological;
KW   antisense; phosphorothioate backbone; B-raf kinase; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
XX
PN   US6410518-B1.
XX
PD   25-JUN-2002.
XX
PF   18-FEB-2000; 2000US-00506073.
XX
PR   31-MAY-1994;   94US-00250856.
PR   31-MAY-1995;   95WO-US007111.
PR   26-NOV-1996;   96US-00756806.
PR   07-JUL-1997;   97US-00888982.
PR   06-JUL-1998;   98WO-US013961.
PR   28-AUG-1998;   98US-00143214.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP;
XX
DR   WPI; 2002-597918/64.
XX
PT   Treating cancer, angiogenesis or neovascularization by administering
PT   antisense oligonucleotides targeted to human raf sequences.
XX
PS   Example 18; Col 26; 41pp; English.
XX
CC   The present invention relates to novel antisense oligonucleotides which
CC   are targetted to nucleic acids encoding human raf proteins and capable of
CC   inhibiting raf expression. The invention also relates to methods of
CC   inhibiting hyperproliferation of cells which involves contacting the
CC   hyperproliferating cells with a therapeutically effective amount of an
CC   oligonucleotide of the invention. The method is useful for treating
CC   cancer, angiogenesis or neovascularisation, especially ocular
CC   angiogenesis or neovascularisation. The present DNA sequence is an
CC   antisense oligonucleotide targetted to human B-raf kinase
XX
SQ   Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1531 AGAAAGGTTAGGAGAGTAG 1549
             ||| || | ||||||||||
Db         20 AGAGAGTTCAGGAGAGTAG 2


RESULT 4078
ABL30917
ID   ABL30917 standard; DNA; 20 BP.
XX
AC   ABL30917;
XX
DT   21-MAR-2002  (first entry)
XX
DE   Human HLA genotyping oligonucleotide SEQ ID NO 406.
XX
KW   Human; human leukocyte antigen; HLA; genotype; polymorphism;
KW   immunogenetic; transplantation; genetic disease; ss.
```

XX
OS Homo sapiens.
XX
PN WO200192572-A1.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-JP004662.
XX
PR 01-JUN-2000; 2000JP-00164798.
XX
PA (NISN) NISSHINBO IND INC.
PA (SYST-) SYSTEM RES INC.
XX
PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX
DR WPI; 2002-122074/16.
XX
PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
PT individuals e.g. by determining immunogenetic differences when
PT transplanting between them.
XX
PS Claim 22; Page 170; 345pp; Japanese.
XX
CC The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
XX
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 255 CCCACCTCTCCTCCGCCGG 273
|| |||||||||||| || ||
Db 1 CTCACCTCTCCTCTGCAGG 19

RESULT 4079
ABI94721/c
ID ABI94721 standard; DNA; 20 BP.
XX
AC ABI94721;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleptide Zip ID#1808 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 498 GAGCGGGGCTGCCCTCGCA 516
||| || |||||| |||||
Db 19 GAGAGGTGCTGCCGTCGCA 1

RESULT 4080
ABK47121
ID ABK47121 standard; DNA; 20 BP.
XX
AC ABK47121;
XX
DT 05-JUN-2002 (first entry)
XX
DE Mouse OtS2-B9 forward PCR primer.
XX
KW PCR; primer; ss; nucleic acid library; immune response; asthma;
KW airway hyperresponsiveness; bronchoalveolar manifestation;
KW signature sequence; SS; chronic obstructive pulmonary disease; COPD;
KW allergic disease; rhinitis; atopic dermatitis; urticaria;
KW autoimmune disease; multiple sclerosis; inflammatory bowel disease;
KW allograft rejection; infectious disease.
XX
OS Mus sp.
XX
PN WO200214366-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-NL000610.
XX

```
PR   16-AUG-2000; 2000EP-00202867.
XX
PA   (UYUT-) RIJKSUNIV UTRECHT.
XX
PI   Groot PC,  Van Bergenhenegouwen BJ,  Van Oosterhout AJM;
XX
DR   WPI; 2002-241888/29.
XX
PT   Nucleic acid library comprising genes which are capable of initiation,
PT   progression and suppression of an immune response, especially an immune
PT   response observed with airway hyper-responsiveness of asthma.
XX
PS   Example 8; Page 76; 120pp; English.
XX
CC   The invention relates to a nucleic acid library comprising genes or their
CC   fragments which are capable of modulating an immune response observed
CC   with airway hyperresponsiveness and/or bronchoalveolar manifestations of
CC   asthma. Also included are a method for modulating an immune response of
CC   an individual comprising modulating a gene comprising a nucleic acid at
CC   least functionally equivalent to a nucleic acid identifiable by a
CC   signature sequence (SS) given in the specification such as R1-SO-R1-A11,
CC   StO1-A10, SvO2-1-C11, StO1-A12, and R1-SO-R1-B7, a substance (for use as
CC   a medicament) capable of modulating a gene comprising a nucleic acid at
CC   least functionally equivalent to a nucleic acid identifiable by SS and
CC   the use of a proteinaceous substance derived from a nucleic acid at least
CC   functionally equivalent to a nucleic acid identifiable by SS for the
CC   production of an antagonist (for use as a medicament) against the
CC   substance. The antagonist and substance are useful for the treatment of
CC   an immune response observed with airway hyperresponsiveness and/or
CC   bronchoalveolar manifestations of asthma. The method is useful for
CC   modulating the above immune response, where the gene encodes a gene
CC   product capable of modulating the immune response. The substance is
CC   useful for treating an immune response, particularly asthma, chronic
CC   obstructive pulmonary disease (COPD), allergic diseases (rhinitis, atopic
CC   dermatitis, urticaria), autoimmune diseases (e.g. multiple sclerosis),
CC   inflammatory bowel disease, allograft rejection and infectious disease.
CC   The present sequence is a PCR primer used to amplify and/or characterise
CC   a mouse signature sequence of the invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        644 GGCCTGGCCGAGAACCTGG 662
              | ||||| ||||| |||||
Db          1 GACCTGGACGAGACCCTGG 19


RESULT 4081
ABS65064
ID   ABS65064 standard; DNA; 20 BP.
XX
AC   ABS65064;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human casein kinase 2-beta antisense oligonucleotide #2.
XX
KW   ss; antisense; casein kinase2-beta; human; antisense gene therapy;
KW   cytostatic; antidiabetic; antiinflammatory; diabetes; cancer; tumour;
KW   hyperproliferative disorder; breast cancer; prostate cancer;
KW   liver cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "All cytidines are 5-methylcytidines"
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phophorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residues"
FT   modified_base   16. .20
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl residues"
XX
PN   WO200262954-A2.
XX
PD   15-AUG-2002.
XX
PF   31-JAN-2002; 2002WO-US003159.
XX
PR   08-FEB-2001; 2001US-00780175.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Freier SM,  Wyatt JR;
XX
DR   WPI; 2002-643409/69.
XX
PT   New antisense oligonucleotides targeted to nucleic acid encoding Casein
PT   kinase 2-beta, useful in diagnostic and research applications, or for
PT   treating a disease or condition associated with the expression of Casein
PT   kinase 2-beta.
XX
PS   Example 15; Page 91; 142pp; English.
XX
CC   The invention relates to a compound that is 8 - 50 nucleobases in length
CC   targeted to a nucleic acid molecule encoding Casein kinase 2-beta, and
CC   which specifically hybridises with and inhibits the expression of Casein
CC   kinase 2-beta, or which specifically hybridises with an 8-nucleobase
CC   portion of an active site on a nucleic acid molecule encoding Casein
CC   kinase 2-beta. Also included are: (1) a composition comprising the
CC   compound, and a carrier or diluent; (2) inhibiting the expression of
CC   Casein kinase 2-beta in cells or tissues by contacting the cells or
CC   tissues with the compound so that the expression of Casein kinase 2-beta
CC   is inhibited; and (3) treating an animal having a disease or condition
CC   associated with Casein kinase 2-beta by administering to the animal the
CC   new compound so that the expression of Casein kinase 2-beta is inhibited.
CC   The antisense compounds are useful for modulating the expression of
CC   Casein kinase 2-beta and for treating diseases or conditions associated
CC   with expression of Casein kinase 2-beta, e.g. diabetes or
CC   hyperproliferative disorders, particularly cancer, such as breast cancer,
CC   prostate cancer, or liver cancer. The antisense compounds are also useful
CC   for diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay
CC   infection, inflammation or tumour formation, as research reagents and
CC   kits, and in distinguishing between functions of various members of a
CC   biological pathway. The present sequence is an antisense oligonucleotide
CC   of the invention targeting human casein kinase 2-beta
XX
SQ   Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1270 AGACCGGACACCCCATGGG 1288
              || ||||| |||||||| |
Db          1 AGTCCGGAGACCCCATGTG 19


RESULT 4082
AAL53492/c
ID   AAL53492 standard; DNA; 20 BP.
XX
AC   AAL53492;
XX
```

```
DT   30-JAN-2003  (first entry)
XX
DE   Signal transducer screening related oligonucleotide #1.
XX
KW   Signal transduction; chimeric; extracellular domain; signal transducer;
KW   intracellular domain; cell proliferation; signal transduction path;
KW   development; differentiation; extracellular signal; defence mechanism;
KW   stress; ds.
XX
OS   Unidentified.
XX
PN   WO200277280-A1.
XX
PD   03-OCT-2002.
XX
PF   26-SEP-2001; 2001WO-JP008370.
XX
PR   26-MAR-2001; 2001JP-00088062.
XX
PA   (SAIT/) SAITO T.
PA   (ARAS/) ARASE H.
XX
PI   Saito T,  Arase H;
XX
DR   WPI; 2003-040592/03.
XX
PT   Screening and identifying nucleic acids encoding signal transducers with
PT   chimeric molecules, for use in studying and regulating cell
PT   proliferation, development and differentiation of organisms, and defense
PT   mechanism.
XX
PS   Example 1; Page 20; 55pp; Japanese.
XX
CC   The invention relates to a novel method for screening nucleic acids
CC   relating to signal transduction. The method comprises using a chimeric
CC   molecule provided with a receptor for transfer of an extracellular domain
CC   as an extracellular signal into a cell, and an intracellular domain as an
CC   extracellular signal into a cell, and an intracellular domain as the test
CC   nucleic acid product. The method of the invention is useful for screening
CC   and identifying nucleic acids encoding signal transducers, which are for
CC   use in studying and regulating cell proliferation, development and
CC   differentiation of organisms, and defense mechanisms against external
CC   factors and stress via their signal transduction path. This sequence
CC   represents an oligonucleotide relating to the novel method of the
CC   invention
XX
SQ   Sequence 20 BP; 12 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTT 2172
              | ||||| ||||||| |||
Db         20 AGTTTTTCCTCCTTTCTTT 2

RESULT 4083
ABX78222/c
ID   ABX78222 standard; DNA; 20 BP.
XX
AC   ABX78222;
XX
DT   17-APR-2003  (first entry)
XX
DE   Human bifunctional apoptosis regulator antisense oligo ISIS NO 143753.
XX
KW   Human; bifunctional apoptosis regulator; antisense; phosphorothioate;
KW   cytostatic; antiinflammatory; inhibitor; infection; inflammation; tumour;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone, nucleotides 1-5 and 16
FT                   -20 are 2'-methoxyethoxy (MOE) nucleotides, nucleotides 7
FT                   -14 are 2'-deoxy- nucleotides, all C nucleotides are 5-
FT                   methyl cytosines"
XX
PN   US6468796-B1.
XX
PD   22-OCT-2002.
XX
PF   27-APR-2001; 2001US-00844525.
XX
PR   27-APR-2001; 2001US-00844525.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Watt AT;
XX
DR   WPI; 2003-196749/19.
XX
PT   New antisense compounds targeted to nucleic acids encoding human
PT   bifunctional apoptosis regulator, for modulating expression of the
PT   regulator and treating diseases associated with expression of the
PT   regulator in humans.
XX
PS   Claim 3; Col 45-46; 42pp; English.
XX
CC   This invention describes a novel compound, 17-50 nucleobases in length
CC   which specifically hybridises with a nucleic acid encoding human
CC   bifunctional apoptosis regulator (BAR) and inhibits the expression of
CC   human BAR. The products of the invention have cytostatic and
CC   antiinflammatory activity and can be used to inhibit human BAR expression
CC   during antisense therapy, useful for inhibiting the expression of human
CC   BAR in cells or tissues and for treating diseases associated with
CC   expression of BAR in an animal, particularly a human suspected of having
CC   or being prone to a disease or condition associated with expression of
CC   human BAR. In addition the antisense oligonucleotides are useful for
CC   diagnostics, therapeutics and as research reagent, e.g. prophylactically
CC   to prevent or delay infection, inflammation or tumor formation. The
CC   oligonucleotides described in the invention have 2'-methoxyethyl (2'-MOE)
CC   wings and a deoxy gap. This sequence represents a human BAR antisense
CC   oligonucleotide described in the disclosure of the invention
XX
SQ   Sequence 20 BP; 9 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTTGAAAG 2197
              ||  |||||||||||| ||
Db         19 TTGCTTTTAACTTTGACAG 1

RESULT 4084
ABZ98046
ID   ABZ98046 standard; DNA; 20 BP.
XX
AC   ABZ98046;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human MCP4 oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
```

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13288; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2009 CAGAGATCAAGTCCTCTGG 2027
||||| ||||||| || ||
Db 1 CAGAGTTCAAGTCTTCAGG 19

RESULT 4085
ABZ90034/c
ID ABZ90034 standard; DNA; 20 BP.
XX
AC ABZ90034;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5276; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1987 AAAAGTGTGTATCTAGCTT 2005
||| |||||| ||||| ||
Db 20 AAATGTGTGTTTCTAGGTT 2

RESULT 4086
ABZ88602/c
ID ABZ88602 standard; DNA; 20 BP.
XX
AC ABZ88602;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3844; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 1 C; 16 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 253 CCCCCACCTCTCCTCCGCC 271
||||| || |||| |||||
Db 20 CCCCCTCCACTCCCCCGCC 2

RESULT 4087
ABZ98097
ID ABZ98097 standard; DNA; 20 BP.
XX
AC ABZ98097;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human MCP4 oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13339; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2009 CAGAGATCAAGTCCTCTGG 2027
||||| ||||||| || ||
Db 1 CAGAGTTCAAGTCTTCAGG 19

RESULT 4088
ABZ98729/c
ID ABZ98729 standard; DNA; 20 BP.
XX
AC ABZ98729;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human tryptase a oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13971; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 555 GGCTGGAGGCGGGCGCGGT 573
|||| ||||||||| |||
Db 20 GGCTACAGGCGGGCGTGGT 2

RESULT 4089
ABZ99386/c
ID ABZ99386 standard; DNA; 20 BP.
XX
AC ABZ99386;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 14628; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 654 AGAACCTGGGGCTCCACGA 672
|||||||||||| || |||
Db 20 AGAACCTGGGGGTCGGCGA 2

RESULT 4090
ABZ85859/c
ID ABZ85859 standard; DNA; 20 BP.
XX
AC ABZ85859;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1101; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1057 TCATGTGACTCTCCTGACA 1075
||||||| ||||||| | ||
Db 19 TCATGTAACTCTCCAGCCA 1

RESULT 4091
ABZ87871
ID ABZ87871 standard; DNA; 20 BP.
XX
AC ABZ87871;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3113; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2552 AAGAGGATGCTGGGCTCTG 2570
|| ||| ||||||| ||||
Db 1 AACAGGCTGCTGGGATCTG 19

RESULT 4092
ABZ92871/c
ID ABZ92871 standard; DNA; 20 BP.
XX
AC ABZ92871;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8113; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 4 T; 0 U; 1 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 448 GCCCACAGGCAGCCAGCAGC 467
||||||||||| ||| |||
Db 20 GCCCACGGGCANGCAGGAGC 1

RESULT 4093
ABZ88203
ID ABZ88203 standard; DNA; 20 BP.
XX
AC ABZ88203;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3445; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 459 GCCAGCAGCAGGCCTGGCC 477
| |||| |||||| |||||
Db 2 GGCAGCTGCAGGCTTGGCC 20

RESULT 4094
ABZ98593
ID ABZ98593 standard; DNA; 20 BP.
XX
AC ABZ98593;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human tryptase a oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 13835; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 2 A; 8 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 211 CGAGGATCGCCACGACGGG 229
|| || |||||| ||||||
Db 1 CGCGGCTCGCCAGGACGGG 19

RESULT 4095
ABZ91192/c
ID ABZ91192 standard; DNA; 20 BP.
XX
AC ABZ91192;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6434; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 651 CCGAGAACCTGGGGCTCCA 669
|| |||| ||||| |||||
Db 20 CCAAGAAGCTGGGTCTCCA 2

RESULT 4096
ABZ88600
ID ABZ88600 standard; DNA; 20 BP.
XX
AC ABZ88600;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

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XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3842; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 4 C; 16 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        554 GGGCTGGAGGCGGGCGCGG 572
              |||| || |||||||| ||
Db          2 GGGCCGGGGGCGGGCGGGG 20


RESULT 4097
ABZ90510/c
ID   ABZ90510 standard; DNA; 20 BP.
XX
AC   ABZ90510;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5752; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 5 A; 3 C; 1 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2119 TTTAGGAAACTTGTAGAAA 2137
              |||||||||||| | |||
Db         20 TTTAGGAAACTTAAAAAAA 2


RESULT 4098
ABZ85536/c
ID   ABZ85536 standard; DNA; 20 BP.
XX
AC   ABZ85536;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
```

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 778; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

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  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTT 2179
              | ||||||||| |||| ||
Db         19 TTTCCTTTTTTCTTTTCTT 1
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RESULT 4099
ABZ88781
ID ABZ88781 standard; DNA; 20 BP.
XX
AC ABZ88781;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4023; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 0 C; 4 G; 16 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              || |||| |||| ||||||
Db          1 TTGTTTTGTTTTGTTTTTT 19
```

RESULT 4100
ABZ88781/c
ID ABZ88781 standard; DNA; 20 BP.
XX
AC ABZ88781;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

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XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
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PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4023; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 0 C; 4 G; 16 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||| |||| |||| ||
Db         19 AAAAAACAAAACAAAACAA 1


RESULT 4101
ABZ90942/c
ID   ABZ90942 standard; DNA; 20 BP.
XX
AC   ABZ90942;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 6184; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 4 A; 2 C; 11 G; 3 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       248 CGGGTCCCCCACCTCTCCT 266
             || | |||| ||||||||||
Db        19 CGTGACCCCAACCTCTCCT 1


RESULT 4102
ABZ85566/c
ID   ABZ85566 standard; DNA; 20 BP.
XX
AC   ABZ85566;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
```

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XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 808; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 5 A; 1 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        342 ACTTTCCCCCTCCCTACCA 360
              ||| | |||||||||| |||
Db         19 ACTCTTCCCCTCCCTCCCA 1


RESULT 4103
ABZ89197
ID   ABZ89197 standard; DNA; 20 BP.
XX
AC   ABZ89197;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4439; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        796 GAAGGAGCTGGTGGGGGCC 814
              |||||| |||| || ||||
Db          2 GAAGGACCTGGAGGTGGCC 20


RESULT 4104
ABZ86102/c
ID   ABZ86102 standard; DNA; 20 BP.
XX
AC   ABZ86102;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
```

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1344; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 10 A; 1 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1812 TGCTATAAGTTTTAGAATC 1830
||||||| ||||| ||||
Db 19 TGCTATATTTTTTAAAATC 1

RESULT 4105
ABZ87395
ID ABZ87395 standard; DNA; 20 BP.
XX
AC ABZ87395;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 2637; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2026 GGTAGGAGGCAAAGGTTCT 2044
| ||||||||| ||| ||||
Db 1 GCTAGGAGGCCAAGTTTCT 19

RESULT 4106
ABZ87364/c
ID ABZ87364 standard; DNA; 20 BP.
XX
AC ABZ87364;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 2606; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1308 TCTTGGAGACGAACATACA 1326
||||||||| ||||| | |
Db 19 TCTTGGAGAAGAACAGAGA 1

RESULT 4107
ABZ89513
ID ABZ89513 standard; DNA; 20 BP.
XX
AC ABZ89513;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4755; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2172 TTTTTTTTTTTTTTTAACT 2190
||||| ||||| ||| |||
Db 1 TTTTTATTTTTGTTTTACT 19

RESULT 4108
ABZ91731/c
ID ABZ91731 standard; DNA; 20 BP.
XX
AC ABZ91731;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6973; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 10 A; 0 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2519 TTTTATTCATATATATACA 2537
||| || ||||||||||
Db 20 TTTCATATATATATATACA 2

RESULT 4109
ABZ98830/c
ID ABZ98830 standard; DNA; 20 BP.
XX
AC ABZ98830;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human tryptase b oligonucleotdie sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 14072; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 555 GGCTGGAGGCGGGCGCGGT 573
|||| |||||||||| |||
Db 20 GGCTACAGGCGGGCGTGGT 2

RESULT 4110
ABZ76530/c
ID ABZ76530 standard; DNA; 20 BP.
XX
AC ABZ76530;
XX
DT 29-APR-2003 (first entry)
XX
DE Lactobacillus brevis PCR primer ORF1 SEQ ID NO:33.
XX
KW Lactobacillus brevis; beer turbidity; beer clouding; beer; detection;
KW lactic acid bacteria; brewing; probe; PCR primer; ss.
XX
OS Lactobacillus brevis.
XX
PN WO200295028-A1.

XX
PD 28-NOV-2002.
XX
PF 23-MAY-2002; 2002WO-JP005022.
XX
PR 23-MAY-2001; 2001JP-00154085.
XX
PA (KIRI) KIRIN BEER KK.
XX
PI Fujii T;
XX
DR WPI; 2003-120803/11.
XX
PT Polynucleotide probes and primers for detecting beer-clouding lactic acid
PT bacteria, for quality control during beer production applicable in
PT brewing industry.
XX
PS Claim 7; Page 29; 94pp; Japanese.
XX
CC The present invention describes a polynucleotide probe, or primer, for
CC detecting beer-clouding lactic acid bacteria containing a nucleotide
CC sequence of (I) with 8056 base pairs (see ABZ76501), or a nucleotide made
CC from not less than 15 nucleotides hybridisable with its complementary
CC sequence. Probes and primers from the present invention can be used for
CC detecting beer-clouding lactic acid bacteria (Lactobacillus brevis) for
CC quality control during beer production, which is applicable in the
CC brewing industry. The present sequence represents a PCR primer for
CC Lactobacillus brevis which is used in the exemplification of the present
CC invention
XX
SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1177 TCATCTTGGAGGACGAAAT 1195
||||||||||||| || ||
Db 20 TCATCTTGGAGGTCGGCAT 2

RESULT 4111
ADA55771
ID ADA55771 standard; DNA; 20 BP.
XX
AC ADA55771;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein-related PCR primer, SEQ ID 3339.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease; PCR; primer;
KW ss.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Example 8; Page 112; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease. The present
CC sequence was used in an example from the invention.
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1917 ATACCTTTTTTTTCAGTGT 1935
||| || || |||||||||
Db 1 ATAGCTCTTGTTTCAGTGT 19

RESULT 4112
ABX33988/c
ID ABX33988 standard; DNA; 20 BP.
XX
AC ABX33988;
XX
DT 10-FEB-2003 (first entry)
XX
DE Human interleukin 12 p40 subunit antisense oligonucleotide ISIS #139161.
XX
KW Human; ss; antisense; interleukin 12 p40 subunit; antibacterial;
KW antiinflammatory; cytostatic; infection; inflammation; tumour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All cytosines are 5-methylcytidines and the
FT nucleotides are linked via a phosphorothioate backbone"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN US6448081-B1.
XX
PD 10-SEP-2002.
XX
PF 07-MAY-2001; 2001US-00851062.
XX
PR 07-MAY-2001; 2001US-00851062.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BF, Freier SM;
XX
DR WPI; 2003-074100/07.
XX
PT New antisense chimeric oligonucleotide, useful for modulating the
PT expression of human Interleukin 12 p40 subunit, in treating or preventing

```
PT   disease states in humans and animals, and as research reagents and
PT   diagnostics.
XX
PS   Claim 3; Col 45; 42pp; English.
XX
CC   The invention relates to an antisense compound 20-50 nucleobases in
CC   length targeted to a start codon region, coding region, a stop codon
CC   region or a 3'-untranslated region of a nucleic acid molecule encoding
CC   human Interleukin 12 p40 subunit. The compound specifically hybridises
CC   with one of the regions and inhibits the expression of human Interleukin
CC   12 p40 subunit. The new compound is useful for inhibiting the expression
CC   of human Interleukin 12 p40 subunit in cells or tissues and comprises
CC   contacting the cells or tissues in vitro with the compound, so that
CC   expression of the human Interleukin 12 p40 subunit is inhibited. The
CC   antisense compound may also be used as research reagents and diagnostics,
CC   and as treatment or prevention of disease states, e.g. to prevent or
CC   delay infection, inflammation or tumour formation, in animals and humans.
CC   The present sequence is an antisense oligonucleotide of the invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1169 ACCAGACCTCATCTTGGAG 1187
              || | | ||||||||||||
Db         20 ACTATAGCTCATCTTGGAG 2


RESULT 4113
ABX34004/c
ID   ABX34004 standard; DNA; 20 BP.
XX
AC   ABX34004;
XX
DT   10-FEB-2003  (first entry)
XX
DE   Human interleukin 12 p40 subunit antisense oligonucleotide ISIS #139177.
XX
KW   Human; ss; antisense; interleukin 12 p40 subunit; antibacterial;
KW   antiinflammatory; cytostatic; infection; inflammation; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "All cytosines are 5-methylcytidines and the
FT                    nucleotides are linked via a phosphorothioate backbone"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   US6448081-B1.
XX
PD   10-SEP-2002.
XX
PF   07-MAY-2001; 2001US-00851062.
XX
PR   07-MAY-2001; 2001US-00851062.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Freier SM;
XX
DR   WPI; 2003-074100/07.
XX
PT   New antisense chimeric oligonucleotide, useful for modulating the
PT   expression of human Interleukin 12 p40 subunit, in treating or preventing
PT   disease states in humans and animals, and as research reagents and
PT   diagnostics.
XX
PS   Example 15; Col 45; 42pp; English.
XX
CC   The invention relates to an antisense compound 20-50 nucleobases in
CC   length targeted to a start codon region, coding region, a stop codon
CC   region or a 3'-untranslated region of a nucleic acid molecule encoding
CC   human Interleukin 12 p40 subunit. The compound specifically hybridises
CC   with one of the regions and inhibits the expression of human Interleukin
CC   12 p40 subunit. The new compound is useful for inhibiting the expression
CC   of human Interleukin 12 p40 subunit in cells or tissues and comprises
CC   contacting the cells or tissues in vitro with the compound, so that
CC   expression of the human Interleukin 12 p40 subunit is inhibited. The
CC   antisense compound may also be used as research reagents and diagnostics,
CC   and as treatment or prevention of disease states, e.g. to prevent or
CC   delay infection, inflammation or tumour formation, in animals and humans.
CC   The present sequence is an antisense oligonucleotide of the invention
XX
SQ   Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1117 TGCCTATGTCTGTGAAGCC 1135
              | || |||||||||||| |
Db         20 TTCCCATGTCTGTGAAGAC 2


RESULT 4114
ABQ84614/c
ID   ABQ84614 standard; DNA; 20 BP.
XX
AC   ABQ84614;
XX
DT   20-FEB-2003  (first entry)
XX
DE   DPP10 related PSQ assay oligonucleotide #99.
XX
KW   DPP10; dipeptidyl peptidase; prolyloligopeptidase; enzyme; asthma;
KW   antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;
KW   antirheumatic; vaccine; gene therapy; inflammatory disease;
KW   inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
KW   chromosome 2q14; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200286113-A2.
XX
PD   31-OCT-2002.
XX
PF   24-APR-2002; 2002WO-GB001887.
XX
PR   24-APR-2001; 2001GB-00010044.
PR   24-APR-2001; 2001GB-00010046.
PR   12-OCT-2001; 2001GB-00024575.
PR   12-OCT-2001; 2001GB-00024594.
XX
PA   (ISIS-) ISIS INNOVATIONS LTD.
XX
PI   Cookson WOCM,  Moffat MF,  Allen M,  Lench N;
XX
DR   WPI; 2003-093132/08.
XX
PT   New nucleic acid sequence comprising DPP10 mRNA, useful for the
PT   manufacture of a medicament for regulating DPP10 protein expression or
PT   for preventing or treating inflammatory disease e.g., inflammatory bowel
PT   disease.
XX
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```
PS   Disclosure; Page 321; 321pp; English.
XX
CC   The present invention describes a new isolated nucleic acid sequence (I)
CC   comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
CC   known as prolyloligopeptidase). (I) has antiinflammatory, antiasthmatic,
CC   antipsoriatic, antiarthritic and antirheumatic activities, and can be
CC   used in vaccines and gene therapy. A composition comprising (I) can be
CC   used for the manufacture of a medicament for regulating DPP10 expression
CC   or for preventing or treating inflammatory disease e.g., inflammatory
CC   bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
CC   also be used in an assay for detecting or measuring DPP10 in a sample. A
CC   host cell comprising (I) can be used for producing recombinant DPP10 gene
CC   products, or in drug screening systems to identify agents for diagnosis
CC   or treatment of individuals having or susceptible to inflammatory
CC   disease. Human DPP10 is located on chromosome 2, more specifically
CC   chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 20 BP; 11 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1624 GTTACCTACCTTACTATTT 1642
              || |||||| || ||||||
Db         20 GTCACCTACTTTTCTATTT 2


RESULT 4115
ACC82913
ID   ACC82913 standard; DNA; 20 BP.
XX
AC   ACC82913;
XX
DT   27-AUG-2003  (first entry)
XX
DE   Human TRIP6 antisense oligonucleotide ISIS #198785.
XX
KW   Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW   OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW   inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW   chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidine residues
FT                   are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2003040328-A2.
XX
PD   15-MAY-2003.
XX
PF   05-NOV-2002; 2002WO-US035479.
XX
PR   08-NOV-2001; 2001US-00008789.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Dobie K;
XX
DR   WPI; 2003-430662/40.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT   hormone receptor interactor 6, useful for diagnosing or treating
PT   hyperproliferative disorders, such as cancer.
XX
PS   Example 15; Page 77; 111pp; English.
XX
CC   The invention relates to antisense compounds targetted to a nucleic acid
CC   encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC   expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC   zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC   Antisense compounds of the invention are useful for modulating the
CC   expression of TRIP6 and for treating diseases or conditions associated
CC   with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC   cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC   to prevent or delay infection, inflammation or tumour formation, as
CC   research reagents and kits and in distinguishing between functions of
CC   various members of a biological pathway. The are also useful in antisense
CC   therapy. The present sequence is an antisense oligo targetted to human
CC   TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ   Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        647 CTGGCCGAGAACCTGGGGC 665
              ||||||| ||| ||||| |
Db          1 CTGGCCGCGAAGCTGGGCC 19


RESULT 4116
ACD42192/c
ID   ACD42192 standard; DNA; 20 BP.
XX
AC   ACD42192;
XX
DT   05-SEP-2003  (first entry)
XX
DE   Antisense oligonucleotide targeting human b-raf, ISIS13742.
XX
KW   Human; ss; antisense; c-raf; a-raf; b-raf; protein kinase; cancer;
KW   signal transduction; cell proliferation; lung carcinoma; cytostatic;
KW   antisense gene therapy; chemotherapeutic agent; angiogenesis;
KW   hyperproliferative condition; neovascularisation; ocular angiogenesis.
XX
OS   Homo sapiens.
XX
PN   US2003032607-A1.
XX
PD   13-FEB-2003.
XX
PF   25-JAN-2002; 2002US-00057550.
XX
PR   31-MAY-1994;   94US-00250856.
PR   31-MAY-1995;   95WO-US007111.
PR   26-NOV-1996;   96US-00756806.
PR   07-JUL-1997;   97US-00888982.
PR   06-JUL-1998;   98WO-US013961.
PR   28-AUG-1998;   98US-00143214.
PR   18-FEB-2000; 2000US-00506073.
XX
PA   (MONI/) MONIA B P.
XX
PI   Monia BP;
XX
DR   WPI; 2003-503332/47.
XX
PT   Novel antisense oligonucleotide which is targeted to mRNA encoding human
PT   raf and which is capable of inhibiting raf expression, useful for
```

```
PT   treating or preventing hyperproliferative conditions such as cancer.
XX
PS   Example 18; Page 14; 42pp; English.
XX
CC   The invention relates to an oligonucleotide 8-50 nucleotides in length
CC   which is targeted to mRNA encoding human c-raf, a-raf or b-raf (raf is a
CC   protein kinase playing a regulatory role in signal transduction,
CC   regulating cell proliferation and has been implicated in lung carcinoma),
CC   and which is capable of inhibiting raf expression. Also included is a
CC   composition comprising the oligonucleotide and a pharmaceutically
CC   acceptable carrier. The antisense oligonucleotide is useful for
CC   inhibiting the expression of human raf in human cells or tissues, by
CC   contacting the human cells or tissues with the oligo. The oligo. is also
CC   is useful for treating or preventing a disease or condition associated
CC   with the expression of raf by administering it in combination with a
CC   chemotherapeutic agent to a human or cells of the human, where the
CC   expression of raf is abnormal expression, and the condition is a
CC   hyperproliferative condition such as cancer, angiogenesis or
CC   neovascularisation (preferably ocular angiogenesis or
CC   neovascularisation). The oligo. is also useful for inhibiting
CC   hyperproliferation of cells. The oligos. are also useful as tools, for
CC   example for detecting and determining the role of raf expression in
CC   various cell functions and physiological processes and conditions and for
CC   diagnosing conditions associated with raf expression and for research
CC   purposes. The present sequence is an antisense oligonucleotide targeting
CC   a human raf mRNA
XX
SQ   Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1531 AGAAAGGTTAGGAGAGTAG 1549
              ||| || | ||||||||||
Db         20 AGAGAGTTCAGGAGAGTAG 2


RESULT 4117
ACA92581/c
ID   ACA92581 standard; DNA; 20 BP.
XX
AC   ACA92581;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human Ki-ras antisense oligonucleotide ISIS 6958.
XX
KW   Human; ras; cancer; cancer cell proliferation; ras oncogene; oncogene;
KW   colorectal cancer; melanoma; liposarcoma; ss; mesothelioma; sarcoma;
KW   colon cancer; pancreatic cancer; antisense.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2003013670-A1.
XX
PD   16-JAN-2003.
XX
PF   30-MAY-2001; 2001US-00870002.
XX
PR   05-OCT-1992;   92US-00958134.
PR   21-JAN-1993;   93US-00007996.
PR   01-OCT-1993;   93WO-US009346.
PR   03-APR-1995;   95US-00411734.
PR   08-JUL-1997;   97US-00889296.
PR   03-AUG-1998;   98US-00128494.
PR   22-MAY-2000; 2000US-00575554.
XX
PA   (MONI/) MONIA B P.
PA   (COWS/) COWSERT L M.
PA   (MANO/) MANOHARAN M.
PA   (DORR/) DORR F A.
PA   (HOLM/) HOLMLUND J.
XX
PI   Monia BP,  Cowsert LM,  Manoharan M,  Dorr FA,  Holmlund J;
XX
DR   WPI; 2003-438917/41.
XX
PT   Composition comprising an antisense oligonucleotide targeted to nucleic
PT   acids encoding human ras, and capable of inhibiting ras expression,
PT   useful for treating or preventing colorectal cancer, melanoma, or
PT   sarcoma.
XX
PS   Disclosure; Page 13; 46pp; English.
XX
CC   The invention relates to a composition comprising an oligonucleotide
CC   which is targeted to a nucleic acid encoding human ras, which is capable
CC   of inhibiting ras expression, and at least one chemotherapeutic agent.
CC   The composition is useful for modulating the expression of human ras in
CC   tissues or cells containing a ras gene. The compostion is also useful for
CC   inhibiting the proliferation of cancer cells, where the cancer cells are
CC   blood cells, preferably peripheral blood mononuclear cells. The
CC   composition is useful for treating or preventing a condition arising from
CC   the activation of ras oncogene which involves contacting an animal
CC   suspected of having a condition (e.g. hyperproliferative condition such
CC   as cancer preferably colorectal cancer, melanoma, liposarcoma,
CC   mesothelioma, sarcoma, colon cancer or pancreatic cancer) arising from
CC   the activation of ras oncogene such as abnormal expression of the ras
CC   oncogene. The present sequence represents a human ras antisense
CC   oligonucleotide
XX
SQ   Sequence 20 BP; 0 A; 12 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAG 69
              || |||| ||||| |||||
Db         19 GCCGCGGCGGCGGAGGCAG 1


RESULT 4118
ADA44763/c
ID   ADA44763 standard; DNA; 20 BP.
XX
AC   ADA44763;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense oligonucleotide  #ISIS 115435 #SEQ ID 61.
XX
KW   Antisense oligonucleotide; cytostatic; immunosuppressive;
KW   antiinflammatory; gene therapy; hyperproliferative disorder; cancer;
KW   autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; ss;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages, all cytosines are 5-
FT                   methylcytosine"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2003031576-A2.
```

```
XX
PD   17-APR-2003.
XX
PF   03-OCT-2002; 2002WO-US031809.
XX
PR   06-OCT-2001; 2001US-00972607.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Wyatt JR;
XX
DR   WPI; 2003-457242/43.
XX
PT   New compound having sequence targeted to nucleic acid encoding inhibitor-
PT   kappa B kinase-gamma, useful for preparing composition for treating e.g.,
PT   cancer, or inflammatory or autoimmune disorder.
XX
PS   Example 15; Page 77; 106pp; English.
XX
CC   The invention relates to an antisense compound that is targeted to a
CC   nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically
CC   hybridising to the nucleic acid encoding inhibitor-kappa B kinase-gamma
CC   and inhibiting its expression. Compounds of the invention are antisense
CC   oligonucleotides comprising at least one modified internucleoside
CC   linkage, which is a phosphorothioate linkage, at least one modified sugar
CC   moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase, which is a 5-methylcytosine. Preferably, the
CC   antisense oligonucleotide is a chimeric oligonucleotide. The compound of
CC   the invention is useful for preparing a composition for treating a
CC   hyperproliferative disorder e.g., cancer, or an autoimmune or
CC   inflammatory disorder. The methods are useful for inhibiting the
CC   expression of inhibitor-kappa B kinase-gamma in cells or tissues, and
CC   treating an animal having a disease or condition associated with
CC   inhibitor-kappa B kinase-gamma. Sequences given in ADA44713-ADA44790
CC   represent antisense oligonucleotides for the inhibition of human
CC   inhibitor-kappa B kinase-gamma mRNA levels.
XX
SQ   Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1001 CGGGAGAAGTTGGACAAGA 1019
              ||||||||| ||| | |||
Db         20 CGGGAGAAGCTGGCCGAGA 2


RESULT 4119
ADA44762/c
ID   ADA44762 standard; DNA; 20 BP.
XX
AC   ADA44762;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Antisense oligonucleotide  #ISIS 115434 #SEQ ID 60.
XX
KW   Antisense oligonucleotide; cytostatic; immunosuppressive;
KW   antiinflammatory; gene therapy; hyperproliferative disorder; cancer;
KW   autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; ss;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages, all cytosines are 5-
FT                   methylcytosine"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   WO2003031576-A2.
XX
PD   17-APR-2003.
XX
PF   03-OCT-2002; 2002WO-US031809.
XX
PR   06-OCT-2001; 2001US-00972607.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Wyatt JR;
XX
DR   WPI; 2003-457242/43.
XX
PT   New compound having sequence targeted to nucleic acid encoding inhibitor-
PT   kappa B kinase-gamma, useful for preparing composition for treating e.g.,
PT   cancer, or inflammatory or autoimmune disorder.
XX
PS   Claim 3; Page 77; 106pp; English.
XX
CC   The invention relates to an antisense compound that is targeted to a
CC   nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically
CC   hybridising to the nucleic acid encoding inhibitor-kappa B kinase-gamma
CC   and inhibiting its expression. Compounds of the invention are antisense
CC   oligonucleotides comprising at least one modified internucleoside
CC   linkage, which is a phosphorothioate linkage, at least one modified sugar
CC   moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one
CC   modified nucleobase, which is a 5-methylcytosine. Preferably, the
CC   antisense oligonucleotide is a chimeric oligonucleotide. The compound of
CC   the invention is useful for preparing a composition for treating a
CC   hyperproliferative disorder e.g., cancer, or an autoimmune or
CC   inflammatory disorder. The methods are useful for inhibiting the
CC   expression of inhibitor-kappa B kinase-gamma in cells or tissues, and
CC   treating an animal having a disease or condition associated with
CC   inhibitor-kappa B kinase-gamma. Sequences given in ADA44713-ADA44790
CC   represent antisense oligonucleotides for the inhibition of human
CC   inhibitor-kappa B kinase-gamma mRNA levels.
XX
SQ   Sequence 20 BP; 1 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1001 CGGGAGAAGTTGGACAAGA 1019
              ||||||||| ||| | |||
Db         19 CGGGAGAAGCTGGCCGAGA 1


RESULT 4120
ACC58274
ID   ACC58274 standard; DNA; 20 BP.
XX
AC   ACC58274;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Vascular endothelial cell growth inhibitor forward PCR primer.
XX
KW   Human; vascular endothelial cell growth inhibitor; VEGI; angiogenesis;
KW   inhibitor; cytostatic; antitumour; vulnerary; gene therapy; PCR; primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO2003039491-A2.
```

```
XX
PD   15-MAY-2003.
XX
PF   12-NOV-2002; 2002WO-US037426.
XX
PR   09-NOV-2001; 2001US-0331190P.
XX
PA   (GEOU ) UNIV GEORGETOWN.
XX
PI   Li L,  Pan H;
XX
DR   WPI; 2003-441465/41.
XX
PT   New vascular endothelial growth inhibitor polynucleotides, useful for
PT   treating disorders needing angiogenesis inhibition, such as solid tumors,
PT   diabetic retinopathy, Kaposi's sarcoma, psoriasis and rheumatoid
PT   arthritis.
XX
PS   Example 7; Page 82; 133pp; English.
XX
CC   The present sequence is that of a forward primer that was used in the
CC   mapping of the human vascular endothelial growth inhibitor (VEGI) gene. 4
CC   Human VEGI isoforms have been identified: novel VEGI-192a and VEGI-192b,
CC   and previously known VEGI-251 and VEGI-174 (see ABR42579-82). The
CC   invention provides angiogenesis inhibitors comprising VEGI-192a, VEGI-
CC   192b or VEGI-251 polynucleotides, polypeptides or derivatives, useful for
CC   treatment of cancer or suppression of tumour growth. Also provided are
CC   accelerators of angiogenesis, e.g. an antibody, antisense
CC   oligonucleotide, antagonist or ribozyme that reduces or eliminates VEGI-
CC   192a, VEGI-192b or VEGI-251 function, useful e.g. for wound healing
XX
SQ   Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        648 TGGCCGAGAACCTGGGGCT 666
              |||||||| | ||||| ||
Db          2 TGGCCGAGGATCTGGGACT 20


RESULT 4121
ACC49680/c
ID   ACC49680 standard; DNA; 20 BP.
XX
AC   ACC49680;
XX
DT   01-JUL-2003  (first entry)
XX
DE   Human KSR chimeric phosphorothioate oligonucleotide SEQ ID NO:50.
XX
KW   Human; kinase suppressor of ras-1; KSR; cytostatic; KSR inhibitor;
KW   antisense gene therapy; hyperproliferative disorder; phosphorothioate;
KW   developmental disorder; antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls (2'-MOE)"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyls (2'-MOE)"
XX
PN   WO2003025144-A2.
XX
PD   27-MAR-2003.
XX
PF   19-SEP-2002; 2002WO-US029705.
XX
PR   20-SEP-2001; 2001US-00961001.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Freier SM;
XX
DR   WPI; 2003-363140/34.
XX
PT   New compounds, particularly antisense oligonucleotides targeted to a
PT   nucleic acid encoding KSR, useful for treating a disease/condition
PT   associated with KSR, such as hyperproliferative or developmental
PT   disorders.
XX
PS   Claim 3; Page 75; 102pp; English.
XX
CC   The present invention describes a compound 8-50 nucleobases in length
CC   targeted to, and which specifically hybridises with a nucleic acid
CC   molecule encoding kinase suppressor of ras-1 (KSR), and inhibits the
CC   expression of KSR. Also described: (1) a compound 8-50 nucleobases in
CC   length that specifically hybridises with at least an 8-nucleobase portion
CC   of an active site on a nucleic acid molecule encoding KSR; (2) a
CC   composition comprising the compound and a carrier or diluent; (3)
CC   inhibiting the expression of KSR in cells or tissues by contacting the
CC   cells or tissues with the compound so that expression of KSR is inhibited
CC   ; and (4) treating an animal having a disease or condition associated
CC   with KSR by administering to the animal a therapeutic or prophylactic
CC   amount of the compound so that expression of KSR is inhibited. The
CC   compound has cytostatic activity and can be used as a KSR inhibitor, and
CC   in antisense gene therapy. The compound, composition and methods are
CC   useful for treating a disease or condition associated with KSR, such as a
CC   hyperproliferative or developmental disorder, or a disease or condition
CC   arising from aberrant apoptosis by inhibiting the expression of KSR. They
CC   are also useful in research and diagnostics for modulating the expression
CC   of KSR. The present sequence represents a chimeric phosphorothioate
CC   antisense oligonucleotide of human KSR, which is used in an example from
CC   the present invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        807 TGGGGGCCGTAATGAACCC 825
              |||||||| ||||||||
Db         19 TGGGGGCCTGCATGAACCC 1


RESULT 4122
ABZ76424/c
ID   ABZ76424 standard; DNA; 20 BP.
XX
AC   ABZ76424;
XX
DT   12-JUN-2003  (first entry)
XX
DE   PRRSV polymerase protein ORF1b specific PCR primer D1.
XX
KW   HCV; IBDV; IBV; ILTV; PRRSV; immunogen; virucide; vaccine; transgenic;
KW   polymerase; ORF1b; PCR; primer; ss.
XX
OS   Porcine reproductive and respiratory syndrome virus.
XX
PN   WO2003013598-A2.
XX
PD   20-FEB-2003.
XX
```

```
PF   08-AUG-2002; 2002WO-US025126.
XX
PR   09-AUG-2001; 2001US-0311106P.
PR   07-AUG-2002; 2002US-00311106.
XX
PA   (LAMD/) LAM D M K.
PA   (ZENG/) ZENG F.
PA   (LEUN/) LEUNG F C.
XX
PI   Lam DMK,  Zeng F,  Leung FC;
XX
DR   WPI; 2003-256496/25.
XX
PT   New orally acceptable immunogenic composition comprising unpurified or
PT   partially purified recombinant HCV, IBDV, IBV, ILTV or PRRSV immunogen
PT   expressed in a plant, useful for producing an immunogenic response
PT   against the antigen.
XX
PS   Example 5; Page 97; 146pp; English.
XX
CC   The invention relates to a new orally acceptable immunogenic composition
CC   comprising unpurified or partially purified recombinant HCV (Hog cholera
CC   virus), IBDV (Infectious Bursal Disease Virus), IBV (infectious
CC   bronchitis virus), ILTV or PRRSV (porcine reproductive and respiratory
CC   syndrome virus) immunogen expressed in a plant, where the immunogen is
CC   expressed in the plant at a level so that upon oral administration of the
CC   composition to an animal, an immunogenic response is observed. The
CC   composition is useful for producing an immunogenic response against HCV,
CC   IBDV, IBV, ILTV or PRRSV antigen. Sequences ABZ76423-28 represent
CC   primers, based on the ORF1b encoding the polymerase protein, used for PCR
CC   amplification and typing of PRRSV
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1212 AGAACATGCTATTGGCGGC 1230
              || ||||| ||||| ||||
Db         19 AGCACATGGTATTGTCGGC 1


RESULT 4123
ABZ74905
ID   ABZ74905 standard; DNA; 20 BP.
XX
AC   ABZ74905;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human acyl coenzyme A cholesterol acyltransferase-1 antisense oligo #25.
XX
KW   Human; acyl coenzyme A cholesterol acyltransferase-1; ACAT; liver;
KW   chromosome 1q25; chromosome 1; chromosome 7; cholesterol metabolism;
KW   free sterol regulation; cholesterol metabolism disorder;
KW   lipid metabolism disorder; atherosclerosis; cardiovascular disease;
KW   cardiant; expression inhibition; phosphorothioate;
KW   antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
FT                   cytosines are 5-methylcytosine"
XX
PN   WO2003012144-A1.
XX
PD   13-FEB-2003.
XX
PF   17-JUL-2002; 2002WO-US022696.
XX
PR   01-AUG-2001; 2001US-00920394.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ,  Lemonidis KM;
XX
DR   WPI; 2003-239532/23.
XX
PT   New antisense oligonucleotides targeted to a nucleic acid encoding acyl
PT   coenzyme A cholesterol acyltransferase-1, useful for treating a
PT   disease/condition involving abnormal lipid or cholesterol metabolism,
PT   e.g. atherosclerosis.
XX
PS   Claim 3; Page 91; 117pp; English.
XX
CC   Sequences ABZ74897-ABZ74942 represent antisense oligonucleotides targeted
CC   to the human or murine acyl coenzyme A cholesterol acyltransferase-1
CC   gene, which inhibit its expression. The antisense oligonucleotides were
CC   designed to target different regions of the human or murine acyl coenzyme
CC   A cholesterol acyltransferase-1 RNA, and were analysed for their effect
CC   on acyl coenzyme A cholesterol acyltransferase-1 mRNA levels by
CC   quantitative real-time PCR. Acyl coenzyme A cholesterol acyltransferase
CC   (ACAT) enzymes catalyse the synthesis of cholesterol esters from free
CC   cholesterol and fatty acyl-CoA, and are also involved in regulating the
CC   concentration of cellular free sterols. The human acyl coenzyme A
CC   cholesterol acyltransferase-1 is the predominant ACAT isoform in the
CC   liver, and the gene encoding it is located on chromosome 1q25, although a
CC   subsequent study has indicated that one acyl coenzyme A cholesterol
CC   acyltransferase-1 mRNA is produced from genes on two different
CC   chromosomes (chromosomes 1 and 7) by a novel RNA recombination mechanism
CC   involving trans-splicing of the two discontinuous precursor mRNAs. The
CC   oligonucleotides of the invention are useful for the prevention and
CC   treatment of conditions associated with acyl coenzyme A cholesterol
CC   acyltransferase-1, such as disorders involving abnormal lipid or
CC   cholesterol metabolism, e.g., atherosclerosis or cardiovascular disease.
CC   They are also useful in research and diagnostics for modulating the
CC   expression of acyl coenzyme A cholesterol acyltransferase-1
XX
SQ   Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1605 TGGCCTGGGGGAAGAGTTT 1623
              ||||| || ||||||| ||
Db          1 TGGCCCGGTGGAAGAGGTT 19


RESULT 4124
ADA26567
ID   ADA26567 standard; DNA; 20 BP.
XX
AC   ADA26567;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human Jun N-terminal kinase, JNK1, antisense oligonucleotide ISIS12551.
XX
KW   ss; human; Jun N-terminal kinase; JNK1; JNK2; JNK3; antisense;
KW   cytostatic; antiinflammatory; apoptosis; prostate cancer;
KW   prostate tumour; inflammation; fibrosis; fibrotic disease;
```

```
KW   fibrotic scarring; peritoneal adhesion; lung fibrosis;
KW   conjunctival scarring; hyperproliferative disease; cancer; probe.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate linkages"
XX
PN   US2003004120-A1.
XX
PD   02-JAN-2003.
XX
PF   31-JAN-2001; 2001US-00774809.
XX
PR   13-AUG-1997;   97US-00910629.
PR   07-AUG-1998;   98US-00130616.
PR   07-APR-1999;   99US-00287796.
PR   15-SEP-1999;   99US-00396902.
XX
PA   (MCKA/) MCKAY R.
PA   (DEAN/) DEAN N M.
PA   (MONI/) MONIA B P.
PA   (NERO/) NERO P.
PA   (GAAR/) GAARDE W A.
XX
PI   Mckay R,  Dean NM,  Monia BP,  Nero P,  Gaarde WA;
XX
DR   WPI; 2003-311908/30.
XX
PT   New oligonucleotides which hybridizes to, and modulates the expression of
PT   Jun N-terminal kinase, useful for treating a disease or condition
PT   characterized by a reduction in apoptosis, e.g. prostate cancer,
PT   inflammation or fibrosis.
XX
PS   Example 3; Page 20; 69pp; English.
XX
CC   The invention relates to an oligonucleotide (antisense, AS) comprising 8-
CC   30 nucleotides connected by covalent linkages, where the oligonucleotide
CC   has a sequence specifically hybridisable with a nucleic acid encoding a
CC   Jun N-terminal kinase (JNK) protein and modulates the expression of the
CC   JNK protein. Also included are a pharmaceutical composition comprising
CC   the AS oligonucleotide (or its bioequivalent, and a pharmaceutical
CC   carrier), treating an animal having/suspected of having/prone to having a
CC   hyperproliferative disease (by administering to a prophylactic or
CC   therapeutic amount of the composition of the AS oligonucleotide),
CC   modulating the expression of a JNK protein in cells or tissues by
CC   contacting the cells or tissues with the AS oligonucleotide, modulating
CC   the cell cycle progression (or the phosphorylation of a protein
CC   phosphorylated by a JNK protein, or expression of a cellular protein that
CC   promotes one or more metastatic events in cultured cells or the cells of
CC   an animal) by administering the oligonucleotide to the cells, inhibiting
CC   the growth of a tumour in an animal by administering the oligonucleotide,
CC   inducing apoptosis in a cell by contacting a cell with an AS
CC   oligonucleotide for JNK2 and treating a human having a disease or
CC   condition associated with a JNK protein or characterised by a reduction
CC   in apoptosis by administering a prophylactic or therapeutic amount of the
CC   AS oligonucleotide. The antisense oligonucleotide is useful for treating
CC   a disease or condition characterised by a reduction in apoptosis, such as
CC   prostate cancer or prostate tumour, inflammation, fibrosis or fibrotic
CC   disease or condition (e.g. fibrotic scarring, peritoneal adhesions, lung
CC   fibrosis or conjunctival scarring), hyperproliferative disease or
CC   condition, such as cancer. The antisense oligonucleotides may also be
CC   used as research agents and diagnostic aids, to detect the presence of
CC   JNK protein-specific nucleic acids in a cell or tissue sample, and to
CC   study the function of one or more genes in the animal. The present
CC   sequence is an antisense oligonucleotide targeting human JNK1.
XX
SQ   Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        813 CCGTAATGAACCCCACTGA 831
              || ||||| ||||||| ||
Db          2 CCATAATGCACCCCACAGA 20


RESULT 4125
ABX95044
ID   ABX95044 standard; cDNA; 20 BP.
XX
AC   ABX95044;
XX
DT   13-JUN-2003  (first entry)
XX
DE   Human RAK mutagenesis primer used to make RAK mutant Y490F.
XX
KW   Human; ss; primer; PCR; cell division cycle; (CDC)2 inhibition; CDC;
KW   neoplastic condition; cancer; non-cancerous proliferative disease; RAK;
KW   cell growth inhibition; beta-actin; mutagenesis; nuclear tyrosine kinase.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6531296-B1.
XX
PD   11-MAR-2003.
XX
PF   20-JUN-1995;   95US-00492723.
XX
PR   20-JUN-1995;   95US-00492723.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Liu ET,  Craven RJ,  Cance WG;
XX
DR   WPI; 2003-361653/34.
XX
PT   New Rak peptide, for use e.g. as a molecular weight marker, or for
PT   treating cancer, other neoplastic conditions or non-cancerous
PT   proliferative diseases.
XX
PS   Example 1; Col 16; 28pp; English.
XX
CC   The invention relates to a peptide, which is a nuclear tyrosine kinase
CC   termed Rak. The Rak peptide is useful in inhibiting cell division cycle
CC   (CDC)2 function that blocks the cell cycle and inhibits cell growth. The
CC   Rak peptide is also useful in diagnostic assays, as a molecular weight
CC   marker, or for treating cancer or other neoplastic conditions, as well as
CC   non-cancerous proliferative diseases. The present sequence represents the
CC   human nuclear tyrosine kinase RAK mutagenesis primer used to make RAK
CC   mutant Y490F
XX
SQ   Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2438 TTACGACTTTTTTGAGACA 2456
              | | |||||||||||| |||
Db          1 TGAAGACTTTTTTGAAACA 19


RESULT 4126
ACH66530
ID   ACH66530 standard; DNA; 20 BP.
XX
AC   ACH66530;
XX
DT   16-OCT-2003  (first entry)
XX
```

```
DE   Antisense PCR primer used to amplify CASP7.
XX
KW   PCR; primer; ss; genomic DNA; gDNA; untranslated region; UTR;
KW   DNA high-density microarray; biosite; large scale production; gDNA probe;
KW   microarray; Type II primer.
XX
OS   Homo sapiens.
XX
PN   US2003073085-A1.
XX
PD   17-APR-2003.
XX
PF   05-OCT-2001; 2001US-00972469.
XX
PR   05-OCT-2001; 2001US-00972469.
XX
PA   (LAIF/) LAI F.
PA   (ZHOU/) ZHOU D.
XX
PI   Lai F, Zhou D;
XX
DR   WPI; 2003-555942/52.
XX
PT   Amplifying expressed genetic sequences from genomic DNA of mammalian or
PT   higher order plant species for printing on DNA microarrays, involves
PT   using the 3' untranslated region of the gene sequence.
XX
PS   Disclosure; Page 7; 15pp; English.
XX
CC   The invention discloses a method for amplifying expressed genetic
CC   sequences from genomic DNA (gDNA) from mammalian or higher order plant
CC   species. The method involves identifying a 3' untranslated region (UTR)
CC   of a gDNA sequence, designing probe, performing PCR, separating the
CC   product by size differentiation and performing a second PCR to amplify
CC   the predetermined sequence. Also claimed is a biological analysis device,
CC   comprising a substrate and an array of a set of expressed genetic
CC   sequences, located on the substrate, which are generated by the method
CC   above and a DNA high-density microarray comprising a substrate upon which
CC   are deposited an array of biosites of genomic DNA fragments having the
CC   sequence of at least one exon, and absent polyadenine and vector
CC   sequences, where the genomic DNA fragments have a sequence length of from
CC   about 75-2000 nucleotides. The method is efficient for amplifying gene
CC   sequences, enables large-scale production of gDNA sequences, generates
CC   large quantities of gDNA probes, which enables greater efficiency for
CC   printing in microarray formats, fabricates high-density DNA arrays of
CC   enhanced, widely varying genetic content and abstains from using RNA-
CC   derived sequences by simple PCR amplifications without cloning. The
CC   method produces amplified sequences that have greater specificity and
CC   size consistency than that observed with cDNA fragments, and allows for
CC   greater signal sensitivity than oligonucleotides. The sequence presented
CC   is a Type II gene specific primer
XX
SQ   Sequence 20 BP; 1 A; 3 C; 6 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2564 GGCTCTGTTCTTGGCTTGG 2582
              |||| |||||||| | |||
Db          2 GGCTTTGTTCTTGTCATGG 20


RESULT 4127
ADA14704/c
ID   ADA14704 standard; DNA; 20 BP.
XX
AC   ADA14704;
XX
DT   06-NOV-2003  (first entry)
XX
DE   PCR primer #1 for human PRKAR1A gene 5' (CA)n.
XX
KW   Human; protein kinase A regulatory subunit 1A; PRKAR1A; Carney complex;
KW   CNC; skin pigmentation defect; freckling; cancer; cytostatic; PCR;
KW   primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2003022180-A1.
XX
PD   30-JAN-2003.
XX
PF   23-AUG-2001; 2001US-00935916.
XX
PR   25-AUG-2000; 2000US-0228211P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Stratakis C,  Kirschner L;
XX
DR   WPI; 2003-540133/51.
XX
PT   New isolated nucleotide sequence of the wild-type or mutant protein
PT   kinase regulatory subunit 1A gene, useful for preparing a composition for
PT   diagnosing or treating cancer or conditions associated with skin
PT   pigmentation defects.
XX
PS   Claim 7; Page 26; 47pp; English.
XX
CC   The present invention relates to wild-type or mutant human protein kinase
CC   A regulatory subunit 1A (PRKAR1A) gene sequences, and methods of
CC   detecting them using gene-specific PCR primers. The compositions and
CC   methods of the invention are useful in the diagnosis and prognosis of
CC   Carney complex (CNC). The method and sequences are useful for treating
CC   conditions associated with skin pigmentation defects such as freckling.
CC   The polynucleotide sequences are useful for preparing a composition for
CC   diagnosing or treating cancer associated with abnormal activity of
CC   protein kinase A. The present sequence represents a PCR primer used to
CC   amplify a region of the human PRKAR1A gene.
XX
SQ   Sequence 20 BP; 5 A; 10 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2662 GTGTGCAGTACAGTGTGTG 2680
              |||| |||||||||| | |
Db         19 GTGTTCAGTACAGTGGGGG 1


RESULT 4128
ADC20037
ID   ADC20037 standard; DNA; 20 BP.
XX
AC   ADC20037;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Synthetic oligonucleotide P31 #SEQ ID 28.
XX
KW   Chimeric animal; Immunoglobulin G; IgG; T cell receptor; myoglobin;
KW   crystallin; renin; albumin; lipase; genetic engineering;
KW   protein analysis; ss.
XX
OS   Synthetic.
XX
PN   WO2003041495-A1.
XX
PD   22-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-JP011236.
XX
PR   15-NOV-2001; 2001JP-00350481.
PR   19-FEB-2002; 2002JP-00042321.
```

XX
PA (KIRI) KIRIN BEER KK.
XX
PI Tomizuka K, Kakitani M, Yoneya T, Ishida I;
XX
DR WPI; 2003-523113/49.
XX
PT Production of chimeric non-human animal expressing a specific protein,
PT useful for functional analysis of the protein.
XX
PS Example 17; SEQ ID NO 28; 108pp; Japanese.
XX
CC The invention relates to the production of a chimeric non-human animal
CC expressing a specific protein. The method of the invention comprises
CC preparing cells of the animal which contain in their genome a sequence
CC encoding the specific protein, inserting the cells into a host embryo of
CC the non-human animal, implanting the chimeric embryo obtained into a host
CC animal, and selecting from the offspring of the host animal those
CC expressing the specific protein. The promoter sequence and the sequence
CC encoding the specific protein are downstream of an internal ribosomal
CC entry site downstream of the stop codon of a gene expressed in the
CC nominated cells or tissues, and upstream of a poly-A signal region. The
CC distance between the poly-A sequence of the upstream gene and the
CC promoter sequence is not more than 1kb. The cells capable of
CC differentiation are preferably embryonic stem cells. The non-human animal
CC is preferably a mouse, but may be a rat, pig, cow, monkey, sheep, goat,
CC rabbit or hamster. The protein is especially light or heavy chain
CC Immunoglobulin (Ig) G in B-cells, T cell receptor in T-cells, myoglobin
CC in skeletal muscle cells, crystallin in the aqueous humor of the eye,
CC renin in kidney tissue, albumin in liver tissue and lipase in pancreas
CC tissue. The method is useful for the functional analysis of the specific
CC protein by comparison of the phenotype of the chimeric animal with that
CC of the corresponding wild-type animal. The current sequence represents a
CC synthetic oligonucleotide related to FGF23 that is used in an example
CC from the invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 752 GGTCCCATTTCCATGACCA 770
||| |||| | |||||||||
Db 1 GGTGCCATCTACATGACCA 19

RESULT 4129
AAD61385/c
ID AAD61385 standard; DNA; 20 BP.
XX
AC AAD61385;
XX
DT 15-JAN-2004 (first entry)
XX
DE Primer #12 used to sequence BS136 specific EST clone.
XX
KW Therapy; breast cancer; cytostatic; tumour; metastasis; BS136; EST;
KW expressed sequence tag; primer; ss.
XX
OS Unidentified.
XX
PN US2003104364-A1.
XX
PD 05-JUN-2003.
XX
PF 25-JUN-1998; 98US-00104750.
XX
PR 25-JUN-1997; 97US-00882369.
XX
PA (BILL/) BILLINGEL P A.
PA (COHE/) COHEN M.
PA (COLP/) COLPITTS T L.
PA (FRIE/) FRIEDMAN P N.
PA (GRAN/) GRANADOS E N.
PA (KLAS/) KLASS M R.
PA (RUSS/) RUSSELL J C.
PA (STRO/) STROUPE S D.
XX
PI Billingel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
PI Klass MR, Russell JC, Stroupe SD;
XX
DR WPI; 2003-801225/75.
XX
PT Novel BS136 polypeptide useful for detecting, diagnosing, staging,
PT monitoring, prognosticating, preventing or treating breast diseases such
PT as breast cancer.
XX
PS Example 2; Page 47; 0pp; English.
XX
CC The present invention relates to a novel BS136 polypeptide useful for
CC detecting, diagnosing, preventing and treating breast diseases such as
CC breast cancer. The invention is useful for preventing action of the
CC tissue-specific BS136 polypeptide and for the therapeutic treatment of
CC tumours and metastases. The present sequence is a primer used to sequence
CC BS136 specific EST clone
XX
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1451 AACCCTGGAGACCAGAGTC 1469
||| |||||||||| |||
Db 20 AACGCTGGAGACCACTGTC 2

RESULT 4130
ADD81486
ID ADD81486 standard; DNA; 20 BP.
XX
AC ADD81486;
XX
DT 29-JAN-2004 (first entry)
XX
DE HIV PRT antisense derived probe #415.
XX
KW ss; oligonucleotide hybridisation potential; efficient hybridisation;
KW large array; minimum oligonucleotide synthesis; probe.
XX
OS Human immunodeficiency virus.
XX
PN US2003054346-A1.
XX
PD 20-MAR-2003.
XX
PF 15-FEB-2001; 2001US-00784674.
XX
PR 10-FEB-1998; 98US-00021701.
XX
PA (SHAN/) SHANNON K W.
PA (WOLB/) WOLBER P K.
PA (DELE/) DELENSTARR G C.
PA (WEBB/) WEBB P G.
PA (KINC/) KINCAID R H.
XX
PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX
DR WPI; 2003-743746/70.
XX
PT Predicting potential of oligonucleotides to hybridize to target
PT nucleotide sequence comprises determining and evaluating for each
PT oligonucleotide a parameter predictive of the oligonucleotides ability to
PT hybridize with target.
XX

PS Example 2; SEQ ID NO 559; 423pp; English.
XX
CC The invention relates to a method of predicting the potential of
CC oligonucleotides to hybridise to target nucleotide sequences. The method
CC is useful for predicting the potential of an oligonucleotide to hybridise
CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
CC contains chemically modified nucleotides. The method is also useful for
CC predicting the potential of the oligonucleotides to hybridise to a
CC complementary target nucleotide sequence. The method is useful to predict
CC efficient hybridisation oligonucleotides for each of multiple target
CC sequences therefore very large arrays may be constructed and tested with
CC minimum synthesis of oligonucleotides. The present sequence represents a
CC HIV PRT antisense derived probe.
XX
SQ Sequence 20 BP; 2 A; 5 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAACTTTG 2193
||||| ||||||||| ||
Db 1 TTTTTCTTTTTTAACCCTG 19

RESULT 4131
ADE15814/c
ID ADE15814 standard; DNA; 20 BP.
XX
AC ADE15814;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PKR exon 13 PCR primer PK13S.
XX
KW ss; primer; PCR; 2',5'-oligoadenylate synthetase; OAS; RNase L;
KW 2'-5' phosphodiesterase; hepatitis C; virucide; hepatotropic;
KW gene therapy; vaccine; human.
XX
OS Homo sapiens.
XX
PN WO2003089003-A1.
XX
PD 30-OCT-2003.
XX
PF 15-APR-2003; 2003WO-GB001625.
XX
PR 19-APR-2002; 2002GB-00008928.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Hill A, Thursz M, Knapp S;
XX
DR WPI; 2003-854045/79.
XX
PT Use of a compound capable of modulating the level of activity of the OAS,
PT RNase L or 2'-5' phosphodiesterase gene or protein in the manufacture of
PT a medicament for treating a patient with or at risk of hepatitis C
PT infection.
XX
PS Example 1; Page 43; 67pp; English.
XX
CC The invention relates to a novel compound capable of modulating the level
CC of activity of the 2',5'-oligoadenylate synthetase (OAS), RNase L or 2'-
CC 5' phosphodiesterase gene or protein, useful in the manufacture of a
CC medicament for treating a patient with or at risk of hepatitis C
CC infection, where the compound is not an interferon or an isoprenoid, such
CC as geranylgeranylacetone (GGA). The method of the invention has virucide
CC and hepatotropic activity. A polynucleotide of the invention may have a
CC use in gene therapy, or in a vaccine. The compound capable of modulating
CC the level of activity of the OAS, RNase L or 2'-5' phosphodiesterase gene
CC and/or activity of the OAS, RNase L or 2'-5' phosphodiesterase protein is
CC useful in the manufacture of a medicament for treating a patient with or
CC at risk of hepatitis C infection. The nucleic acid that hybridises
CC selectively to OAS nucleic acid is useful in the manufacture of a
CC medicament or diagnostic reagent for treating or diagnosing a patient
CC with or at risk of hepatitis C infection. The present sequence is used in
CC the exemplification of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1238 CTGTGTAAAGAATTCACAG 1256
||| ||| | |||||||||
Db 19 CTGGGTATAAAATTCACAG 1

RESULT 4132
ADE43612/c
ID ADE43612 standard; DNA; 20 BP.
XX
AC ADE43612;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human KNSL1 sequencing primer, SEQ ID 217.
XX
KW Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW Chromosome 10; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003054143-A2.
XX
PD 03-JUL-2003.
XX
PF 25-OCT-2002; 2002WO-US034679.
XX
PR 25-OCT-2001; 2001US-0339525P.
PR 08-NOV-2001; 2001US-0336929P.
PR 08-NOV-2001; 2001US-0338010P.
PR 09-NOV-2001; 2001US-0338363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
PA (NEUR-) NEUROGENETICS INC.
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;
XX
DR WPI; 2003-559131/52.
XX
PT Determining a predisposition for or the occurrence of neurodegenerative
PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT the presence or absence of an allelic variant of one or more polymorphic
PT regions.
XX
PS Example 3; Page 287; 848pp; English.
XX
CC The present invention relates to a method (M1) for determining a
CC predisposition for or the occurrence of neurodegenerative disease in a
CC subject. The method comprises detecting in a target nucleic acid obtained
CC from the subject the presence or absence of an allelic variant of one or
CC more polymorphic regions of one or more genes selected from uPA
CC (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC presence of at least one of the allelic variant of one or more
CC polymorphic regions is indicative of a predisposition for or the
CC occurrence of neurodegenerative disease. The genes are all located on
CC chromosome 10. M1 is useful for determining a predisposition for or the

```
CC   occurrence of, and for treating neurodegenerative disease, particularly
CC   Alzheimer's disease. The present sequence is a PCR primer, which was used
CC   in the method of the invention.
XX
SQ   Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2797
              ||| | |||||| ||||||
Db         20 AGACTAGAAAAACAAAAAA 2

RESULT 4133
ADE43690/c
ID   ADE43690 standard; DNA; 20 BP.
XX
AC   ADE43690;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human KNSL1 sequencing primer, SEQ ID 295.
XX
KW   Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
KW   Alzheimer's disease; neuroprotective; nootropic; gene therapy;
KW   Chromosome 10; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003054143-A2.
XX
PD   03-JUL-2003.
XX
PF   25-OCT-2002; 2002WO-US034679.
XX
PR   25-OCT-2001; 2001US-0339525P.
PR   08-NOV-2001; 2001US-0336929P.
PR   08-NOV-2001; 2001US-0338010P.
PR   09-NOV-2001; 2001US-0338363P.
PR   04-DEC-2001; 2001US-0337052P.
PR   28-MAR-2002; 2002US-0368919P.
XX
PA   (NEUR-) NEUROGENETICS INC.
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Becker KD,  Velicelebi G,  Elliott KJ,  Wang X,  Tanzi RE,  Bertram L;
PI   Saunders AJ,  Mullin KM,  Sampson AJ,  Blacker DL;
XX
DR   WPI; 2003-559131/52.
XX
PT   Determining a predisposition for or the occurrence of neurodegenerative
PT   disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT   the presence or absence of an allelic variant of one or more polymorphic
PT   regions.
XX
PS   Example 3; Page 290; 848pp; English.
XX
CC   The present invention relates to a method (M1) for determining a
CC   predisposition for or the occurrence of neurodegenerative disease in a
CC   subject. The method comprises detecting in a target nucleic acid obtained
CC   from the subject the presence or absence of an allelic variant of one or
CC   more polymorphic regions of one or more genes selected from uPA
CC   (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC   degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC   lypase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the
CC   presence of at least one of the allelic variant of one or more
CC   polymorphic regions is indicative of a predisposition for or the
CC   occurrence of neurodegenerative disease. The genes are all located on
CC   chromosome 10. M1 is useful for determining a predisposition for or the
CC   occurrence of, and for treating neurodegenerative disease, particularly
CC   Alzheimer's disease. The present sequence is a PCR primer, which was used
CC   in the method of the invention.
XX
SQ   Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 20;
  Best Local Similarity   84.2%;  Pred. No. 3.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2730 CAAATAATTGTTGTGTGTA 2748
              |||||||||  | ||||||
Db         19 CAAATAATTCCTCTGTGTA 1

RESULT 4134
AAX14731/c
ID   AAX14731 standard; DNA; 21 BP.
XX
AC   AAX14731;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix third strand of Beta-globin gene nucleotides 917-937.
XX
KW   Triplex formation; DNA detection; triple helix; identification; bacteria;
KW   oncogene; virus; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 17-18; 168pp; English.
XX
CC   The present sequence represents a polynucleotide that is able to form a
CC   triple helix with a double stranded sequence. Cytosine bases in the
CC   present can be replaced with 5-methylcytosine for increased triplex
CC   stability. The present sequence is used in the assay of the invention,
CC   where it can be part of the anchor DNA or reporter DNA sequence. The
CC   assay comprises adding a sample containing double-stranded DNA test
CC   sequences to an aqueous medium containing at least one complex of anchor
CC   DNA, attached to a solid support, and reporter DNA, where either a part
CC   of the anchor DNA or reporter DNA is designed to form a triple-strand
CC   structure with part of the test sequence. Triplex formation results in
CC   displacement of the reporter DNA which is detected as an indication of
CC   the presence of the DNA test sequence. The method is used to detect DNA
CC   sequences, particularly for identification of bacteria (by detecting
CC   genes for ribosomal RNA) in clinical samples, but also detection of
CC   oncogenes and Hepatitis B virus
XX
SQ   Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
```

```
                  |||| |||||||||| || |
Db          21 GAAAGAAAAAAAAAGAAGA 3
```

RESULT 4135
AAT42561/c
ID AAT42561 standard; cDNA; 21 BP.
XX
AC AAT42561;
XX
DT 14-JAN-1997 (first entry)
XX
DE 3' primer #1087-1107 for DHPS:chloroplast transit peptide fusion protein.
XX
KW Dihydrodipicolinic acid synthase; DHPS; chloroplast transit peptide; PCR;
KW chloroplast; maize; L-Lysine; recombinant plant; nutrition; grain crop;
KW forage plant; clover; fescue; alfalfa; processed plant; tomatoe; lupin;
KW soyabean; feed; food; food additive; polymerase chain reaction; primer;
KW amplify; ss.
XX
OS Synthetic.
XX
PN US5545545-A.
XX
PD 13-AUG-1996.
XX
PF 27-APR-1993; 93US-00053867.
XX
PR 27-APR-1993; 93US-00053867.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Sellner JM, Somers DA, Bittel DC, Gengenbach BG, Shaver JM;
XX
DR WPI; 1996-383670/38.
XX
PT DNA encoding maize di:hydro:di:picolinic acid synthase mutant - resistant
PT to feedback inhibition by lysine.
XX
PS Example 7; Col 20; 35pp; English.
XX
CC AAT42552-T42561 represent amplification primers for the recombinant DNA
CC sequence used in the method of the invention. The method of the invention
CC is for increasing the level of L-Lysine in a plant. In the method, a
CC recombinant DNA sequence is introduced into the cells of a plant tissue
CC source. The recombinant sequence comprises an altered mature Zea mays
CC dihydrodipicolinic acid (DHPS) sequence (see AAT42547) which is
CC substantially resistant to feedback inhibition by endogenously produced
CC free L-Lysine, and a second sequence which encodes a chloroplast transit
CC sequence (see AAT42549). The DHPS used has at least one amino acid
CC alteration contained within residues 100-125, and is more than 400 times
CC less sensitive to lysine than wild-type DHPS. The chloroplast transit
CC sequence localises the altered mature DHPS in the chloroplasts of the
CC plant cells. The transfected plant cells are then used to generate plants
CC expressing the recombinant DNA in their cells. The plants regenerated
CC from the transformed cells have increased levels of free L-Lysine, which
CC improves their nutritional value. The plants which can be improved by
CC this transformation include maize and other grain crops, forage plants
CC (such as clover, fescue, and alfalfa), and processed plants (such as
CC tomatoes, soyabeans and lupins). The plants can be used directly as feed
CC or food, or the L-Lysine can be extracted for use as a feed or food
CC additive
XX
SQ Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.2; DB 1; Length 21;
 Best Local Similarity 84.2%; Pred. No. 4.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2027 GTAGGAGGCAAAGGTTCTA 2045
              | ||||||| ||||||||
Db         19 GAAGGAGGCCCAGGTTCTA 1
```

RESULT 4136
AAT46179/c
ID AAT46179 standard; DNA; 21 BP.
XX
AC AAT46179;
XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
DE Pyruvate decarboxylase primer PDC1186 (antisense).
XX
KW Pyruvate decarboxylase; PCR; mutant; PDC; acyloin; ephedrine; W392A;
KW Zymomonas mobilis; ss.
XX
OS Synthetic.
XX
PN WO9637620-A2.
XX
PD 28-NOV-1996.
XX
PF 22-MAY-1996; 96WO-DE000928.
XX
PR 26-MAY-1995; 95DE-01018809.
PR 29-JUN-1995; 95DE-01023269.
XX
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Bruhn H, Pohl M, Mesch K, Kula M;
XX
DR WPI; 1997-033996/03.
XX
PT DNA encoding mutant pyruvate carboxylase - for prepn. of acyloin(s) of
PT high optical purity useful for prodn. of phenyl:acetyl:carbinol, an
PT intermediate for ephedrine.
XX
PS Example 1; Page 12; 27pp; German.
XX
CC Example 1 describes the prodn. of PDC mutant W392A from Zymomonas
CC mobilis. The primers given in AAT46178 and AAT46179 are used in the
CC synthesis of the 5' fragment of the mutant gene. The primers given in
CC AAT46180 and AAT46181 are used in the synthesis of the 3' fragment of the
CC mutant gene. Fusion primers are given in AAT46182 and AAT46183. The wild-
CC type PDC gene is given in AAT46184. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 21 BP; 7 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

 Query Match 0.5%; Score 14.2; DB 1; Length 21;
 Best Local Similarity 84.2%; Pred. No. 4.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1061 GTGACTCTCCTGACATCCT 1079
              |||||||||||   |||||
Db         20 GTGACTCTCCTTCAATCCT 2
```

RESULT 4137
AAT48456
ID AAT48456 standard; DNA; 21 BP.
XX
AC AAT48456;
XX
DT 12-APR-1997 (first entry)
XX
DE Human beta-globin gene third-strand binding site.
XX
KW Haemoglobinopathy; sickle cell anaemia; beta-thalassaemia; haemoglobin;
KW beta-globin; triple helix; triplex; HbS; HbA; gene therapy;
KW targetted DNA replacement; homologous recombination; mutagenesis; ds.
XX
OS Homo sapiens.
XX

```
PN   WO9640271-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009430.
XX
PR   07-JUN-1995;   95US-00473845.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Glazer PM;
XX
DR   WPI; 1997-099895/09.
XX
PT   Repairing mutation(s) in haemoglobin by targetted mutagenesis or
PT   homologous recombination - mediated by a triplex forming
PT   oligo:nucleotide, opt. carrying a mutagen, partic. for treatment of
PT   sickle cell anaemia or thalassemia.
XX
PS   Claim 34; Page 45; 70pp; English.
XX
CC   A third-strand binding site (AAT48456) is located in the second intron of
CC   the human beta-globin gene, beginning at position 2825 of the sequence
CC   given in AAT48454. It comprises 21 uninterrupted pyrimidines in the
CC   coding strand. Third-strand binding sites (see also AAT48455-59) can be
CC   used in targetted DNA replacement (TDR). This method for genetic defect
CC   repair involves targetting third strands (see also AAT48467-70) to native
CC   DNA sequences to induce DNA damage that stimulates homologous
CC   recombination with an introduced donor nucleic acid strand. The method is
CC   used to correct mutations in a target region, esp. for treatment of beta-
CC   thalassaemia and sickle cell anaemia. TDR is highly specific and, since
CC   the corrected gene is in its native chromosome, the cure is permanent
XX
SQ   Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              |||| ||||||||| || |
Db          1 CTTTCTTTTTTTTTCTTCT 19


RESULT 4138
AAT48456/c
ID   AAT48456 standard; DNA; 21 BP.
XX
AC   AAT48456;
XX
DT   12-APR-1997  (first entry)
XX
DE   Human beta-globin gene third-strand binding site.
XX
KW   Haemoglobinopathy; sickle cell anaemia; beta-thalassaemia; haemoglobin;
KW   beta-globin; triple helix; triplex; HbS; HbA; gene therapy;
KW   targetted DNA replacement; homologous recombination; mutagenesis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9640271-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009430.
XX
PR   07-JUN-1995;   95US-00473845.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Glazer PM;
XX
DR   WPI; 1997-099895/09.
XX
PT   Repairing mutation(s) in haemoglobin by targetted mutagenesis or
PT   homologous recombination - mediated by a triplex forming
PT   oligo:nucleotide, opt. carrying a mutagen, partic. for treatment of
PT   sickle cell anaemia or thalassemia.
XX
PS   Claim 34; Page 45; 70pp; English.
XX
CC   A third-strand binding site (AAT48456) is located in the second intron of
CC   the human beta-globin gene, beginning at position 2825 of the sequence
CC   given in AAT48454. It comprises 21 uninterrupted pyrimidines in the
CC   coding strand. Third-strand binding sites (see also AAT48455-59) can be
CC   used in targetted DNA replacement (TDR). This method for genetic defect
CC   repair involves targetting third strands (see also AAT48467-70) to native
CC   DNA sequences to induce DNA damage that stimulates homologous
CC   recombination with an introduced donor nucleic acid strand. The method is
CC   used to correct mutations in a target region, esp. for treatment of beta-
CC   thalassaemia and sickle cell anaemia. TDR is highly specific and, since
CC   the corrected gene is in its native chromosome, the cure is permanent
XX
SQ   Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              || || ||||||||| |||
Db         20 GAGAAGAAAAAAAAAGAAA 2


RESULT 4139
AAT48469
ID   AAT48469 standard; DNA; 21 BP.
XX
AC   AAT48469;
XX
DT   12-APR-1997  (first entry)
XX
DE   Third-strand oligonucleotide pyrimidine/parallel motif for TDR.
XX
KW   Haemoglobinopathy; sickle cell anaemia; haemoglobin; beta-globin; HbS;
KW   HbA; gene therapy; triple helix; triplex; psoralen; mutagen;
KW   targeted DNA replacement; TDR; homologous recombination; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 2
FT                   /*tag=  a
FT                   /note= "psoralen attachment site"
XX
PN   WO9640271-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009430.
XX
PR   07-JUN-1995;   95US-00473845.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Glazer PM;
XX
DR   WPI; 1997-099895/09.
XX
PT   Repairing mutation(s) in haemoglobin by targetted mutagenesis or
PT   homologous recombination - mediated by a triplex forming
PT   oligo:nucleotide, opt. carrying a mutagen, partic. for treatment of
PT   sickle cell anaemia or thalassemia.
XX
PS   Claim 35; Page 47; 70pp; English.
XX
```

```
CC   Third-strand oligonucleotides (AAT48467-70) bind to a purine-rich region
CC   (see also AAT48455) located at position 2655 in the beta-globin gene (see
CC   also AAT48454). They can be utilised in a targetted DNA replacement (TDR)
CC   method to correct a mutation that leads to sickle cell anaemia. In TDR, a
CC   third-strand oligonucleotide is targetted to a binding region in the
CC   gene, where it induces DNA damage. This stimulates homologous
CC   recombination with an introduced donor nucleic acid strand. TDR is highly
CC   specific and, since the corrected gene is in its native chromosome, the
CC   cure is permanent
XX
SQ   Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTT 2173
              |||| ||| ||||| ||||
Db          3 TTTTCTTCCCCTTTCTTTT 21


RESULT 4140
AAV60859/c
ID   AAV60859 standard; DNA; 21 BP.
XX
AC   AAV60859;
XX
DT   25-JAN-1999  (first entry)
XX
DE   Primer #2 for the B. flavum fumarase gene.
XX
KW   Fumarase; recombinant vector; inactivation; homologous recombination;
KW   amino acid; aspartic acid; alanine; primer; PCR; amplification; ss.
XX
OS   Synthetic.
OS   Brevibacterium flavum.
XX
PN   JP10262684-A.
XX
PD   06-OCT-1998.
XX
PF   19-AUG-1997;   97JP-00237758.
XX
PR   23-JAN-1997;   97JP-00024407.
XX
PA   (MITU ) MITSUBISHI CHEM CORP.
XX
DR   WPI; 1998-587296/50.
XX
PT   Nucleic acids and vectors encoding fumarase gene - used for producing
PT   fumarase gene-destroying bacterial strain, for production of aspartic
PT   acid and alanine.
XX
PS   Example 4; Page 9; 14pp; Japanese.
XX
CC   Primers AAV60858-V60859 are used to PCR amplify the fumarase gene from
CC   the microorganism Brevibacterium flavum (AAV60855). The product is then
CC   cloned into the E. coli vector JM109. The DNA, and recombinant vectors
CC   containing it, can be used for the preparation of a microbial strain in
CC   which the fumarase gene is inactivated by homologous recombination with
CC   the DNA. The fumarase-negative strain can be used for the preparation of
CC   the amino acids aspartic acid or alanine
XX
SQ   Sequence 21 BP; 3 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1598 CCCCTCCTGGCCTGGGGGA 1616
              | |||||| ||| ||||||
Db         19 CGCCTCCTAGCCCGGGGGA 1


RESULT 4141
AAV51661
ID   AAV51661 standard; DNA; 21 BP.
XX
AC   AAV51661;
XX
DT   02-FEB-1999  (first entry)
XX
DE   Zea mays genome forward PCR primer #261.
XX
KW   Polymorphic marker; allele-specific; probe; amplification; PCR primer;
KW   hybridisation; plant; hybrid certification; genetic contribution;
KW   progeny; back-cross; hybrid; ancestry; corn; ss.
XX
OS   Synthetic.
OS   Zea mays.
XX
PN   WO9824796-A1.
XX
PD   11-JUN-1998.
XX
PF   01-DEC-1997;   97WO-US021782.
XX
PR   02-DEC-1996;   96US-0032069P.
PR   07-MAR-1997;   97US-00813507.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Lemieux B,  Landry BS,  Sapolsky RJ,  Murigneux A;
XX
DR   WPI; 1998-333252/29.
XX
PT   Brassica species allele-specific oligonucleotide probes and primers -
PT   useful for plant breeding.
XX
PS   Example 1; Page 54; 65pp; English.
XX
CC   AAV51401-V51704 are forward PCR primers used to amplify fragments of the
CC   Zea mays genome in order to detect polymorphic markers. Such markers can
CC   be used in the construction of allele-specific primers and probes for
CC   amplification or hybridisation, e.g. to determine common or disparate
CC   ancestry between 2 or more plants, to monitor the genetic contribution of
CC   an ancestral plant, to trace the progeny of proprietary plants, in
CC   certification of a hybrid plant or to identify the progeny of a back-
CC   crossed plant with an ancestral plant
XX
SQ   Sequence 21 BP; 8 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1728 TATTATCAGAAGGTGACAA 1746
              ||||| | | |||||||||
Db          2 TATTACCCGTAGGTGACAA 20


RESULT 4142
AAV05205/c
ID   AAV05205 standard; DNA; 21 BP.
XX
AC   AAV05205;
XX
DT   18-MAY-1998  (first entry)
XX
DE   Antisense primer used to amplify part of exon 9 of the BRCA1 gene.
XX
KW   BRCA1 gene; identification; mutation; multiplex amplification process;
KW   ovarian cancer; breast cancer; large scale diagnostic screening;
KW   PCR primer; amplify; ds.
XX
OS   Synthetic.
```

OS Homo sapiens.
XX
PN WO9743441-A1.
XX
PD 20-NOV-1997.
XX
PF 13-MAY-1997; 97WO-CA000321.
XX
PR 14-MAY-1996; 96US-00649950.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R, Leushner J, Dunn JM;
XX
DR WPI; 1998-008902/01.
XX
PT Detecting mutation(s) in the BRCA1 gene by exon amplification - then
PT comparing amplification products with those from wild type gene,
PT optionally followed by sequencing.
XX
PS Claim 15; Page 11; 65pp; English.
XX
CC PCR primers AAV05204-05 are used to amplify exon 9 of the BRCA1 gene. A
CC fragment of 197 bp is produced. The primers are used in a method for
CC identifying mutations in the BRCA1 gene using a multiplex amplification
CC process. BRCA1 mutations are associated with ovarian and breast cancer. A
CC sample is tested for mutations in the BRCA1 gene by amplifying at least
CC one (partial) exon of the gene, and comparing the sizes and amounts of
CC amplification products with corresponding products of the wild-type gene.
CC Any differences indicate a mutation. If no mutations are detected, the
CC sequence of at least one exon may be determined. This method is
CC inexpensive enough to be used for large scale diagnostic screening
XX
SQ Sequence 21 BP; 11 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2149 GATTGATTTTTTTCTCCTT 2167
||||||| ||| |||| ||
Db 19 GATTGATGTTTCTCTCTTT 1

RESULT 4143
AAV40600/c
ID AAV40600 standard; DNA; 21 BP.
XX
AC AAV40600;
XX
DT 21-DEC-1998 (first entry)
XX
DE Human TSC gene exon 17 reverse primer hTSCex17.
XX
KW Thiazide-sensitive Na-Cl cotransporter; TSC; hTSC gene; human;
KW ion transport; Gitelman's syndrome; Bartter's syndrome;
KW hypokalaemic alkalosis; hypocalciuria; hypomagnesemia; diagnosis;
KW therapy; SSCP; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9829431-A1.
XX
PD 09-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US023553.
XX
PR 31-DEC-1996; 96US-00778052.
XX
PA (UYYA) UNIV YALE.
XX
PI Lifton RP, Simon DB;
XX
DR WPI; 1998-388029/33.
XX
PT Thiazide sensitive cotransporter and ATP sensitive potassium channel
PT genes - useful for developing products for the diagnosis and treatment of
PT ion transport disorders, e.g. Gitelman's Syndrome or Bartter's Syndrome.
XX
PS Example 1; Page 51; 105pp; English.
XX
CC Primers hTSCex17 forward and reverse (see AAV40599 and AAV40600,
CC respectively) are designed to amplify exon 17 of the human hTSC gene (see
CC AAV40561) that codes for thiazide-sensitive Na-Cl cotransporter TSC (see
CC AAW29682). Both primers are located within introns of hTSC. 27 Sets of
CC specific primers (see AAV40565-V40618) were used for SSCP analysis of
CC hTSC. Amplified products were analysed for molecular variants by
CC electrophoresis, and identified variants were sequenced. Complete linkage
CC of Gitelman's syndrome with TSC was demonstrated. Identification of the
CC molecular basis of Gitelman's syndrome allows for the genetic diagnosis
CC of this disorder. The invention provides products and methods useful for
CC diagnosis and treatment of Gitelman's syndrome and other ion transport
CC disorders
XX
SQ Sequence 21 BP; 5 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 97 GGATTTACCGCTTGGGGGC 115
||| |||| |||||| |||
Db 19 GGACTTACGGCTTGGTGGC 1

RESULT 4144
AAZ26264
ID AAZ26264 standard; DNA; 21 BP.
XX
AC AAZ26264;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 453.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor

CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 7 A; 3 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       1914 ACAATACCTTTTTTTTCAG 1932
              || ||| |||||||||  ||
Db          1 ACCATAACTTTTTTTTAAG 19
```

RESULT 4145
AAZ26012
ID AAZ26012 standard; DNA; 21 BP.
XX
AC AAZ26012;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 201.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP; 6 A; 4 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1914 ACAATACCTTTTTTTTCAG 1932
              | || |||||||||||| |
Db          3 AAAAAACCTTTTTTTTCTG 21
```

RESULT 4146
AAZ40513
ID AAZ40513 standard; DNA; 21 BP.
XX
AC AAZ40513;
XX
DT 18-FEB-2000 (first entry)
XX
DE Human STE20-related protein kinase gene primer #15.
XX
KW Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;
KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist;
KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW myocardial infarction; cardiovascular disease; stroke; renal failure;
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW mesangial disorder; growth regulation; wound healing; T cell activation;
KW immunosuppressant; primer; PCR; amplification; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953036-A2.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US008150.
XX
PR 14-APR-1998; 98US-0081784P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman G, Martinez R, Whyte D;
XX
DR WPI; 1999-611301/52.
XX
PT Novel kinase-related polypeptides used for the diagnosis and treatment of
PT kinase-related diseases and disorders.
XX
PS Disclosure; Page 322; 387pp; English.
XX
CC This sequence represents a PCR primer used to amplify the coding sequence

```
CC   for a novel STE20-related protein kinase. The invention relates to
CC   nucleic acid molecule encoding a kinase polypeptide selected from STLK2,
CC   STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1,
CC   SULU3, GEK2, PAK4 and PAK5. The proteins are used to identify agonists
CC   and antagonists, and to raise antibodies. The polynucleotides are useful
CC   in gene therapy protocols. The polynucleotides, polypeptides, antibodies,
CC   antagonists and agonists may be used to treat diseases such as immune-
CC   related disorders and diseases (e.g. rheumatoid arthritis,
CC   artherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's
CC   disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis,
CC   autoimmunity, and organ transplantation, chronic inflammatory pelvic
CC   disease, multiple sclerosis, organ transplantation, myocardial
CC   infarction, cardiovascular disease, stroke, renal failure, oxidative
CC   stress-related neurodegenerative disorders (e.g. amylotrophic lateral
CC   sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC   cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC   mellitus, fibrotic and mesangial disorders. The proteins may also be
CC   useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants
XX
SQ   Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        919 GTCCCCACCTGAATGCTTA 937
              ||||||||| ||| | |||
Db          2 GTCCCCACCAGAAGGTTTA 20


RESULT 4147
AAX27494/c
ID   AAX27494 standard; DNA; 21 BP.
XX
AC   AAX27494;
XX
DT   22-JUN-1999  (first entry)
XX
DE   Human TFIID gene control primer TFIID-R.
XX
KW   INSL-4; insulin-like gene; EPIL; early placental insulin-like; antibody;
KW   vector; probe; hybridisation; tumour; hypoglycaemia; hyperglycaemia;
KW   diabetes; cardiovascular; primer; PCR; amplification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9909172-A1.
XX
PD   25-FEB-1999.
XX
PF   12-AUG-1998;   98WO-FR001799.
XX
PR   14-AUG-1997;   97FR-00010387.
PR   03-NOV-1997;   97FR-00013802.
XX
PA   (INSR ) INST ROUSSY GUSTAVE.
XX
PI   Bellet D,  Troalen F,  Bidart J,  Mock P;
XX
DR   WPI; 1999-181038/15.
XX
PT   EPIL polypeptides encoded by insulin-like gene 4 - and corresponding
PT   nucleic acids, antibodies, probes, primers, etc.
XX
PS   Example 5; Page 52; 119pp; French.
XX
CC   The invention relates to a novel INSL-4 (insulin-like gene 4) gene
CC   encoding an EPIL (early placental insulin-like) polypeptide. Primers
CC   AAX27493-X27494 were used to PCR amplify a fragment of the TFIID gene
CC   from cytotrophoblast and syncytiotrophoblast cell lines as a control in a
CC   quantitation assay for the level of expression of INSL4 in these cells.
CC   The polypeptide, antibodies to the polypeptide, vectors containing the
CC   coding sequence and probes derived from the coding sequence, can be used
CC   to treat tumours, preferably angioproliferative tumours, especially
CC   Kaposi's sarcoma, tumours of the pancreas, liver, uterus or breast,
CC   angiosarcomas, glioblastomas, neuroblastomas, rhabdomyosarcomas or
CC   leiomyosarcomas; to promote vascularisation of specific tissues; to treat
CC   retinopathy, macular degeneration, psoriasis, endometriosis, rheumatoid
CC   arthritis, atherosclerosis or hyperthyroidism; to treat post-angioplastic
CC   restenosis; to promote or inhibit embryo implantation; to prevent and/or
CC   treat disorders directly or indirectly connected with insulin-like
CC   activity; to prevent and/or treat disorders directly or indirectly
CC   connected with a dysfunction in carbohydrate metabolism, especially
CC   connected with hypo glycaemia or hyperglycaemia, especially gestational
CC   diabetes and diabetic complications, especially cardiovascular
CC   complications
XX
SQ   Sequence 21 BP; 13 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTT 2179
              ||||||| ||||| ||| |
Db         21 TCTCCTTATTTTTGTTTCT 3


RESULT 4148
AAX14729
ID   AAX14729 standard; DNA; 21 BP.
XX
AC   AAX14729;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix third strand of Beta-globin gene nucleotides 742-762.
XX
KW   Triplex formation; DNA detection; triple helix; identification; bacteria;
KW   oncogene; virus; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 17-18; 168pp; English.
XX
CC   The present sequence represents a polynucleotide that is able to form a
CC   triple helix with a double stranded sequence. Cytosine bases in the
CC   present can be replaced with 5-methylcytosine for increased triplex
CC   stability. The present sequence is used in the assay of the invention,
CC   where it can be part of the anchor DNA or reporter DNA sequence. The
CC   assay comprises adding a sample containing double-stranded DNA test
CC   sequences to an aqueous medium containing at least one complex of anchor
CC   DNA, attached to a solid support, and reporter DNA, where either a part
CC   of the anchor DNA or reporter DNA is designed to form a triple-strand
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```
CC   structure with part of the test sequence. Triplex formation results in
CC   displacement of the reporter DNA which is detected as an indication of
CC   the presence of the DNA test sequence. The method is used to detect DNA
CC   sequences, particularly for identification of bacteria (by detecting
CC   genes for ribosomal RNA) in clinical samples, but also detection of
CC   oncogenes and Hepatitis B virus
XX
SQ   Sequence 21 BP; 0 A; 7 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTT 2173
              |||| ||| ||||| ||||
Db          3 TTTTCTTCCCCTTTCTTTT 21


RESULT 4149
AAX14730
ID   AAX14730 standard; DNA; 21 BP.
XX
AC   AAX14730;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 917-937 of Beta-globin gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 17-18; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              |||| ||||||||| || |
Db          1 CTTTCTTTTTTTTCTTCT 19


RESULT 4150
AAX14730/c
ID   AAX14730 standard; DNA; 21 BP.
XX
AC   AAX14730;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 917-937 of Beta-globin gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 17-18; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              || || ||||||||| |||
Db         20 GAGAAGAAAAAAAAAGAAA 2


RESULT 4151
AAZ23796
ID   AAZ23796 standard; RNA; 21 BP.
XX
AC   AAZ23796;
XX
DT   14-JAN-2000  (first entry)
XX
```

```
DE   HSV RNA fragment 14.
XX
KW   Antisense; DNA library; identification; multiple cloning site; MCS;
KW   inhibition; ss.
XX
OS   Herpes simplex virus unknown type.
XX
PN   WO9950457-A1.
XX
PD   07-OCT-1999.
XX
PF   28-MAR-1999;   99WO-US006742.
XX
PR   28-MAR-1998;   98US-0079792P.
PR   06-NOV-1998;   98US-0107504P.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Ruffner DE,  Pierce ML,  Chen Z;
XX
DR   WPI; 1999-610866/52.
XX
PT   Production of antisense libraries, used for identifying antisense agents
PT   and for identifying target sites for antisense-mediated inhibition of a
PT   selected gene.
XX
PS   Example 4; Page 60; 63pp; English.
XX
CC   This invention describes a novel method for generating an antisense
CC   library targeted to a selected RNA transcript. The methods can be used
CC   for identifying antisense agents and for identifying target sites for
CC   antisense-mediated inhibition of a selected gene. The use of a direct
CC   library for target site selection significantly simplifies the screening
CC   process, since only very small libraries need be prepared and assayed.
CC   AAZ23783-Z23798 represent RNA fragments derived from the Herpes simplex
CC   virus genome which are used to illustrate the method of the invention
XX
SQ   Sequence 21 BP; 4 A; 8 C; 8 G; 0 T; 1 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 4.1e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        151 GGGGACGCCGGACGCCATG 169
              ||||||  | |||||||:|
Db          1 GGGGACCACCGACGCCAUG 19


RESULT 4152
AAZ18469/c
ID   AAZ18469 standard; DNA; 21 BP.
XX
AC   AAZ18469;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Polymorphic fragment in region 5' to ASTH1I.
XX
KW   ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTHIJ; genetic locus;
KW   therapeutic; immunogen; polymorphism; ss.
XX
OS   Homo sapiens.
XX
PN   WO9937809-A1.
XX
PD   29-JUL-1999.
XX
PF   21-JAN-1998;   98WO-US001260.
XX
PR   21-JAN-1998;   98WO-US001260.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Brooks-Wilson AR,  Buckler A,  Cardon L,  Carey AH,  Galvin M;
PI   Miller A,  North M;
XX
DR   WPI; 1999-479058/40.
XX
PT   Mammalian asthma related genes, useful for diagnosis of a predisposition
PT   to development of asthma.
XX
PS   Disclosure; Page 63; 195pp; English.
XX
CC   The invention identifies a genetic locus ASTH1, associated with asthma,
CC   mapped to human chromosome 11p. ASTH1I and ASTHIJ are genes present
CC   within the locus, located close to each other on human chromosome 11p,
CC   and have similar patterns of expression, and common sequence motifs. The
CC   ASTH1 genes and fragments, encoded protein, genomic regulatory regions
CC   and anti-ASTH1 antibodies are useful in the identification of individuals
CC   predisposed to development of asthma, and for the modulation of gene
CC   activity in vivo for prophylactic and therapeutic purposes. The ASTH1
CC   protein is useful as an immunogen to raise specific antibodies, in drug
CC   screening for compositions that mimic or modulate ASTH1 activity or
CC   expression, including altered forms of ASTH1 protein, and as a
CC   therapeutic. Sequences AAZ18366-Z18509 represent polymorphisms in the
CC   ASTH1I and ASTH1J genes
XX
SQ   Sequence 21 BP; 6 A; 9 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              ||||||||  |:||||   | ||
Db         21 CTGGGGGGTTYCTGGTGTCAA 1


RESULT 4153
AAZ18390/c
ID   AAZ18390 standard; DNA; 21 BP.
XX
AC   AAZ18390;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Polymorphic fragment in ASTH1J transcribed region.
XX
KW   ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTHIJ; genetic locus;
KW   therapeutic; immunogen; polymorphism; ss.
XX
OS   Homo sapiens.
XX
PN   WO9937809-A1.
XX
PD   29-JUL-1999.
XX
PF   21-JAN-1998;   98WO-US001260.
XX
PR   21-JAN-1998;   98WO-US001260.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Brooks-Wilson AR,  Buckler A,  Cardon L,  Carey AH,  Galvin M;
PI   Miller A,  North M;
XX
DR   WPI; 1999-479058/40.
XX
PT   Mammalian asthma related genes, useful for diagnosis of a predisposition
PT   to development of asthma.
XX
PS   Disclosure; Page 61; 195pp; English.
XX
CC   The invention identifies a genetic locus ASTH1, associated with asthma,
CC   mapped to human chromosome 11p. ASTH1I and ASTHIJ are genes present
CC   within the locus, located close to each other on human chromosome 11p,
```

```
CC   and have similar patterns of expression, and common sequence motifs. The
CC   ASTH1 genes and fragments, encoded protein, genomic regulatory regions
CC   and anti-ASTH1 antibodies are useful in the identification of individuals
CC   predisposed to development of asthma, and for the modulation of gene
CC   activity in vivo for prophylactic and therapeutic purposes. The ASTH1
CC   protein is useful as an immunogen to raise specific antibodies, in drug
CC   screening for compositions that mimic or modulate ASTH1 activity or
CC   expression, including altered forms of ASTH1 protein, and as a
CC   therapeutic. Sequences AAZ18366-Z18509 represent polymorphisms in the
CC   ASTH1I and ASTH1J genes
XX
SQ   Sequence 21 BP; 6 A; 9 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              ||||||||  |:||||  | ||
Db         21 CTGGGGGGTTYCTGGTGTCAA 1


RESULT 4154
AAZ01252/c
ID   AAZ01252 standard; DNA; 21 BP.
XX
AC   AAZ01252;
XX
DT   27-SEP-1999  (first entry)
XX
DE   PCR primer for PG1 biallelic marker 99-1462-238.
XX
KW   PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW   cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW   PSA; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9932644-A2.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-IB002133.
XX
PR   22-DEC-1997;   97US-00996306.
PR   09-SEP-1998;   98US-0099658P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I,  Bougueleret L;
XX
DR   WPI; 1999-405178/34.
XX
PT   Use of a prostate cancer associated gene and biallelic markers derived
PT   from it.
XX
PS   Claim 4; Page 357; 385pp; English.
XX
CC   The invention relates to a mammalian PG1 gene and protein, and a set of
CC   PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are
CC   used in a hybridisation assay, a sequencing assay, or in an allele-
CC   specific amplification assay for determining the identity of a nucleotide
CC   at a PG1-related biallelic marker. The methods can be used to detect and
CC   to assess the risk of developing cancer or prostate cancer. Early-stage
CC   diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC   dosage. However, the effectiveness of this is limited due to its
CC   inability to discriminate between malignant and non-malignant affections
CC   of the organ. A need exists for both a reliable diagnostic procedure
CC   which would enable early-stage diagnosis, and for preventative and
CC   curative treatments of the disease. The PG1 gene can be used for
CC   detection of prostate cancer, and the risk of developing it in the
CC   future, and can also be used to determine therapies for the disease
XX
SQ   Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2685 TGAAATGGAGATTTGGAAT 2703
              |||||||||  | ||||||
Db         20 TGAAATGGACTTCTGGAAT 2


RESULT 4155
AAD00468
ID   AAD00468 standard; DNA; 21 BP.
XX
AC   AAD00468;
XX
DT   29-AUG-2000  (first entry)
XX
DE   Human MINT1 clone specific PCR primer-1.
XX
KW   Methylated CpG island Amplification; MCA; CGI; CpG site; DNA methylation;
KW   restriction endonuclease; SmaI; isoschizomer; XmaI; neoplastic cell;
KW   diagnosis; age-related disorder; dementia; artherosclerosis; astrocytoma;
KW   diabetes mellitus; cell proliferative disorder; cancer; kidney; colon;
KW   breast; uterus; prostate; lung; leukaemia; glioblastoma; neuroblastoma;
KW   modulating agent; screen; hypermethylation; human; Methylated IN Tumour;
KW   MINT; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200026401-A1.
XX
PD   11-MAY-2000.
XX
PF   02-NOV-1999;   99WO-US025251.
XX
PR   03-NOV-1998;   98US-0106925P.
PR   10-MAY-1999;   99US-00309175.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Issa J,  Baylin S,  Toyota M;
XX
DR   WPI; 2000-365641/31.
XX
PT   Methylated CpG island amplification (MCA) used to determine DNA
PT   methylation status of CpG sites in a given locus, useful for diagnosis of
PT   age-related disorders e.g. colon cancer and dementia.
XX
PS   Example 8; Page 69; 100pp; English.
XX
CC   The patent discloses a method known as Methylated CpG island (CGI)
CC   Amplification (MCA) to identify methylated CpG sites (cytosine residues
CC   5' of neighbouring guanine). The method uses a methylation-sensitive
CC   restriction endonuclease SmaI, that cleaves unmethylated CpG sites and
CC   its isoschizomer XmaI, that cleaves both methylated and unmethylated
CC   CGIs. It involves amplification of closely spaced methylated SmaI sites.
CC   This method is used to determine the DNA methylation status of CpG sites
CC   in a given locus, in normal and neoplastic cells. It can be used for
CC   diagnosis of age-related disorders, associated with methylation of CGIs,
CC   e.g. dementia, artherosclerosis and diabetes mellitus, cell proliferative
CC   disorders, e.g. cancer of the kidney, colon, breast, uterus, prostate and
CC   lung, leukaemia, glioblastoma, astrocytoma and neuroblastoma. It is also
CC   used to evaluate the cell response to a methylation modulating agent. It
CC   can also be used to screen samples for the presence of hypermethylation
CC   of specific genes. The present DNA sequence is the human MINT1 clone
CC   (Methylated IN Tumour) specific PCR primer-1, used for amplification and
CC   bisulphite-restriction methylation analysis
XX
SQ   Sequence 21 BP; 4 A; 0 C; 12 G; 5 T; 0 U; 0 Other;
```

```
  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1536 GGTTAGGAGAGTAGGGAAG 1554
              || | |||||||||||| ||
Db          1 GGGTTGGAGAGTAGGGGAG 19


RESULT 4156
AAZ59336
ID   AAZ59336 standard; DNA; 21 BP.
XX
AC   AAZ59336;
XX
DT   05-APR-2000  (first entry)
XX
DE   Human STP2 intron 2 polymorphism sequence 94.
XX
KW   Single nucleotide polymorphism; SNP; STP2; phenol sulphotransferase;
KW   probe; genotyping; human; drug metabolism; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       11
FT                   /*tag=  a
FT                   /note= "Site of polymorphism"
XX
PN   WO9964630-A1.
XX
PD   16-DEC-1999.
XX
PF   09-JUN-1999;   99WO-US013094.
XX
PR   10-JUN-1998;   98US-0088710P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Guida M,  Kurth J;
XX
DR   WPI; 2000-105892/09.
XX
PT   Novel nucleic acid used for genotyping, e.g. to predict rate of drug
PT   metabolism.
XX
PS   Claim 2; Page 16; 46pp; English.
XX
CC   Sequences AAZ59305-Z59352 are fragments of the human STP2 gene. The
CC   fragments are from the 8 exons, the promoter region, 3' and 5'
CC   untranslated regions of the STP2 gene. Each sequence contains a newly
CC   identified STP2 gene single nucleotide polymorphism (SNP). STP2 is a
CC   phenol sulphotransferase. Substrates for STP2 include minoxidil,
CC   acetaminophen, and paranitrophenol. Several of the nucleotide changes
CC   identified at the polymorphism sites, give rise to an amino acid change.
CC   Amino acid changes may result in altered enzyme activity. The sequences
CC   can be used as probes for detecting STP2 polymorphisms. The polymorphic
CC   probes are used in screening and genotyping, i.e. to predict the rate of
CC   metabolism of STP2 substrates, potential drug-drug interactions and
CC   adverse side effects. They can also be used to detect diseases resulting
CC   from accidental or occupational exposure to toxins and to establish
CC   animal, cell or in vitro models for drug metabolism
XX
SQ   Sequence 21 BP; 2 A; 11 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        373 CTCCCAGTCGGCCGACCCC 391
              ||||||| |||| | ||||
Db          3 CTCCCAGGCGGCAGTCCCC 21


RESULT 4157
AAA14463
ID   AAA14463 standard; RNA; 21 BP.
XX
AC   AAA14463;
XX
DT   21-AUG-2000  (first entry)
XX
DE   AUUUA RNA target sequence.
XX
KW   AUUUA sequence; RNA target molecule; RNA binding protein identification;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200020637-A1.
XX
PD   13-APR-2000.
XX
PF   16-SEP-1999;   99WO-US021672.
XX
PR   02-OCT-1998;   98US-00165868.
XX
PA   (MESS-) MESSAGE PHARM INC.
XX
PI   Giordano T,  Beach DL,  Temeles GL;
XX
DR   WPI; 2000-303802/26.
XX
PT   Nucleic acid molecules useful for identifying compounds affecting
PT   interactions between RNA molecules and identifying RNA binding proteins.
XX
PS   Example 1; Page 33; 58pp; English.
XX
CC   The invention relates to mRNA sequences which bind to RNA binding
CC   proteins, and their use for identifying RNA binding proteins and
CC   compounds which have an effect on the interactions between an RNA binding
CC   protein and an RNA molecule. The disclosed sequences are the 3'
CC   untranslated region (3' UTR) sequences APP-R1, APP-D3 and APP-I1 from the
CC   human amyloid precursor protein mRNA (AAA14456-A14458); the 3' UTR of
CC   human interleukin-10 (IL-10) mRNA (AAA14459); the 3' UTR of human erb-B2
CC   mRNA (AAA14460); and the 5' UTR of human insulin-like growth factor I
CC   receptor (IGF-IR) mRNA (AAA14461). The disclosed mRNA sequences may be
CC   used to identify compounds affecting interactions between an RNA molecule
CC   comprising the sequence and an RNA binding protein. Such compounds can
CC   then be included with a carrier in pharmaceutical compositions for
CC   altering expression of a gene comprising the sequences, which can be
CC   administered to individuals or cells requiring altered expression of the
CC   gene. The mRNA sequences are also useful to identify RNA binding proteins
CC   which interact with them. Compounds identified as having the ability to
CC   affect such RNA binding interactions may therefore be useful as drugs for
CC   modulating protein levels in disease states. The present sequence
CC   represents an AUUUA RNA sequence used as a target molecule in an
CC   exemplification of the invention in an assay for detecting interactions
CC   between RNA molecules and RNA binding proteins
XX
SQ   Sequence 21 BP; 6 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   15.8%;  Pred. No. 4.1e+03;
  Matches    3;  Conservative   13;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATTT 2273
              :::|:::   :|:::|:::
Db          2 UUUAUUUAUUUAUUUAUUU 20


RESULT 4158
AAZ69623/c
ID   AAZ69623 standard; DNA; 21 BP.
XX
AC   AAZ69623;
```

XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:3979.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1079; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 21 BP; 4 A; 3 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2280 TTTCGAGTAAACTTGAAAA 2298
|| |||| ||||| ||||||
Db 20 TGTCGAATAAACCTGAAAA 2

RESULT 4159
AAZ73890/c
ID AAZ73890 standard; DNA; 21 BP.
XX
AC AAZ73890;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:8246.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1989; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2685 TGAAATGGAGATTTGGAAT 2703
||||||||| | ||||||
Db 20 TGAAATGGACTTCTGGAAT 2

RESULT 4160
AAZ75985
ID AAZ75985 standard; DNA; 21 BP.
XX
AC AAZ75985;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10341.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.

XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 9; Page 2435; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 21 BP; 4 A; 10 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 340 CTACTTTCCCCCTCCCTAC 358
||||||||||| || | ||
Db 3 CTACTTTCCCCATCTCCAC 21

RESULT 4161
AAD00964/c
ID AAD00964 standard; DNA; 21 BP.
XX
AC AAD00964;
XX
DT 21-SEP-2000 (first entry)
XX
DE Primer PAD4.5 to sequence Arabidopsis thaliana PAD4 and pad4-1 alleles.
XX
KW PAD4; pAtgPAD4 clone; disease resistance; phytoalexin; PR-1; PR-5;
KW pathogenesis-related protein; BGL2; beta-glucanase; ASA1;
KW anthranilate synthase; defence response; salicylic acid; SA;
KW signal transduction; transgenic plant; pathogen; bacteria; fungi;
KW nematode; Phytophthora; Peronospora; Pseudomonas; plant; agronomy; crop;
KW chromosome 3; pad4-1 allele; primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200029595-A1.
XX
PD 25-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026106.
XX
PR 12-NOV-1998; 98US-00190733.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Glazebrook J, Jirage D, Tootle T, Feys BJF;
XX
DR WPI; 2000-387805/33.
XX
PT New PAD4 polypeptide from Arabidopsis thaliana, useful to enhance plant
PT resistance to diseases due to pathogens such as Phytophthora e.g. to
PT improve crop quality or yields.
XX
PS Disclosure; Page 147; 181pp; English.
XX
CC The present sequence is a primer PAD4.5 which is used to sequence
CC Arabidopsis thaliana PAD4 and pad4-1 alleles and corresponds to positions
CC 8293-8273 of Arabidopsis genomic clone pAtgPAD4. PAD4 gene is located on
CC Arabidopsis chromosome 3 and encodes a protein which plays an important
CC role in disease resistance in plants. The protein has positive regulatory
CC effect on phytoalexin levels and PR-1 (pathogenesis-related protein)
CC expression levels, but has no effect on PR-5 (pathogenesis- related
CC protein), BGL2 (beta-glucanase) or ASA1 (anthranilate synthase)
CC expression levels in a disease defence response by a host plant. PAD4 is
CC required upstream from salicylic acid in the signal transduction pathway
CC leading from infection to activation of defence responses. It is used to
CC produce transgenic plants which have enhanced resistance to diseases
CC caused due to pathogens such as bacteria, fungi, and nematodes,
CC especially Phytophthora, Peronospora or Pseudomonas. Such transgenic
CC plants are useful agronomically e.g. to improve crop quality or yield
XX
SQ Sequence 21 BP; 7 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1096 TGTTCATTTGGCTAGGGAC 1114
|| |||||||||| || |
Db 20 TGATCATTTGGCTATGGGC 2

RESULT 4162
AAZ46461/c
ID AAZ46461 standard; DNA; 21 BP.
XX
AC AAZ46461;
XX
DT 13-MAR-2000 (first entry)
XX
DE Rat opsin gene specific forward primer.
XX
KW Retinal stem cell precursor; growth factor; photoreceptor; opsin;
KW retinal disorder; retinitis pigmentosa; macular degeneration; rat;
KW cell-survival factor; PCR primer; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN WO9955838-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US007377.
XX
PR 24-APR-1998; 98US-0082970P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Ahmad I;
XX
DR WPI; 2000-072175/06.
XX
PT Multipotent retinal stem cell precursors, for treating retinal
PT degeneration, especially retinitis pigmentosa.
XX
PS Example 1; Page 21; 62pp; English.

```
XX
CC   The invention provides multipotent retinal stem cell precursors (A). (A)
CC   can be prepared by dissociating embryonic retinal explants to form a
CC   suspension of retinalspheres, plating these, and exposing them to a
CC   growth factor so that they remain proliferative and uncommited, then
CC   isolating (A). (A) are used: by transplantation, to treat or prevent
CC   disorders of the retina associated with inherited or age-related
CC   degeneration of photoreceptors (retinitis pigmentosa and macular
CC   degeneration); to screen for agents that promote survival or
CC   differentiation of (A), i.e. agents potentially useful for preventing
CC   death of photoreceptors; for studying differentiation mechanisms that
CC   lead to photoreceptors; possibly as a source of cell-survival factors,
CC   and in diagnosis. (A) can differentiate into photoreceptors; can be
CC   expanded in culture and remain viable for a long time. They represent an
CC   alternative to use of fetal tissue. Sequences AAZ46461-462 represent rat
CC   opsin gene specific PCR primers used for amplifying the opsin transcript
XX
SQ   Sequence 21 BP; 4 A; 3 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1441 ATCCTACATGAACCCTGGA 1459
                ||||  |||||||| ||| |
Db         21 ATCCCACATGAACACTGCA 3


RESULT 4163
AAA80291/c
ID   AAA80291 standard; DNA; 21 BP.
XX
AC   AAA80291;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human ASTH1J transcribed region polymorphic site, SEQ ID NO:40.
XX
KW   ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KW   bronchial hyperreactivity; ets family; transcription factor;
KW   splice variant; genetic predisposition; polymorphism; antibody;
KW   drug screening; prophylaxis; therapy; diagnosis;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
PN   US6087485-A.
XX
PD   11-JUL-2000.
XX
PF   21-JAN-1998;   98US-00009913.
XX
PR   21-JAN-1997;   97US-0035663P.
PR   01-JUL-1997;   97US-0051432P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  North M,  Cardon L,  Buckler A;
PI   Brooks-Wilson AR,  Carey AH;
XX
DR   WPI; 2000-505109/45.
XX
PT   New nucleic acids other than naturally occurring chromosomes encoding
PT   ASTH1 protein, for e.g. screening compositions that modulate expression
PT   or function of ASTH1 proteins or as diagnostics for genetic
PT   predisposition to asthma.
XX
PS   Example; Col 39-40; 131pp; English.
XX
CC   The invention relates to the ASTH1 locus on the short arm of human
CC   chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
CC   are associated with a genetic predisposition to asthma and bronchial
CC   hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
CC   directions with the ASTH1 locus, and have similar patterns of expression
CC   and common sequence motifs. They are both expressed in trachea, lung and
CC   several other tissues. ASTH1I and ASTH1J are novel members of the ets
CC   family of transcription factors, which have been implicated in the
CC   activation of a variety of genes including the TCRa gene and cytokine
CC   genes known to be important in the aetiology of asthma. Both ASTH1I and
CC   ASTH1J mRNAs are alternatively spliced. Alternative splicing of
CC   transcripts has no effect on the open reading frame of ASTH1J, as the
CC   exons involved are all 5' to the start codon in exon b. In contrast,
CC   alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
CC   isoforms. The invention also encompasses mouse asth1j protein. The ASTH1
CC   nucleic acids are useful as diagnostics to identify a hereditary
CC   predisposition to asthma, as probes for identifying ASTH1 related genes,
CC   for identifying expression of the gene in a biological specimen, and for
CC   generating genetically modified non-human animals or site specific gene
CC   modifications in cell lines. The encoded ASTH1 proteins are useful as
CC   immunogens to raise specific antibodies; in drug screening for
CC   compositions that mimic or modulate activity or expression of ASTH1I
CC   and/or ASTH1J (including altered forms of these proteins); and as a
CC   therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC   ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
CC   antibodies are useful in the identification of individuals predisposed to
CC   development of asthma, and for modulation of gene activity in vivo for
CC   prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
CC   proteins or active fragments thereof may be used to modulate or reduce
CC   bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC   represent polymorphic sites within the ASTH1J or ASTH1I genes
XX
SQ   Sequence 21 BP; 6 A; 9 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       115 CTGGGGGGATCCTGGATTTAA 135
             |||||||| |:|||| | ||
Db        21 CTGGGGGGTTYCTGGTGTCAA 1


RESULT 4164
AAA80375/c
ID   AAA80375 standard; DNA; 21 BP.
XX
AC   AAA80375;
XX
DT   22-NOV-2000  (first entry)
XX
DE   Human ASTH1I 5' region polymorphic site, SEQ ID NO:119.
XX
KW   ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
KW   bronchial hyperreactivity; ets family; transcription factor;
KW   splice variant; genetic predisposition; polymorphism; antibody;
KW   drug screening; prophylaxis; therapy; diagnosis;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
PN   US6087485-A.
XX
PD   11-JUL-2000.
XX
PF   21-JAN-1998;   98US-00009913.
XX
PR   21-JAN-1997;   97US-0035663P.
PR   01-JUL-1997;   97US-0051432P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  North M,  Cardon L,  Buckler A;
PI   Brooks-Wilson AR,  Carey AH;
XX
DR   WPI; 2000-505109/45.
XX
```

```
PT   New nucleic acids other than naturally occurring chromosomes encoding
PT   ASTH1 protein, for e.g. screening compositions that modulate expression
PT   or function of ASTH1 proteins or as diagnostics for genetic
PT   predisposition to asthma.
XX
PS   Example; Col 41-42; 131pp; English.
XX
CC   The invention relates to the ASTH1 locus on the short arm of human
CC   chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
CC   are associated with a genetic predisposition to asthma and bronchial
CC   hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
CC   directions with the ASTH1 locus, and have similar patterns of expression
CC   and common sequence motifs. They are both expressed in trachea, lung and
CC   several other tissues. ASTH1I and ASTH1J are novel members of the ets
CC   family of transcription factors, which have been implicated in the
CC   activation of a variety of genes including the TCRa gene and cytokine
CC   genes known to be important in the aetiology of asthma. Both ASTH1I and
CC   ASTH1J mRNAs are alternatively spliced. Alternative splicing of
CC   transcripts has no effect on the open reading frame of ASTH1J, as the
CC   exons involved are all 5' to the start codon in exon b. In contrast,
CC   alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
CC   isoforms. The invention also encompasses mouse asth1j protein. The ASTH1
CC   nucleic acids are useful as diagnostics to identify a hereditary
CC   predisposition to asthma, as probes for identifying ASTH1 related genes,
CC   for identifying expression of the gene in a biological specimen, and for
CC   generating genetically modified non-human animals or site specific gene
CC   modifications in cell lines. The encoded ASTH1 proteins are useful as
CC   immunogens to raise specific antibodies; in drug screening for
CC   compositions that mimic or modulate activity or expression of ASTH1I
CC   and/or ASTH1J (including altered forms of these proteins); and as a
CC   therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
CC   ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
CC   antibodies are useful in the identification of individuals predisposed to
CC   development of asthma, and for modulation of gene activity in vivo for
CC   prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
CC   proteins or active fragments thereof may be used to modulate or reduce
CC   bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
CC   represent polymorphic sites within the ASTH1J or ASTH1I genes
XX
SQ   Sequence 21 BP; 6 A; 9 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        115 CTGGGGGGATCCTGGATTTAA 135
              ||||||| |:||||  | ||
Db         21 CTGGGGGGTTYCTGGTGTCAA 1


RESULT 4165
AAA87655/c
ID   AAA87655 standard; DNA; 21 BP.
XX
AC   AAA87655;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:579.
XX
KW   Rat; phenobarbitol; carcinogenesis marker; carcinogenesis; detection;
KW   identification; carcinogenic; probe; primer; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO200044902-A2.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-US000503.
XX
PR   29-JAN-1999;   99US-0118078P.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bunch RT,  Curtis SW,  Rodi CP,  Morris DL;
XX
DR   WPI; 2000-505977/45.
XX
PT   New nucleic acid encoding a carcinogenic biomarker, induced by
PT   phenobarbitol treatment of rat hepatocytes, useful for identifying
PT   carcinogenic compounds.
XX
PS   Claim 1; Page 240; 240pp; English.
XX
CC   AAA87080 to AAA87656 represent nucleic acid sequences (N1) encoding a
CC   carcinogenesis biomarkers. The carcinogenesis biomarkers are induced by
CC   treating rat hepatocytes with phenobarbitol. The nucleic acids are useful
CC   for identifying carcinogenic compounds. The nucleic acid molecules can be
CC   used to derive probes and/or primers for detecting or inducing
CC   carcinogenesis, respectively
XX
SQ   Sequence 21 BP; 7 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2313 CAATTTGTTGCTGCTTGTC 2331
              |||| || |||||||| ||
Db         19 CAATGTGCTGCTGCTTCTC 1


RESULT 4166
AAF96485/c
ID   AAF96485 standard; DNA; 21 BP.
XX
AC   AAF96485;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1246.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
```

```
XX
PS   Example; Page 136; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 5 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2764 AAAAGTATTCTTGTTAGAA 2782
              ||||||  ||| |||||||
Db         20 AAAAGTGGTCTCGTTAGAA 2

RESULT 4167
AAF97089/c
ID   AAF97089 standard; DNA; 21 BP.
XX
AC   AAF97089;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1850.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 173; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 6 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       711 ACCAGCACCTGTTGCTGCA 729
             ||||||||||| | || ||
Db        19 ACCAGCACCTGGTTCTCCA 1

RESULT 4168
AAF96326
ID   AAF96326 standard; DNA; 21 BP.
XX
AC   AAF96326;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1087.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 126; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
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```
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 7 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2004 TTCTTCAGAGATCAAGTCC 2022
              | || ||||| ||||||||
Db          1 TACTCCAGAGGTCAAGTCC 19


RESULT 4169
AAC92911/c
ID   AAC92911 standard; DNA; 21 BP.
XX
AC   AAC92911;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Mouse ISF PCR primer S5R, SEQ ID NO:7.
XX
KW   ISF; immune suppressor factor; kidney; cancer; infectious disease;
KW   autoimmune disease; thrombosis; cytostatic; antibacterial, antiviral;
KW   immunomodulatory; anticoagulant; PCR primer; ss.
XX
OS   Mus musculus.
XX
PN   WO200073442-A1.
XX
PD   07-DEC-2000.
XX
PF   31-MAY-2000; 2000WO-JP003505.
XX
PR   01-JUN-1999;   99JP-00154365.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Tulin EE,  Onoda N;
XX
DR   WPI; 2001-061529/07.
XX
PT   Cytokine C121 forming part of immune suppressor factor for development of
PT   remedies for cytokine-mediated disorders including cancer and infectious
PT   and autoimmune diseases.
XX
PS   Example 9; Page 55; 128pp; Japanese.
XX
CC   The invention relates to a novel mouse cytokine, C121 (AAB48976) and to
CC   cDNA encoding it (AAC92907). C121 corresponds to the C-terminus of mouse
CC   immune suppressor factor (ISF), but is a complete protein as the cDNA
CC   encoding it is full-length, rather than just being a 3' fragment of mouse
CC   ISF cDNA. The C121 cDNA was isolated from a mouse myeloid stroma cell
CC   line (ST2) cDNA library, using a retrovirus-based expression cloning
CC   method. The C121 protein can be present as a soluble or a membrane-bound
CC   protein, and both forms support the proliferation of S21 cells. The
CC   invention also discloses the cDNA and protein sequence of human ISF
CC   (AAC92908, AAB48977). Human ISF cDNA was isolated from a human kidney
CC   cDNA library using primers and probes based on the mouse ISF and C121
CC   sequences. The invention further relates to recombinant vectors and host
CC   cells comprising mouse C121 or human ISF nucleic acids, and the
CC   recombinant production of mouse C121 and human ISF. The invention also
CC   encompasses C121-specific antibodies, and methods of screening for agents
CC   which bind to C121 and C121 activity modulators. C121, and nucleic acids
CC   which encode it may be used in the diagnosis, treatment and prevention of
CC   diseases in which C121 expression is implicated, including cancer,
CC   infectious diseases, autoimmune diseases and thrombosis. The present
CC   sequence represents a PCR primer used in the isolation of human ISF cDNA
CC   in an exemplification of the invention
XX
SQ   Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1169 ACCAGACCTCATCTTGGAG 1187
              |||||||||| ||  |||
Db         19 ACCAGACCTCAGCTATGAG 1


RESULT 4170
AAH62338/c
ID   AAH62338 standard; DNA; 21 BP.
XX
AC   AAH62338;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Transcription factor polymorphism containing DNA fragment #239.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 48; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 6 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy        495 AGGGAGCGGGGCTGCCCTC 513
              || |||| |||||| ||||
Db         21 AGTGAGCTGGGCTGTCCTC 3
```

RESULT 4171
AAH20432
ID AAH20432 standard; DNA; 21 BP.
XX
AC AAH20432;
XX
DT 06-AUG-2001 (first entry)
XX
DE PCR primer used in pTalpha assay for immature T cell detection.
XX
KW T cell production; haematopoietic T cell progenitor; immunodeficiency;
KW immunoproliferative disorder; immune disorder; AIDS; DiGeorge's syndrome;
KW lymphoma; pTalpha; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200132841-A2.
XX
PD 10-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US029655.
XX
PR 29-OCT-1999; 99US-0162574P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Ruiz M, Kinter A, Dybul M, Catanzaro A, Fauci AS;
XX
DR WPI; 2001-335829/35.
XX
PT In vitro production of T cells, useful for treating immune disorders e.g.
PT AIDS, lymphoma and DiGeorge's Syndrome, involves culturing a lymph node
PT cell in vitro with a primate hematopoietic T cell progenitor cell.
XX
PS Example 6; Page 22; 41pp; English.
XX
CC This invention relates to a method for the in vitro production of T
CC cells. The T cells are generated from a population of haematopoietic T
CC cell progenitor cells. One example comprises culturing a lymph node cell
CC in vitro with a primate haematopoietic T-cell progenitor cell. The method
CC is useful for modifying a haematopoietic stem cell to produce a
CC descendent cell containing a nucleotide sequence of interest. This
CC comprises contacting the primate hematopoietic T cell progenitor cell and
CC the lymph node cells with an expression vector such as a viral vector,
CC comprising a nucleotide sequence of interest, so as to allow the virus to
CC enter the haematopoietic T cell progenitor cell. The method is also
CC useful for treating a subject having an immune disorder such as an
CC immunodeficiency or immunoproliferative disorder, further comprising
CC administering the progenitor cell or its descendent to the subject.
CC Factors such as cytokines are also administered to the lymph node in the
CC subject. The method is useful for treating immune disorders such as AIDS,
CC DiGeorge's Syndrome (Complete Athymia), and immunoproliferative disorders
CC such as lymphoma. Haematopoietic T cells produced by the method and their
CC progeny are used as carriers for the production of a wide variety of
CC products where the host cell is genetically deficient or as a result of
CC subsequent diseases as become genetically deficient. The present sequence
CC represents a PCR primer used to amplify cDNA in a pTalpha assay. The
CC assay is used to determine the presence or absence of immature T cells,
CC in an example illustrating the method of the invention
XX
SQ Sequence 21 BP; 2 A; 9 C; 3 G; 7 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1786 CCCATTCTTTCCTTCTCTG 1804
              | ||  ||||||||||||||
Db          3 CACACCCTTTCCTTCTCTG 21
```

RESULT 4172
AAS23721
ID AAS23721 standard; DNA; 21 BP.
XX
AC AAS23721;
XX
DT 04-DEC-2001 (first entry)
XX
DE Primer A #35 used as probe for identifying C. albicans GRACE strain.
XX
KW Gene identification; essential gene; GRACE; pathogenic fungus;
KW gene replacement and conditional expression; fungal infection; probe; ss.
XX
OS Candida albicans.
OS Synthetic.
XX
PN WO200160975-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005551.
XX
PR 18-FEB-2000; 2000US-0183534P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H;
XX
DR WPI; 2001-489080/53.
XX
PT Identifying genes essential to fungal metabolisms and identifying
PT potential therapeutic agents that target these genes.
XX
PS Disclosure; Page 307; 324pp; English.
XX
CC The present invention relates to novel methods for constructing fungal
CC strains useful for identification and validation of gene products as
CC targets for therapeutic agents, for creating a collection of identified
CC essential genes, and screening assays for the discovery of new drugs. The
CC invention provides the GRACE (gene replacement and conditional
CC expression) method for the construction of mutant organisms referred to
CC as GRACE strains of the organism. The invention can be applied to any
CC organism, particularly a pathogenic fungus e.g. Candida albicans,
CC Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful
CC to identify agents that may be used in the treatment of fungal
CC infections. AAS23687-AAS23747 represent primers A #1-61 used as probes
CC for identifying C. albicans GRACE strains
XX
SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1888 TTGATGTGCCCTAGATCAA 1906
              |||||| | || |||||||
Db          1 TTGATGGGTCCGAGATCAA 19
```

RESULT 4173
ABS58442/c
ID ABS58442 standard; DNA; 21 BP.
XX
AC ABS58442;
XX
DT 05-NOV-2002 (first entry)
XX
DE Bovine CVM disease gene forward PCR primer HUJ246.
XX
KW Cow; bovine; complex vertebral malformation; CVM; PCR; primer; ss.

XX
OS Bos taurus.
XX
PN WO200240709-A2.
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-DK000756.
XX
PR 16-NOV-2000; 2000DK-00001717.
PR 15-MAY-2001; 2001DK-00000765.
XX
PA (DAFO-) DANMARKS MIN FODERVARER LANDBRUG OG FISK.
PA (DAKV-) DANSK KVAEGAVL.
XX
PI Bendixen C, Svendsen S, Jensen H, Panitz F, Aasberg A, Holm L;
PI Horn P, Hoj A, Thomsen B, Jeppesen M, Nielsen VH, Jonker M;
XX
DR WPI; 2002-490145/52.
XX
PT Detecting bovine complex vertebral malformation in a subject, involves
PT detecting presence or absence of a genetic marker linked to a bovine
PT complex vertebral malformation disease trait in a bovine genetic
PT material.
XX
PS Claim 29; Page 15; 47pp; English.
XX
CC The presents invention relates to a new method of detecting bovine
CC complex vertebral malformation (CVM) in a bovine subject, where the
CC presence of a genetic marker associated with bovine CVM is identified.
CC The method of the invention involves providing a bovine genetic material,
CC and detecting in the genetic material, the presence or absence of at
CC least one genetic marker that is linked to a bovine CVM disease trait.
CC The method is useful for detecting bovine CVM in a bovine subject and is
CC also useful for detecting the presence of the genetic marker associated
CC with bovine CVM in a bovine subject. The present nucleic acid sequence
CC represents a PCR primer that was used in the method of the invention for
CC genetic mapping of bovine CVM
XX
SQ Sequence 21 BP; 2 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1508 CACAGGAAATAAAATTGGA 1526
| ||||||| |||| ||||
Db 21 CCCAGGAAAGAAAACTGGA 3

RESULT 4174
AAD33350/c
ID AAD33350 standard; DNA; 21 BP.
XX
AC AAD33350;
XX
DT 01-JUL-2002 (first entry)
XX
DE TGF-beta type II receptor antisense oligonucleotide.
XX
KW Transforming growth factor; TGF-beta type II receptor; cancer; thymoma;
KW germ cell tumour; multiple myeloma; melanoma; haematopoietic disease;
KW thrombocytopaenia; gene therapy; cytostatic; haemostatic; ss.
XX
OS Unidentified.
XX
PN WO200204479-A1.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-US021420.
XX
PR 06-JUL-2000; 2000US-0216256P.
XX
PA (AVIB-) AVI BIOPHARMA INC.
XX
PI Bartelmez SH, Iversen PL;
XX
DR WPI; 2002-195761/25.
XX
PT New human stem cell composition, useful for treating various cancers,
PT e.g. ovarian cancer, melanoma, testicular cancer, lung cancer or brain
PT cancer, as well as for other non-malignant hematopoietic diseases, e.g.
PT thrombocytopenia.
XX
PS Claim 5; Page 47; 59pp; English.
XX
CC The present invention relates to transforming growth factor (TGF)-beta
CC blocking agent-treated human stem cell compositions which are capable of
CC rapid in vivo reconstitution of the haematopoietic system of a subject.
CC The composition comprises a cell population enriched for human stem
CC cells, the stem cells treated ex vivo with an oligomer antisense to TGF-
CC beta, where the viability and differentiation state of the stem cells is
CC preserved in culture longer than stem cells not subjected to TGF-beta
CC antisense treatment. The human stem cell composition is useful for
CC promoting the rapid engraftment of long term repopulating haematopoietic
CC stem cells (LTR-HSC) following in vivo administration and facilitate the
CC rapid proliferation of LTR-HSC in vitro. The HSC- containing cell
CC population is useful for treating various cancers, including ovarian
CC cancer, thymomas, germ cell tumours, multiple myeloma, melanoma,
CC testicular cancer, lung cancer and brain cancer as well as for other non-
CC malignant haematopoietic diseases, e.g. thrombocytopaenia. Sequences of
CC the invention are also used in gene therapy. The present sequence is TGF-
CC beta type II receptor antisense oligonucleotide
XX
SQ Sequence 21 BP; 3 A; 10 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 223 CGACGGGAGCAGCAATGGG 241
||||||| || || |||||
Db 21 CGACGGGGGCTGCCATGGG 3

RESULT 4175
ABK65500
ID ABK65500 standard; DNA; 21 BP.
XX
AC ABK65500;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human single nucleotide polymorphism #120.
XX
KW Human; single nucleotide polymorphism; SNP; sickle cell anaemia;
KW agammaglobulinaemia; diabetes insipidus; Lesch-Nyhan syndrome;
KW muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease;
KW familial hypercholesterolaemia; polycystic kidney disease; cancer;
KW hereditary spherocytosis; Von Willebrand's disease; tuberous sclerosis;
KW hereditary haemorrhagic telangiectasia; familial colonic polyposis;
KW Ehlers-Danlos syndrome; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; inflammation; nervous system disorder;
KW infection; rheumatoid arthritis; multiple sclerosis; diabetes;
KW systemic lupus erythematosus; Graves disease; longevity; obesity;
KW baldness; fertility; forensic; paternity testing; ss.
XX
OS Homo sapiens.
XX
PN US2002037508-A1.
XX
PD 28-MAR-2002.
XX
PF 18-JAN-2001; 2001US-00765081.
XX

```
PR   19-JAN-2000; 2000US-0176861P.
XX
PA   (CARG/) CARGILL M.
PA   (IREL/) IRELAND J S.
PA   (LAND/) LANDER E S.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2002-315108/35.
XX
PT   Nucleic acid comprising single nucleotide polymorphisms, useful in
PT   forensics, paternity testing and diagnosis of disease.
XX
PS   Claim 1; Page 49; 96pp; English.
XX
CC   The invention relates to a nucleic acid comprising single nucleotide
CC   polymorphisms (SNPs) associated with diseases. The nucleic acids
CC   comprising the SNPs and probes and primers for detecting them may be used
CC   in assays for the diagnosis of diseases associated with SNPs (such as
CC   sickle cell anaemia, agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan
CC   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC   familial hypercholesterolaemia, polycystic kidney disease, hereditary
CC   spherocytosis, Von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, and acute intermittent porphyria,
CC   symptoms of, or susceptibility to, multifactorial diseases of which a
CC   component is or may be genetic, such as autoimmune diseases,
CC   inflammation, cancer, diseases of the nervous system, and infection by
CC   pathogenic microorganisms, autoimmune diseases including rheumatoid
CC   arthritis, multiple sclerosis, diabetes (insulin-dependent and non-
CC   independent), systemic lupus erythematosus and Graves disease, cancers
CC   including cancers of the bladder, brain, breast, colon, oesophagus,
CC   kidney, leukaemia, liver, lung, oral cavity, ovary, pancreas, prostate,
CC   skin, stomach and uterus, longevity, appearance (e.g., baldness,
CC   obesity), strength, speed, endurance, fertility, and susceptibility or
CC   receptivity to particular drugs or therapeutic treatments), in forensics
CC   and in paternity testing. ABK65381-ABK65841 represent human single
CC   nucleotide polymorphisms of the invention
XX
SQ   Sequence 21 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        765 TGACCAAGAACCCTCTGAACC 785
              ||||||||  :||| || |||
Db          1 TGACCAAGGCSCCTGTGGACC 21


RESULT 4176
ABK65490/c
ID   ABK65490 standard; DNA; 21 BP.
XX
AC   ABK65490;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human single nucleotide polymorphism #110.
XX
KW   Human; single nucleotide polymorphism; SNP; sickle cell anaemia;
KW   agammaglobulinaemia; diabetes insipidus; Lesch-Nyhan syndrome;
KW   muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease;
KW   familial hypercholesterolaemia; polycystic kidney disease; cancer;
KW   hereditary spherocytosis; Von Willebrand's disease; tuberous sclerosis;
KW   hereditary haemorrhagic telangiectasia; familial colonic polyposis;
KW   Ehlers-Danlos syndrome; osteogenesis imperfecta; autoimmune disease;
KW   acute intermittent porphyria; inflammation; nervous system disorder;
KW   infection; rheumatoid arthritis; multiple sclerosis; diabetes;
KW   systemic lupus erythematosus; Graves disease; longevity; obesity;
KW   baldness; fertility; forensic; paternity testing; ss.
XX
OS   Homo sapiens.
XX
PN   US2002037508-A1.
XX
PD   28-MAR-2002.
XX
PF   18-JAN-2001; 2001US-00765081.
XX
PR   19-JAN-2000; 2000US-0176861P.
XX
PA   (CARG/) CARGILL M.
PA   (IREL/) IRELAND J S.
PA   (LAND/) LANDER E S.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2002-315108/35.
XX
PT   Nucleic acid comprising single nucleotide polymorphisms, useful in
PT   forensics, paternity testing and diagnosis of disease.
XX
PS   Claim 1; Page 48; 96pp; English.
XX
CC   The invention relates to a nucleic acid comprising single nucleotide
CC   polymorphisms (SNPs) associated with diseases. The nucleic acids
CC   comprising the SNPs and probes and primers for detecting them may be used
CC   in assays for the diagnosis of diseases associated with SNPs (such as
CC   sickle cell anaemia, agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan
CC   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC   familial hypercholesterolaemia, polycystic kidney disease, hereditary
CC   spherocytosis, Von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, and acute intermittent porphyria,
CC   symptoms of, or susceptibility to, multifactorial diseases of which a
CC   component is or may be genetic, such as autoimmune diseases,
CC   inflammation, cancer, diseases of the nervous system, and infection by
CC   pathogenic microorganisms, autoimmune diseases including rheumatoid
CC   arthritis, multiple sclerosis, diabetes (insulin-dependent and non-
CC   independent), systemic lupus erythematosus and Graves disease, cancers
CC   including cancers of the bladder, brain, breast, colon, oesophagus,
CC   kidney, leukaemia, liver, lung, oral cavity, ovary, pancreas, prostate,
CC   skin, stomach and uterus, longevity, appearance (e.g., baldness,
CC   obesity), strength, speed, endurance, fertility, and susceptibility or
CC   receptivity to particular drugs or therapeutic treatments), in forensics
CC   and in paternity testing. ABK65381-ABK65841 represent human single
CC   nucleotide polymorphisms of the invention
XX
SQ   Sequence 21 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   76.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2374 GCGTTGAGTGTACAGATTTTA 2394
              || |||||  :|||| |||||
Db         21 GCATTGAGCAKACAGGTTTTA 1


RESULT 4177
ABT13236/c
ID   ABT13236 standard; DNA; 21 BP.
XX
AC   ABT13236;
XX
DT   30-JAN-2003  (first entry)
XX
DE   Fanconi anaemia FANCD exon amplifying PCR primer SEQ ID No 139.
XX
KW   Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect;
KW   Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome;
KW   cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer;
KW   Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy;
KW   Xeroderma pigmentosum; PCR; primer; ss.
XX
```

OS Unidentified.
XX
PN WO200236761-A2.
XX
PD 10-MAY-2002.
XX
PF 02-NOV-2001; 2001WO-US045561.
XX
PR 03-NOV-2000; 2000US-0245756P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI D'andrea AD, Taniguchi T, Timmers C, Grompe M;
XX
DR WPI; 2002-519251/55.
XX
PT Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2,
PT useful for treating Fanconi anemia pathway defect in cell target or for
PT treating patient with defective FANCD2 gene.
XX
PS Claim 8; Page 55; 103pp; English.
XX
CC The invention relates to an isolated Fanconi anaemia protein complex
CC (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472
CC amino acids fully defined in the specification, its 90% identical
CC sequence, a sequence encoded by a polynucleotide that is at least 90%
CC identical to sequences given in specification such as a 5127 base pair
CC sequence, or a fragment which is at least 50 amino acids in length. The
CC FANCD2 protein is useful for treating an FA pathway defect in a cell
CC target or for treating a patient with a defective FANCD2 gene. The FANCD2
CC gene is useful for making a recombinant expression vector. The FANCD2
CC protein and its gene are useful as a novel target for therapeutic
CC development, and in diagnostic test and screening assays for diseases
CC associated with DNA repair and cell cycle abnormalities such as Fanconi
CC anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis
CC colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2
CC gene is useful in producing probes and primers for screening patients in
CC genetic based test, for diagnosing Fanconi anaemia and cancer, for
CC preparing an experimental mouse model for use in screening new
CC therapeutics for treating conditions involving defective DNA repair, and
CC in gene therapy methods. A recombinant vector containing the FANCD2 gene
CC of the invention is useful in gene therapy. This polynucleotide sequence
CC represents a PCR primer for amplifying a FANCD exon relating to the
CC invention
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       231 GCAGCAATGGGAATCCGCG 249
             ||| |||||||| ||| ||
Db        21 GCATCAATGGGATTCCACG 3
```

RESULT 4178
ABK41517/c
ID ABK41517 standard; DNA; 21 BP.
XX
AC ABK41517;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human CTNNA3 exon-specific lower PCR primer #4.
XX
KW Human; mouse; alpha-catenin; primer; ss; cytostatic; antiinfertility;
KW cadherin-catenin related pathway; heart testis; cancer; gene therapy;
KW cadherin-catenin related disease; specifically dilated cardiomyopathy;
KW cardiomyopathy; male infertility; CTNNA3; PCR; alpha T-catenin.
XX
OS Homo sapiens.
XX
PN WO200204636-A1.
XX
PD 17-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-EP007392.
XX
PR 12-JUL-2000; 2000EP-00202472.
PR 14-JUL-2000; 2000US-0218309P.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Van Roy F, Goossens S, Janssens B, Vanpoucke G;
XX
DR WPI; 2002-171717/22.
XX
PT New alpha catenin polypeptides and polynucleotides encoding them, useful
PT for predicting, diagnosing or treating cadherin-catenin related diseases,
PT particularly cardiomyopathies, cancer and male infertility.
XX
PS Example; Page 35; 132pp; English.
XX
CC The invention relates to human and mouse alpha-catenin polypeptides and
CC their associated polynucleotides. The polypeptides and related antibodies
CC are useful for modulating the cadherin-catenin related pathway in
CC selected organs, such as the heart and testis. The nucleic acids and the
CC antibodies are useful in the diagnosis and/or prediction of the
CC likelihood of developing cadherin-catenin related diseases. The nucleic
CC acids may also be used to predict the likelihood of developing cancer or
CC in diagnosing cancer, and in gene therapy. The polypeptide, the nucleic
CC acid or the antibody is useful in manufacturing a medicament for treating
CC cadherin-catenin related diseases, such as cancer, cardiomyopathy,
CC specifically dilated cardiomyopathy, and male infertility. Sequences
CC ABK41510-ABK41599 represent PCR primers used to amplify DNA encoding
CC human and mouse alpha-catenin polypeptides, including the CTNNA3 gene
CC which encodes human alpha T-catenin
XX
SQ Sequence 21 BP; 8 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1793 TTTCCTTCTCTGAAAGTGG 1811
              |||| |||||||||  |||
Db         20 TTTCATTCTCTGAACCTGG 2
```

RESULT 4179
ABS55055
ID ABS55055 standard; DNA; 21 BP.
XX
AC ABS55055;
XX
DT 29-AUG-2003 (revised)
DT 09-DEC-2002 (first entry)
XX
DE R. obamensis DNA polymerase 1 PCR primer 202-154.
XX
KW ss; PCR; DNA polymerase I; thermostability; 3'-5' exonuclease; GroEL;
KW DNA amplification; primer.
XX
OS Rhodothermus marinus; strain JCM 9785.
XX
PN US6440715-B1.
XX
PD 27-AUG-2002.
XX
PF 12-MAR-1999; 99US-00267311.
XX
PR 12-MAR-1999; 99US-00267311.
XX
PA (NEWE) NEW ENGLAND BIOLABS INC.
XX

PI Xu S;
XX
DR WPI; 2002-730567/79.
XX
PT Novel thermostable DNA polymerase I obtainable from Rhodothermus
PT obamensis, useful for improving the fidelity of DNA amplification
PT reactions, has 3'-5' exonuclease activity and a specified half life.
XX
PS Example 1; Col 5; 25pp; English.
XX
CC The invention relates to a substantially pure thermostable DNA polymerase
CC I obtainable from Rhodothermus obamensis (JCM 9785), and having a
CC molecular weight of 104 kDa, possessing 3'-5' exonuclease activity and
CC having a half-life of 35 minutes at 94 plusoC. Also included are (1) a
CC recombinant R. obamensis DNA polymerase I large fragment, having a
CC molecular weight of about 71 kDa, possessing 3'-5' exonuclease activity
CC and having a half-life of about 35 minutes at 94 plusoC and (2) a DNA
CC polymerase I composition comprising R. obamensis DNA polymerase I large
CC fragment and an approximately 60 kDa Escherichia coli GroEL protein,
CC where the thermostability of R. obamensis DNA polymerase I large fragment
CC is increased by the presence of GroEL protein. The thermostable DNA
CC polymerase is useful for improving the fidelity of DNA amplification
CC reactions. The present sequence is a PCR primer used to isolate DNA
CC encoding R. obamensis DNA polymerase I. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 21 BP; 1 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1373 CAGGCCATCTGTGCCGCGG 1391
              |||| | | ||||||||||
Db          3 CAGGGCGTTTGTGCCGCGG 21
```

RESULT 4180
ABZ29935
ID ABZ29935 standard; DNA; 21 BP.
XX
AC ABZ29935;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans GRACE strain PCR primer SEQ ID NO 4086.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR WPI; 2002-566694/60.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 36; SEQ ID NO 4086; 167pp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1888 TTGATGTGCCCTAGATCAA 1906
              |||||| | || |||||||
Db          1 TTGATGGGTCCGAGATCAA 19
```

RESULT 4181
ABS98382
ID ABS98382 standard; DNA; 21 BP.
XX
AC ABS98382;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance associated protein 3 polymorphic sequence #4.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.

XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 24; Page 152; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or haematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX
SQ Sequence 21 BP; 8 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

```
  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        979 GAAAAATGGAGGCCGGTCC 997
              || ||||||| || |||||
Db          1 GAGAAATGGAAGCAGGTCC 19
```

RESULT 4182
ABS98479/c
ID ABS98479 standard; DNA; 21 BP.
XX
AC ABS98479;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human orphan nuclear receptor (NR1I2) gene polymorphic sequence #17.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.
XX
PR 28-NOV-2000; 2000US-00724389.
XX
PA (DNAS-) DNA SCI LAB INC.
XX
PI Guida M, Hall J;
XX
DR WPI; 2002-698522/75.
XX
PT Isolated nucleic acid molecules having polymorphisms in known human genes
PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.
XX
PS Example 25; Page 155; 714pp; English.
XX
CC This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterising the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered

```
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a
CC   polymorphic DNA sequence of the invention
XX
SQ   Sequence 21 BP; 0 A; 6 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        448 GCCCACAGGCAGCCAGCAG 466
              ||||||||||| | || |||
Db         19 GCCCACAGGCCGGCACCAG 1


RESULT 4183
ABS56153
ID   ABS56153 standard; DNA; 21 BP.
XX
AC   ABS56153;
XX
DT   29-JAN-2003  (first entry)
XX
DE   Sperm formation relative protein Sgrg related RT-PCR primer YN11RT-R.
XX
KW   Sperm formation relative protein Sgrg protein; infertility; RT-PCR;
KW   reverse transcriptase-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1352138-A.
XX
PD   05-JUN-2002.
XX
PF   09-NOV-2000; 2000CN-00127314.
XX
PR   09-NOV-2000; 2000CN-00127314.
XX
PA   (SHAN-) SHANGHAI BIOLOGICAL ENG RES CENT ACAD S.
XX
PI   Kong X,  Yang J,  Zhao G;
XX
DR   WPI; 2002-714424/78.
XX
PT   New sperm formation relative protein Sgrg protein and polynucleotides
PT   encoding it, for treating infertility and other diseases.
XX
PS   Example 12; Page 16 (disclosure); 26pp; Chinese.
XX
CC   The present invention relates to the isolation of a novel sperm formation
CC   relative protein Sgrg protein, and the polynucleotide sequence encoding
CC   it. Also described is the process for preparing the protein by DNA
CC   recombination and the application of the polypeptide and polynucleotide
CC   in treating various diseases such as infertility and other diseases. The
CC   present invention also discloses a machine composite containing the Sgrg
CC   protein. The present sequence represents a reverse transcriptase (RT)-PCR
CC   primer used in the examples of the present invention
XX
SQ   Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        222 ACGACGGGAGCAGCAATGG 240
              | || || ||||||||||||
Db          3 ATGATGGCAGCAGCAATGG 21


RESULT 4184
ABK14355/c
ID   ABK14355 standard; DNA; 21 BP.
XX
AC   ABK14355;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human interleukin-13 sense PCR primer.
XX
KW   Human; ss; PCR; primer; interleukin-13; neuroprotective; nootropic;
KW   anticonvulsant; cerebroprotective; antiparkinsonian; vulnerary;
KW   immunosuppressive; microglia cell line; autoimmune disease;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   Huntington's disease; amyotrophic lateral sclerosis; stroke;
KW   spinal cord injury; ataxia; brain trauma; multiple sclerosis;
KW   acquired immunodeficiency syndrome; AIDS-dementia.
XX
OS   Homo sapiens.
XX
PN   WO200204604-A2.
XX
PD   17-JAN-2002.
XX
PF   09-JUL-2001; 2001WO-IB001770.
XX
PR   10-JUL-2000; 2000WO-US018777.
PR   15-MAY-2001; 2001US-00855468.
PR   22-JUN-2001; 2001US-00887145.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Kim SU;
XX
DR   WPI; 2002-148175/19.
XX
PT   Genetically modified human microglia cell for treating neurodegenerative
PT   disease, comprises demonstrable phagocytic properties, produces progeny
PT   in culture, presents surface antigens, and contains modified human
PT   genomic DNA.
XX
PS   Example; Page 23; 46pp; English.
XX
CC   The invention relates to a genetically modified human microglia cell
CC   maintained stably in vitro which has (i) has demonstrable phagocytic
CC   properties; (ii) produces progeny continuously in culture; (iii) presents
CC   CD11b and CD68 as surface antigens; and (iv) contains human genomic DNA
CC   that has been genetically modified to include a viral vector carrying at
CC   least one DNA segment encoding an exogenous gene for intracellular
CC   expression. The microglia cell line is useful for screening compounds for
CC   the treatment of autoimmune disease, and is used in the treatment of a
CC   neurodegenerative disorder e.g. Alzheimer's disease, Parkinson's disease,
CC   Huntington's disease, amyotrophic lateral sclerosis, stroke, spinal cord
CC   injuries, ataxia, brain trauma, multiple sclerosis and AIDS-(acquired
CC   immunodeficiency syndrome)-dementia. The cell line is also useful for
CC   isolating neurotoxic or neurotrophic molecules naturally produced by
CC   human microglia. The present sequence is an RT-PCR (reverse transcriptase
CC   PCR) primer which amplifies a segment of the mRNA for an expressed marker
CC   gene, used to characterise the cell line
XX
SQ   Sequence 21 BP; 7 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2106 GGGGCCTTCTGGTTTTAGG 2124
              || |||||||||| | ||
Db         20 GGAGCCTTCTGGTTCTGGG 2


RESULT 4185
ABK37957/c
```

```
ID   ABK37957 standard; DNA; 21 BP.
XX
AC   ABK37957;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Forward RT-PCR primer for NOV7.
XX
KW   Human; NOVX; ss; cardiomyopathy; atherosclerosis; diabetes; PCR; primer;
KW   cell signal processing disorder; metabolic disorder; obesity; infection;
KW   anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; immune disorder;
KW   haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW   osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW   myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW   psychosis; neurological disorder; anxiety; schizophrenia;
KW   manic depression; dementia; dyskinesia; Huntington's disease;
KW   Gilles de la Tourette's syndrome; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200210216-A2.
XX
PD   07-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US024225.
XX
PR   28-JUL-2000; 2000US-0221409P.
PR   04-AUG-2000; 2000US-0222840P.
PR   04-AUG-2000; 2000US-0223752P.
PR   04-AUG-2000; 2000US-0223762P.
PR   04-AUG-2000; 2000US-0223769P.
PR   04-AUG-2000; 2000US-0223770P.
PR   14-AUG-2000; 2000US-0225146P.
PR   15-AUG-2000; 2000US-0225392P.
PR   15-AUG-2000; 2000US-0225470P.
PR   16-AUG-2000; 2000US-0225697P.
PR   01-FEB-2001; 2001US-0263662P.
PR   05-APR-2001; 2001US-0281645P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Padigaru M,  Mezes P,  Mishra V,  Burgess C,  Casman S,  Grosse WM;
PI   Alsobrook JP,  Lepley DM,  Gerlach VL,  Macdougall JR,  Smithson G;
XX
DR   WPI; 2002-180074/23.
XX
PT   New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT   polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT   infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT   immune disorders.
XX
PS   Example 7; Page 173; 213pp; English.
XX
CC   The invention relates to an isolated cytoplasmic, nuclear, membrane
CC   bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC   form. Also included are the nucleic acids encoding the NOVX proteins, a
CC   vector comprising the nucleic acid, a cell comprising the vector, an anti
CC   -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC   antibody are useful for treating or preventing a NOVX-associated
CC   disorder, where the disorder is selected from cardiomyopathy,
CC   atherosclerosis, diabetes, a disorder related to cell signal processing
CC   and metabolic pathway modulation, metabolic disorders, obesity,
CC   infectious disease, anorexia, cancer-associated cachexia, cancer,
CC   neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC   immune disorders, haematopoietic disorders, and the various
CC   dyslipidaemias, metabolic disturbances associated with obesity, the
CC   metabolic syndrome X and wasting disorders associated with chronic
CC   diseases, bacterial, fungal, protozoal and viral infections, pain,
CC   bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC   disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC   pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC   hypertrophy, and psychotic and neurological disorders, including anxiety,
CC   schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC   such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC   nucleic acid is useful in gene therapy. The present sequence is an RT-PCR
CC   (reverse transcriptase PCR) primer used to quantitate tissue specific
CC   expression of a NOVX transcript
XX
SQ   Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match          0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity  84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1992 TGTGTATCTAGCTTCTTCA 2010
              ||||| ||| ||||||||
Db         20 TGTGTTTCTGCCTTCTTCA 2


RESULT 4186
AAL40172
ID   AAL40172 standard; DNA; 21 BP.
XX
AC   AAL40172;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Isoprenoid related PCR primer SEQ ID No 84.
XX
KW   Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS; DDS;
KW   decaprenyl diphosphate synthase; PCR; primer; ss.
XX
OS   Sphingomonas trueperi.
OS   Synthetic.
XX
PN   WO200226933-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-US030328.
XX
PR   29-SEP-2000; 2000US-0236580P.
XX
PA   (CRGI ) CARGILL INC.
XX
PI   Gokarn R,  Jessen H,  Zidwick MJ;
XX
DR   WPI; 2002-416480/44.
XX
PT   Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate
PT   synthase activity, useful for the production of isoprenoids, especially
PT   CoQ(10).
XX
PS   Example 4; Page 64; 246pp; English.
XX
CC   The invention relates to methods and materials for the production of
CC   isoprenoids. More particularly the invention provides isolated nucleic
CC   acids, substantially pure polypeptides, host cells, and methods for
CC   producing various isoprenoid compounds. The polypeptides are useful for
CC   the production of isoprenoids, especially CoQ(10). Expressing the pure
CC   polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS)
CC   activity or decaprenyl diphosphate synthase (DDS) activity, is useful for
CC   increasing production of CoQ(10) in a cell having endogenous DDS
CC   activity. This polynucleotide sequence represents a PCR primer relating
CC   to the isoprenoid production of the invention
XX
SQ   Sequence 21 BP; 6 A; 5 C; 1 G; 1 T; 0 U; 8 Other;

  Query Match          0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity  52.4%;  Pred. No. 4.1e+03;
  Matches   11;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        698 CAGAATGTCGACGACCAGCAC 718
              :|::| :||: |:||:||:||
Db          1 VAKRAARTCSCCSACSAGSAC 21
```

```
RESULT 4187
ABK94369
ID   ABK94369 standard; DNA; 21 BP.
XX
AC   ABK94369;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Endothelin converting enzyme 1 (ECE-1) SNP detection primer #157.
XX
KW   Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW   EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW   hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW   diabetes; familial hypercholesterolaemia; forensic marker;
KW   transgenic animal; solid support; cardiovascular regulator; SNP;
KW   single nucleotide polymorphism; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200224747-A2.
XX
PD   28-MAR-2002.
XX
PF   31-AUG-2001; 2001WO-EP010087.
XX
PR   19-SEP-2000; 2000EP-00120123.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brinkmann U,  Hoffmeyer S;
XX
DR   WPI; 2002-435060/46.
XX
PT   Novel polynucleotide of the endothelin/endothelin converting
PT   enzyme/receptors of endothelin and endothelin converting enzyme signaling
PT   system associated with cardiovascular disease, useful for treating the
PT   disease.
XX
PS   Example 6; Page 67; 190pp; English.
XX
CC   The invention describes a polynucleotide (I) of the endothelin
CC   (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC   signaling system which is associated with a cardiovascular disease. (I),
CC   the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC   or (II) is useful for producing cells capable of expressing a molecular
CC   variant polypeptide which is associated with a cardiovascular disease.
CC   (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a
CC   molecular variant gene comprising (I) is useful for identifying and
CC   obtaining a pro-drug or drug capable of modulating the activity of a
CC   molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC   or its gene product, or for identifying and obtaining an inhibitor of the
CC   activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC   signaling system or its gene product. The isolated proteins and
CC   polynucleotides encoding them are useful for preparation of a
CC   pharmaceutical composition for treating a cardiovascular disease such as
CC   coronary heart disease, hypertension, atherosclerosis, or related to
CC   abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC   hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC   EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC   creating a transgenic animal and in creation of a solid support
CC   comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC   host cells of the invention. This sequence represents a PCR primer used
CC   to identify single nucleotide polymorphisms in DNA encoding
CC   cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway
XX
SQ   Sequence 21 BP; 8 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        818 ATGAACCCCACTGAGGTCT 836
              | ||||||||  |||||||
Db          2 AAGAACCCCAGAGAGGTCT 20


RESULT 4188
ABK94370/c
ID   ABK94370 standard; DNA; 21 BP.
XX
AC   ABK94370;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Endothelin converting enzyme 1 (ECE-1) SNP detection primer #158.
XX
KW   Endothelin; EDN; endothelin converting enzyme; ECE; endothelin receptor;
KW   EDNR; signaling system; cardiovascular disease; coronary heart disease;
KW   hypertension; atherosclerosis; angiogenesis; fatty acid metabolism;
KW   diabetes; familial hypercholesterolaemia; forensic marker;
KW   transgenic animal; solid support; cardiovascular regulator; SNP;
KW   single nucleotide polymorphism; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200224747-A2.
XX
PD   28-MAR-2002.
XX
PF   31-AUG-2001; 2001WO-EP010087.
XX
PR   19-SEP-2000; 2000EP-00120123.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Brinkmann U,  Hoffmeyer S;
XX
DR   WPI; 2002-435060/46.
XX
PT   Novel polynucleotide of the endothelin/endothelin converting
PT   enzyme/receptors of endothelin and endothelin converting enzyme signaling
PT   system associated with cardiovascular disease, useful for treating the
PT   disease.
XX
PS   Example 6; Page 67; 190pp; English.
XX
CC   The invention describes a polynucleotide (I) of the endothelin
CC   (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)
CC   signaling system which is associated with a cardiovascular disease. (I),
CC   the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)
CC   or (II) is useful for producing cells capable of expressing a molecular
CC   variant polypeptide which is associated with a cardiovascular disease.
CC   (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a
CC   molecular variant gene comprising (I) is useful for identifying and
CC   obtaining a pro-drug or drug capable of modulating the activity of a
CC   molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system
CC   or its gene product, or for identifying and obtaining an inhibitor of the
CC   activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE
CC   signaling system or its gene product. The isolated proteins and
CC   polynucleotides encoding them are useful for preparation of a
CC   pharmaceutical composition for treating a cardiovascular disease such as
CC   coronary heart disease, hypertension, atherosclerosis, or related to
CC   abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial
CC   hypercholesterolaemia. The gene or a polynucleotide fragment of the
CC   EDN/ECE/EDNR signaling system are useful as forensic markers, for
CC   creating a transgenic animal and in creation of a solid support
CC   comprising polynucleotides, genes, vectors, polypeptides, antibodies or
CC   host cells of the invention. This sequence represents a PCR primer used
CC   to identify single nucleotide polymorphisms in DNA encoding
CC   cardiovascular regulator proteins of the EDN/ECE/EDNR signaling pathway
XX
SQ   Sequence 21 BP; 2 A; 5 C; 6 G; 8 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
```

```
 Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
 Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        818 ATGAACCCCACTGAGGTCT 836
              | ||||||||  |||||||
Db         20 AAGAACCCCAGAGAGGTCT 2


RESULT 4189
AAL50228
ID   AAL50228 standard; mRNA; 21 BP.
XX
AC   AAL50228;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human ARE-mRNA sequence #1.
XX
KW   ARE-mRNA; protein secretion inhibition; ARE-mRNA regulation;
KW   inflammation; arthritis; autoimmune disease; septic shock; blood clot;
KW   stroke; TNFalpha; tumour necrosis factor alpha; antiinflammatory;
KW   antiarthritic; antibacterial; immunosuppressive; cerebroprotective;
KW   antipyretic; immunomodulator; adenylate-uridylate rich element; ss.
XX
OS   Homo sapiens.
XX
PN   WO200283842-A2.
XX
PD   24-OCT-2002.
XX
PF   08-APR-2002; 2002WO-US010898.
XX
PR   10-APR-2001; 2001US-0282974P.
XX
PA   (MESS-) MESSAGE PHARM INC.
XX
PI   Giordano T,  Sturgess MA;
XX
DR   WPI; 2003-046924/04.
XX
PT   Modulating Adenylate-Uridylate Rich element-mRNA regulation involves
PT   administering new amide compound that inhibits secretion of protein
PT   encoded by ARE-mRNA, useful for treating inflammation, arthritis and
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 5; 147pp; English.
XX
CC   The present invention relates to a method of modulating the regulation of
CC   an adenylate-uridylate rich element (ARE)-mRNA, which involves
CC   administering new compounds that inhibits secretion of a protein encoded
CC   by an ARE-mRNA. This can be used in the treatment of inflammation,
CC   arthritis, autoimmune diseases, septic shock, blood clot, stroke, fever,
CC   acute respiratory distress syndrome (ARDS) and cachexia. The present
CC   sequence is an ARE-mRNA shown in the exemplification of the invention
XX
SQ   Sequence 21 BP; 6 A; 0 C; 0 G; 1 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   21.1%;  Pred. No. 4.1e+03;
  Matches    4;  Conservative   12;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATTT 2273
              :|:|:::   :|:::|:::
Db          2 UTTUAUUUAUUUAUUUAUUU 20


RESULT 4190
ABZ24198/c
ID   ABZ24198 standard; DNA; 21 BP.
XX
AC   ABZ24198;
XX
DT   14-APR-2003  (first entry)
XX
DE   Humanised R. reniformis GFP DNA amplifying 5' retro primer.
XX
KW   Polymerase chain reaction; PCR; mutagenesis; nucleic acid amplification;
KW   green fluorescent protein; GFP; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200297078-A1.
XX
PD   05-DEC-2002.
XX
PF   23-MAY-2002; 2002WO-US016280.
XX
PR   30-MAY-2001; 2001US-0294341P.
XX
PA   (STRA-) STRATAGENE.
XX
PI   Hogrefe HH,  Cline JM;
XX
DR   WPI; 2003-167269/16.
XX
PT   Polymerase chain reaction amplification for mutagenesis, by incubating
PT   reaction mixture having template, primers, archaeal exo-DNA polymerase
PT   and amplification enhancing factor to produce mutated amplified product.
XX
PS   Example 3; Page 37; 57pp; English.
XX
CC   The invention relates to polymerase chain reaction (PCR) amplification
CC   for mutagenesis. The method involves incubating a reaction mixture
CC   comprising a nucleic acid template, at least two PCR primers, an archaeal
CC   exo-DNA polymerase, and PCR enhancing factor under conditions which
CC   permit amplification of the nucleic acid template by the archaeal exo-DNA
CC   polymerase to produce a mutated amplified product. The method is useful
CC   for performing PCR mutagenesis. The method is useful for making nucleic
CC   acid mutant libraries, and as control for the mutazyme error prone PCR.
CC   The method is simple for controlling mutation frequencies of target
CC   nucleic acid template, allows the amplification of highly complex
CC   targets, and provides higher product yields. The present sequence
CC   represents a PCR primer for amplifying a 720 bp gene encoding a humanised
CC   R. reinformis green fluorescent protein (GFP), used as mutational target
CC   for Mutazyme PCR mutagenesis
XX
SQ   Sequence 21 BP; 1 A; 7 C; 11 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1355 ACCCACGGGTTTGGCAGCC 1373
              |||| |||| | |||||||
Db         19 ACCCCCGGGGTCGGCAGCC 1


RESULT 4191
AAL53707
ID   AAL53707 standard; RNA; 21 BP.
XX
AC   AAL53707;
XX
DT   07-FEB-2003  (first entry)
XX
DE   Adenylate Uridylate-rich element motif SEQ ID No 1.
XX
KW   Target RNA; target RNA:support-attached test compound; flow cytometry;
KW   mass spectrometry; high-throughput screening; RNA motif; ss.
XX
OS   Homo sapiens.
XX
PN   WO200283837-A1.
XX
PD   24-OCT-2002.
XX
```

PF 11-APR-2002; 2002WO-US011758.
XX
PR 11-APR-2001; 2001US-0282966P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Almstead NG;
XX
DR WPI; 2003-075534/07.
XX
PT Identifying a test compound that binds to a target RNA molecule by
PT separating the detectably labeled target RNA:support-attached test
PT compound complex from uncomplexed target RNA molecules and test compounds
PT by flow cytometry.
XX
PS Disclosure; Page 16; 131pp; English.
XX
CC The invention relates to a novel method for identifying a test compound
CC that binds to a target RNA molecule comprising separating the detectably
CC labeled target RNA:support-attached test compound complex from
CC uncomplexed target RNA molecules and test compounds. The separating
CC process is carried out by flow cytometry and determining a structure of
CC the type of test compound of the RNA:support-attached test compound
CC complex by mass spectrometry. The method is useful for high-throughput
CC screening of libraries of compounds to identify pharmaceutical leads.
CC This polynucleotide sequence represents one of the target RNA motifs/
CC regions of the invention
XX
SQ Sequence 21 BP; 6 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 15.8%; Pred. No. 4.1e+03;
Matches 3; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

Qy 2255 TTTATTTGCATATTTATTT 2273
:::|::: :|:::|:::
Db 2 UUUAUUUAUUUAUUUAUUU 20

RESULT 4192
AAD49639
ID AAD49639 standard; mRNA; 21 BP.
XX
AC AAD49639;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human adenylate uridylate-rich element (ARE) motif mRNA #1.
XX
KW Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;
KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
KW neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;
KW haemostatic; antibacterial; nootropic; neuroprotective; cytostatic;
KW fungicide; human; adenylate uridylate-rich element; ARE; ss.
XX
OS Homo sapiens.
XX
PN WO200283953-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011757.
XX
PR 11-APR-2001; 2001US-0282965P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Rando R, Welch E;
XX
DR WPI; 2003-075561/07.
XX
PT Identifying a test compound that binds to a target RNA molecule for
PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,
PT diabetes, by contacting a detectably labeled target RNA molecule with a
PT library of test compounds.
XX
PS Example; Page 18; 152pp; English.
XX
CC The invention relates to a method for identifying a test compound that
CC binds to a target RNA molecule, which comprises contacting a detectably
CC labelled target RNA molecule with a library of test compounds under
CC conditions that permit direct binding of the labelled target RNA to a
CC member of the library of test compounds so that a detectably labeled
CC target RNA:test compound complex is formed. The method is useful for
CC screening libraries of compounds for those that are selectively bind to a
CC pre-selected target RNA. The compounds are useful for inhibiting the
CC formation of a specific bound RNA:host cell factor complexes in vivo.
CC They are also useful for treating or preventing diseases associated with
CC overproduction or decreased protein function, such as amyloidosis,
CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,
CC dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,
CC inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative
CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).
CC The invention is also used in gene therapy. The present sequence is human
CC adenylate uridylate-rich element (ARE) motif mRNA. This sequence is used
CC to illustrate the method of the invention
XX
SQ Sequence 21 BP; 6 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 15.8%; Pred. No. 4.1e+03;
Matches 3; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

Qy 2255 TTTATTTGCATATTTATTT 2273
:::|::: :|:::|:::
Db 2 UUUAUUUAUUUAUUUAUUU 20

RESULT 4193
ACC83520
ID ACC83520 standard; mRNA; 21 BP.
XX
AC ACC83520;
XX
DT 08-SEP-2003 (first entry)
XX
DE AU rich element (ARE).
XX
KW AU-rich element; ARE; exosome; mRNA turnover; antiinflammatory;
KW cytostatic; ss.
XX
OS Unidentified.
XX
PN WO2003044166-A2.
XX
PD 30-MAY-2003.
XX
PF 14-NOV-2002; 2002WO-US036665.
XX
PR 15-NOV-2001; 2001US-0334712P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen C, Karin M;
XX
DR WPI; 2003-457602/43.
XX
PT New purified mammalian exosome, useful for treating immune diseases e.g.
PT diabetes, cirrhosis, scleroderma, lupus, arthritis, or multiple
PT sclerosis, inflammatory diseases, cancer, or hormone deficiency disease
PT e.g. osteoporosis.
XX
PS Disclosure; Page 53; 127pp; English.
XX
CC The present sequence is that of a Group I Cluster AU rich element (ARE).

CC AREs play a role in mRNA stability. The invention provides methods of
CC altering the level of ARE-containing RNA, e.g. an RNA containing the
CC present motif. The human exosome has been purified and characterised. It
CC promotes the degradation of ARE-containing RNAs. A claimed method for
CC altering the level of an ARE-containing RNA involves contacting the RNA
CC with an ARE-binding protein, a mammalian (human) exosome and an agent
CC that alters the level of binding of the exosome to the ARE-binding
CC protein. Levels of mRNA are decreased or increased by impacting the level
CC of degradation of the mRNA. Reducing the level of a cytokine, proto-
CC oncogene or growth factor RNA can be used to treat an immune disease,
CC inflammatory disease or cancer. Increasing the level of a target RNA can
CC be performed in a subject capable of developing a hormone deficiency
XX
SQ Sequence 21 BP; 6 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 15.8%; Pred. No. 4.1e+03;
Matches 3; Conservative 13; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2255 TTTATTTGCATATTTATTT 2273
              :::|:::   :|:::|:::
Db          2 UUUAUUUAUUUAUUUAUUU 20
```

RESULT 4194
ADC42473/c
ID ADC42473 standard; DNA; 21 BP.
XX
AC ADC42473;
XX
DT 18-DEC-2003 (first entry)
XX
DE FANCD2 PCR primer MG755 SEQ ID NO:139.
XX
KW cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;
KW chemosensitising; ss; PCR; primer.
XX
OS Synthetic.
XX
PN WO2003039327-A2.
XX
PD 15-MAY-2003.
XX
PF 06-JUN-2002; 2002WO-US018153.
XX
PR 02-NOV-2001; 2001US-00998027.
PR 02-NOV-2001; 2001WO-US045561.
XX
PA (DAND) DANA FARBER CANCER INST.
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI D'andrea AD, Taniguchi T, Timmers C, Grompe M, Fox EA;
XX
DR WPI; 2003-441436/41.
XX
PT Diagnosing or determining cancer or increased risk of cancer in a
PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a
PT cancer-associated defect, that indicates cancer or increased risk of
PT cancer.
XX
PS Claim 11; SEQ ID NO 139; 160pp; English.
XX
CC The invention relates to a novel method of diagnosing or determining if a
CC patient has cancer or is at increased risk of cancer, involving testing a
CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a
CC cancer-associated defect, where the presence of one or more cancer-
CC associated defects is indicative of cancer or an increased risk of cancer
CC in the patient. The method of the invention has cytostatic activity. The
CC method is useful for determining if a patient has cancer, or is at
CC increased risk of developing cancer, e.g. breast, ovarian or prostate
CC cancer. A microarray of the invention is useful for determining if a
CC patient has cancer, or is at increased risk of developing cancer, by
CC hybridising a nucleic acid sample to the nucleic acid sequences from the
CC array, and detecting the presence of mutations in FA/BRCA pathway genes
CC in the nucleic acid sample from the patient, where detecting the presence
CC of mutations is indicative of a patient who has cancer, or is at
CC increased risk of developing cancer. A method of the invention is useful
CC for screening a chemosensitising agent, and the agent obtained is useful
CC for treating a patient having a cancer. The present sequence is used in
CC the exemplification of the invention.
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        231 GCAGCAATGGGAATCCGCG 249
              ||| |||||||| ||| ||
Db         21 GCATCAATGGGATTCCACG 3
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RESULT 4195
ADD14366/c
ID ADD14366 standard; DNA; 21 BP.
XX
AC ADD14366;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human src biomarker forward PCR primer SEQ ID NO:555.
XX
KW predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003062395-A2.
XX
PD 31-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-US001981.
XX
PR 18-JAN-2002; 2002US-0350061P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Huang F, Fairchild CR, Lee FY, Shaw P;
XX
DR WPI; 2003-636735/60.
XX
PT New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX
PS Example 2; SEQ ID NO 555; 139pp; English.
XX
CC The present invention describes a predictor set comprising a plurality of
CC polynucleotides or polypeptides whose expression pattern is predictive of
CC the response of cells to treatment with a compound that modulates protein
CC tyrosine kinase activity or members of the protein tyrosine kinase
CC pathway. Also described: (1) predicting whether a compound is capable of
CC modulating the activity of cells, comprising obtaining a sample of cells,
CC determining whether the cells express a plurality of markers, and
CC correlating the expression of the markers to the compound's ability to
CC modulate the activity of the cells; (2) a plurality of cell lines for
CC identifying polynucleotides and polypeptides whose expression levels
CC correlate with compound sensitivity or resistance of cells associated
CC with a disease state; and (3) identifying polynucleotides and
CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting

```
CC   polynucleotides or polypeptides that predict the sensitivity or
CC   resistance of cells associated with a disease state by using the
CC   expression pattern of the microarray. The polynucleotides and
CC   polypeptides have cytostatic activities, and can be used in gene therapy.
CC   The polynucleotides and polypeptides are useful in predicting the
CC   activity of compounds that interact with protein tyrosine kinases and/or
CC   protein tyrosine kinase pathways. These may be used in determining drug
CC   sensitivity in patients to allow the development of individualized
CC   genetic profiles which aid in treating diseases and disorders (e.g.
CC   cancer) based on patient response at a molecular level. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1073 ACATCCTTAGTAGAAGGTG 1091
              ||||||||  |  | ||||||
Db         21 ACATCCTTCGGATAAGGTG 3


RESULT 4196
AAD61847/c
ID   AAD61847 standard; DNA; 21 BP.
XX
AC   AAD61847;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Mouse MORC exon 1 specific RT-PCR primer.
XX
KW   Germ cell; MORC; male infertility; cancer; spermatogenesis;
KW   male contraceptive agent; gene therapy; PCR; primer; mouse; ss.
XX
OS   Mus musculus.
XX
PN   US6632934-B1.
XX
PD   14-OCT-2003.
XX
PF   30-SEP-1999;   99US-00409604.
XX
PR   30-SEP-1998;   98US-0102575P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Moreadith RW,  Zinn AR,  Watson ML,  Inoue N,  Hess KD,  Albright GM;
XX
DR   WPI; 2003-810560/76.
XX
PT   New nucleic acid segment encoding a male germ cell specific protein,
PT   designated MORC, useful for preparing a composition for treating
PT   infertility, germ cell cancer or microrchidia, altering spermatogenesis
PT   or as a male contraceptive.
XX
PS   Example 2; Col 84; 0pp; English.
XX
CC   The invention relates to an isolated male germ cell specific nucleic acid
CC   designated MORC. The nucleic acid segment is useful for preparing a
CC   composition for treating male infertility, germ cell cancer or
CC   microrchidia, altering spermatogenesis or as a male contraceptive agent.
CC   The invention is useful in gene therapy. The present sequence is MORC
CC   exon specific PCR primer used in the exemplification of the invention
XX
SQ   Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 4.1e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        611 CTGCTGCCCCACGCACACG 629
              ||| || |||||||  ||||
Db         19 CTGTTGGCCCACGCCCACG 1


RESULT 4197
ADE86000
ID   ADE86000 standard; RNA; 21 BP.
XX
AC   ADE86000;
XX
DT   29-JAN-2004  (first entry)
XX
DE   AU-rich element motif.
XX
KW   Human; AU-rich element; antiinflammatory; Hu-antigen R; ss.
XX
OS   Synthetic.
XX
PN   WO2003087815-A2.
XX
PD   23-OCT-2003.
XX
PF   16-APR-2003; 2003WO-EP004008.
XX
PR   17-APR-2002; 2002US-0373207P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
XX
PI   Auer M,  Meisner N,  Uhl V;
XX
DR   WPI; 2003-833795/77.
XX
PT   Identifying an agent having inhibitory effects on the complex-formation
PT   of ARE-containing mRNA and HuR protein, useful for treating disorders
PT   with aberrant production of a cytokine, growth factor, proto-oncogene or
PT   a viral protein.
XX
PS   Example 5; Page 20; 32pp; English.
XX
CC   The present sequence is that of an AU-rich element (ARE) motif. A 2-
CC   dimensional FIDA anisotropy analysis was performed to determine the
CC   affinity of human Hu-antigen R (HuR) for this, and other, AREs. Kd values
CC   of soluble and non-soluble forms of full-length HuR ADE85987 for the ARE
CC   were 0.4 +/- 0.05 and 23.47 +/- 8.92 nM, respectively. The RNA sequence
CC   motif NNUUNNUUU was identified as the binding site for HuR. The complex
CC   formation of an ARE-containing mRNA with an HuR protein induces the
CC   expression of various disease causing/mediating substances, such as
CC   inflammatory acting substances, e.g. cytokines, growth factors, proto-
CC   oncogenes and viral proteins. Agents which inhibit complex formation may
CC   thus prevent the expression of such substances and may be used in the
CC   treatment of e.g. inflammatory diseases. The invention provides an assay
CC   for identifying compounds with an inhibitory effect on selected HuR-ARE
CC   target interactions. A pharmaceutical composition comprising an agent
CC   identified by the assay can be used to treat a disorder having an
CC   aetiology associated with the production of a cytokine, growth factor
CC   proto-oncogene or a viral protein.
XX
SQ   Sequence 21 BP; 6 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   15.8%;  Pred. No. 4.1e+03;
  Matches    3;  Conservative   13;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2255 TTTATTTGCATATTTATTT 2273
              :::|:::   :|:::|:::
Db          2 UUUAUUUAUUUAUUUAUUU 20


RESULT 4198
ABL35690/c
ID   ABL35690 standard; DNA; 22 BP.
XX
```

```
AC   ABL35690;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 616.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .22
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 63; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 22 BP; 0 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              \\\\\\\\\ | || |||
Db         22 AAAAAAAAAAGAGAACAAA 4


RESULT 4199
AAT28054/c
ID   AAT28054 standard; DNA; 22 BP.
XX
AC   AAT28054;
XX
DT   31-DEC-1996  (first entry)
XX
DE   3'-primer L for human fibroblasts.
XX
KW   Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW   enhanced differential display; EDD; mRNA preparation; senescent cell;
KW   quiescent cell; dividing cell; senescence-related gene; gene expression;
KW   non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW   donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS   Synthetic.
XX
PN   WO9613610-A2.
XX
PD   09-MAY-1996.
XX
PF   24-AUG-1995;   95WO-US011230.
XX
PR   31-OCT-1994;   94US-00332420.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Hirsch KS,  Villeponteau B,  Feng J,  Funk W,  West MD;
XX
DR   WPI; 1996-251464/25.
XX
PT   Identifying, isolating and regulating senescence-related genes - useful
PT   to ameliorate problems associated with accumulation of senescent cells,
PT   e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS   Claim 6; Page 25; 135pp; English.
XX
CC   AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC   differential display (EDD), which is used in conjuncture with the method
CC   of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC   represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC   5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC   complementary to the poly-A tail of the mRNA. In the method of the
CC   invention, mRNA is isolated from a senescent cell, and a young quiescent
CC   cell, and the mRNAs are amplified in separate reaction mixtures. The
CC   amplified sequences are then separated by size or charge, and the
CC   products are analysed to identify a gene from young quiescent cells and
CC   dividing cells, that is present at a different level from senescent
CC   cells. The method can be used for the rapid and efficient identification
CC   and isolation of senescence-related genes and gene products, and to
CC   detect and distinguish between senescent and non-senescent cells. It can
CC   also be used to destroy cells expressing senescence specific (or related)
CC   gene products, and to screen for compounds capable of altering gene
CC   expression in senescent cells. The method can also be used to ameliorate
CC   problems associated with the accumulation of senescent cells such as age-
CC   related lipofuscin accumulation in the retina, and in the treatment of
CC   AIDS. Also, the method can be used to distinguish young cells from
CC   senescent cells in donor tissue, which is useful in removing senescent
CC   melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC   spots
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              ||||||||| |||||  ||
Db         22 TGAAAAAAAAAAAAGCTTG 4


RESULT 4200
AAT58494/c
ID   AAT58494 standard; DNA; 22 BP.
XX
AC   AAT58494;
XX
```

```
DT   24-MAR-1997  (first entry)
XX
DE   First primer #11 for use in enhanced differential display method.
XX
KW   Differential Display; Enhanced Differential Display; EDD; screening;
KW   gene expression; cell type; different; cell development; gene typing;
KW   identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS   Synthetic.
XX
PN   US5580726-A.
XX
PD   03-DEC-1996.
XX
PF   29-APR-1994;   94US-00235180.
XX
PR   29-APR-1994;   94US-00235180.
XX
PA   (GERO-) GERON CORP.
XX
PI   Linskens MHK,  Feng J,  Villeponteau B,  Funk W;
XX
DR   WPI; 1997-033564/03.
XX
PT   Detection of differentially expressed mRNA mols. - using two-step
PT   polymerase chain reaction amplification method.
XX
PS   Claim 9; Col 17; 15pp; English.
XX
CC   An improved method of Differential Display, named Enhanced Differential
CC   Display (EDD) has been designed as a technique for screening differences
CC   in gene expression between various cell types or between different stages
CC   of cell development. The technique is highly reproducible, leading to
CC   precise typing of the expressed genes in any given cell. EDD analysis
CC   permits the identification of novel genes involved in differentiation,
CC   aging and disease, and enables direct comparisons of different cell types
CC   and disease states. By using longer primers, and/or an alteration in the
CC   annealing temperatures, the number of false positives can be reduced.
CC   First, cDNA is prepared from total cellular RNA using 12 different 22-
CC   base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC   of pol II mRNA transcripts. The last two bases of each primer varies so
CC   as to anchor the primer to the 3' end of different sets of mRNAs. A
CC   second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC   randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC   amplification of a subset of cDNAs is carried out in a two step process
CC   using particular 5' and 3' primers. The amplified gene products can then
CC   be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              ||||||||| |||||  ||
Db         22 TGAAAAAAAAAAAAGCTTG 4


RESULT 4201
AAZ47352/c
ID   AAZ47352 standard; DNA; 22 BP.
XX
AC   AAZ47352;
XX
DT   06-MAR-2000  (first entry)
XX
DE   PCR primer L used in differential display analysis of Aspergillus oryzae.
XX
KW   Dopa decarboxylase; DDC2; DDC3; increased yield; hormone; receptor;
KW   antibody; reporter; enzyme; polypeptide production; primer; ss.
XX
OS   Synthetic.
XX
OS   Aspergillus oryzae.
XX
PN   WO9960136-A1.
XX
PD   25-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US010689.
XX
PR   15-MAY-1998;   98US-00079344.
PR   15-MAY-1998;   98US-00079601.
XX
PA   (NOVO ) NOVO NORDISK BIOTECH INC.
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Wahleithner J,  Christensen T;
XX
DR   WPI; 2000-062459/05.
XX
PT   New isolated Aspergillus oryzae signaling sequences, used to increase the
PT   production of polypeptides by recombinant host filamentous fungal cells.
XX
PS   Example 2; Page 35; 78pp; English.
XX
CC   Sequences AAZ47342-Z47353 are oligo(dT12N2) primers used in the
CC   differential display analysis of the Aspergillus oryzae strains HC4.01
CC   and 27. The strains were analysed to find the genetic basis for phenotype
CC   differences in the strains which are used in a method for producing a
CC   polypeptide in an enhanced amount. The method involves cultivating a
CC   mutant of a parent filamentous fungal cell in suitable nutrient medium.
CC   The mutant cell contains the nucleotide sequence encoding the polypeptide
CC   to be synthesised and one or more second nucleotide sequences encoding a
CC   DDC polypeptide (see AAZ47338-Z47339). The mutant cell produces more of
CC   the polypeptide than the parent cell and the polypeptide can be recovered
CC   from the nutrient medium of the mutant cell. The method can be used for
CC   the production of polypeptides such as hormones, receptors, antibodies,
CC   reporters or enzymes, e.g. an aminopeptidase, amylase, carbohydrase,
CC   carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin
CC   glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase,
CC   beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase,
CC   invertase, laccase, lipase, mannosidase, mutanase, oxidase, pectinolytic
CC   enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme,
CC   ribonuclease, transglutaminase or xylanase
XX
SQ   Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1977 TGAAAAAAAGAAAAGTGTG 1995
              ||||||||| |||||  ||
Db         22 TGAAAAAAAAAAAAGCTTG 4


RESULT 4202
AAH22195/c
ID   AAH22195 standard; DNA; 22 BP.
XX
AC   AAH22195;
XX
DT   20-AUG-2001  (first entry)
XX
DE   Human hepatocyte auxin related 3'-(T-rich) primer K.
XX
KW   Human; hepatocyte; auxin; liver; hepatitis; chronic hepatitis;
KW   liver fibrosis; cirrhosis; liver damage; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1280985-A.
XX
PD   24-JAN-2001.
XX
```

PF 20-JUL-1999; 99CN-00110801.
XX
PR 20-JUL-1999; 99CN-00110801.
XX
PA (HOSP-) HOSPITAL NO 458 CHINESE PLA.
XX
PI Kong X, Yi X, Zeng P;
XX
DR WPI; 2001-291394/31.
XX
PT Novel recombinant human hepatocyte auxin, its preparation and clinical
PT application.
XX
PS Example 1; Page 2 (disclosure); 13pp; Chinese.
XX
CC The present invention describes a differential indication PCR (polymerase
CC chain reaction) technique which is used to obtain a new complete gene
CC able to promote the repair of damaged liver cells and with substance
CC total length of 0.7 kb by screening the cDNA library of human foetal
CC liver. The induction expression of engineering bacteria, the separation
CC and cracking of inclusion body and the process for restoring and
CC decontaminating proteins are built up to obtain high purity recombinant
CC human hepatocyte auxin. It can externally promote the reproduction of
CC primary culture liver cells and liver cancer cells BEL-7402 and
CC internally promote the synthesis of mouse liver cell DNA after CCL4 is
CC damaged and the repair of liver cells. The method may be used to treat
CC serious hepatitis, chronic hepatitis, liver fibrosis and cirrhosis. The
CC present sequence represents a primer which is used in the exemplification
CC of the present invention
XX
SQ Sequence 22 BP; 3 A; 4 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 22;
Best Local Similarity 84.2%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1977 TGAAAAAAAGAAAAGTGTG 1995
||||||||| ||||| ||
Db 22 TGAAAAAAAAAAAAGCTTG 4

RESULT 4203
AAH28299/c
ID AAH28299 standard; RNA; 22 BP.
XX
AC AAH28299;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from neuronal cadherin gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 22 BP; 2 A; 1 C; 1 G; 0 T; 18 U; 0 Other;

Query Match 0.5%; Score 14.2; DB 1; Length 22;
Best Local Similarity 84.2%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1503 AGAAACACAGGAAATAAAA 1521
| ||| |||| ||||||||
Db 21 AAAAATACAGAAAATAAAA 3

RESULT 4204
AAH28297/c
ID AAH28297 standard; RNA; 22 BP.
XX
AC AAH28297;
XX
DT 05-SEP-2001 (first entry)
XX
DE 3' untranslated region sequence from neuronal cadherin gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a

```
CC   biological sample comprising mRNP complex with ligand that specifically
CC   binds a component of mRNP complex, separating mRNP complex by binding the
CC   ligand with a molecule specific for ligand, which is attached to the
CC   solid support and then collecting the mRNP complex by removing the
CC   complex from the support. The method is useful for in vivo partitioning
CC   of cellular mRNA protein complexes in a biological sample. The method is
CC   useful for determining the ribonomic profile of a cell which has numerous
CC   uses including monitoring of tumour development, state of growth or state
CC   of development, perturbations of a biological system such as disease,
CC   drug or toxin treatment and the state of cell aging or death,
CC   distinguishing ribonomic profiles among organisms, to discriminate
CC   between transcriptional and post-transcriptional contributions to gene
CC   expression and to track the movement of RNAs through RNP complexes,
CC   including the interactions of combinations of proteins with RNAs in RNP
CC   complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC   untranslated region (UTR) of mRNA of various genes. The sequences contain
CC   target sequences for RNA-binding proteins
XX
SQ   Sequence 22 BP; 2 A; 1 C; 1 G; 0 T; 18 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 22;
  Best Local Similarity   84.2%;  Pred. No. 4.3e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1503 AGAAACACAGGAAATAAAA 1521
              | ||| |||| ||||||||
Db         21 AAAAATACAGAAAATAAAA 3


RESULT 4205
ADD28129/c
ID   ADD28129 standard; DNA; 23 BP.
XX
AC   ADD28129;
XX
DT   15-JAN-2004  (first entry)
XX
DE   HIV-1 LTR region DNA fragment PNAI.
XX
KW   conjugate; peptide nucleic acid; PNA; transport mediator;
KW   addressing protein; nuclear importation; penetratin family; tat gene;
KW   rev gene; anti-HIV; primer; ss.
XX
OS   Human immunodeficiency virus 1.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    16. .17
FT                   /*tag= a
FT                   /note= "continous DNA sequence interrupted by an
FT                   undisclosed peptide linker"
FT   modified_base   21
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "Optionally pseudo-isocytosine or cytosine"
XX
PN   WO2003006065-A2.
XX
PD   23-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-DE002564.
XX
PR   12-JUL-2001; 2001DE-01033307.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
XX
PI   Braun K,  Waldeck W,  Pipkorn R,  Braun I,  Debus J;
XX
DR   WPI; 2003-256334/25.
XX
PT   New conjugate for delivery to the cell nucleus, useful for treating
PT   infection by human immune deficiency virus, comprises targeting peptides
PT   and peptide nucleic acid.
XX
PS   Disclosure; Page 8; 30pp; German.
XX
CC   This invention describes a novel conjugate for mediating specific
CC   transport to the cell nucleus of a peptide nucleic acid (PNA) that
CC   hybridizes to an HIV (human immune deficiency virus) gene, or part of it.
CC   The conjugate comprises a transport mediator for the cell membrane, an
CC   addressing protein or peptide for nuclear importation and the PNA being
CC   delivered. The transport mediator is a peptide or protein able to pass
CC   through the plasma membrane, particularly derived from the penetratin
CC   family protein. The PNA is designed to hybridize to at least part of the
CC   tat or rev genes and is especially targeted to the long terminal repeat
CC   or the polypurine tract, the central DNA flap, Nef, NCp7 or the gag slice
CC   site, at the RNA level. The conjugate has the structure transport
CC   mediator-addressing protein-PNA, particularly with a spacer (e.g.
CC   polylysine or a synthetic polymer) between addressing protein and PNA.
CC   The conjugate of the invention has anti-HIV activity. The transport
CC   mediator/addressing protein combination provide rapid and efficient
CC   transport of PNA to the nucleus and PNA is resistant to proteases and
CC   nucleases. The conjugate can be used in both early and late stages of
CC   infection. This sequence represents a fragment of HIV-1 LTR region used
CC   to construct PNA's used in the method of the invention.
XX
SQ   Sequence 23 BP; 0 A; 8 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 23;
  Best Local Similarity   84.2%;  Pred. No. 4.5e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1979 AAAAAAAGAAAAGTGTGTA 1997
              |||||||||||||| | | |
Db         19 AAAAAAAGAAAAGGGGGGA 1


RESULT 4206
ABQ73262/c
ID   ABQ73262 standard; DNA; 24 BP.
XX
AC   ABQ73262;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human ribosomal protein L312.54 PCR primer 2 SEQ ID NO:4.
XX
KW   Human; ribosomal protein L312.54; malignant tumour; inflammation;
KW   development disorder; immunological disease; haemopathy; HIV infection;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1339454-A.
XX
PD   13-MAR-2002.
XX
PF   23-AUG-2000; 2000CN-00119720.
XX
PR   23-AUG-2000; 2000CN-00119720.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-455356/49.
XX
PT   New polypeptide-ribosomal protein L312.54 and polynucleotide for encoding
PT   said polypeptide.
XX
PS   Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The present invention describes human ribosomal protein L312.54 (I). Also
CC   described is a process for producing (I) using DNA recombination
CC   technology. (I) and the polynucleotide encoding it can be used for
CC   treating various diseases, such as malignant tumour, inflammations,
CC   development disorder, immunological diseases, haemopathy and HIV
```

```
CC   infection. The present sequence represents a PCR primer for (I), which is
CC   used in an example from the present invention
XX
SQ   Sequence 24 BP; 3 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 24;
  Best Local Similarity   84.2%;  Pred. No. 4.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||| |  ||||
Db         24 AAAAAAAAAAACATTAAAA 6


RESULT 4207
ABL55230
ID   ABL55230 standard; DNA; 24 BP.
XX
AC   ABL55230;
XX
DT   14-JUN-2002  (first entry)
XX
DE   Pax protein 11 RT-PCR primer, SEQ ID NO:3.
XX
KW   Pax protein 11; human; recombinant production; malignant tumour; cancer;
KW   blood disease; HIV infection; human immunodeficiency virus;
KW   immune disorder; inflammatory condition; cytostatic; gene therapy;
KW   anti-HIV; antiinflammatory; immunomodulator; reverse transcription-PCR;
KW   RT-PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1329025-A.
XX
PD   02-JAN-2002.
XX
PF   21-JUN-2000; 2000CN-00116687.
XX
PR   21-JUN-2000; 2000CN-00116687.
XX
PA   (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-305398/35.
XX
PT   A novel polypeptide-Pax protein 11 and polynucleotide for coding this
PT   polypeptide.
XX
PS   Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC   The invention relates to pax protein 11 (AAM49189) and to nucleic acids
CC   encoding it (ABL55229). The protein has a molecular weight of 11 kD. The
CC   invention also relates to a method for the recombinant production of the
CC   protein, an antagonist of the protein, and the use of the protein, gene
CC   and antagonist in therapeutic applications. Pax protein 11 can be used in
CC   the treatment of a variety of diseases such as malignant tumours, blood
CC   diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC   and inflammatory conditions. Sequences ABL55230-ABL55231 represent
CC   reverse transcription-PCR (RT-PCR) primers used in an exemplification of
CC   the invention to isolate human pax protein 11 cDNA
XX
SQ   Sequence 24 BP; 19 A; 4 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 24;
  Best Local Similarity   84.2%;  Pred. No. 4.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                | |||||  ||| |||||||
Db          3 ACAAAAACAAACAAAAAAA 21


RESULT 4208
ABZ21302/c
ID   ABZ21302 standard; DNA; 24 BP.
XX
AC   ABZ21302;
XX
DT   24-FEB-2003  (first entry)
XX
DE   DNA binding protein (RCCI) 10.45 related primer 1.
XX
KW   DNA binding protein; RCCI; 10.45; malignant tumour; haemopathy;
KW   inflammation; immunological disease; human immunodeficiency virus; HIV;
KW   PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1351992-A.
XX
PD   05-JUN-2002.
XX
PF   02-NOV-2000; 2000CN-00127118.
XX
PR   02-NOV-2000; 2000CN-00127118.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-714393/78.
XX
PT   New DNA binding protein 10.45 polypeptide for treating malignant tumors,
PT   hemopathy, inflammations, immunological diseases, and human
PT   immunodeficiency virus infection.
XX
PS   Example 2; Page 16 (disclosure); 32pp; Chinese.
XX
CC   The present invention discloses a new kind of polypeptide, RCCI protein
CC   10.45, a polynucleotide encoding the polypeptide and a DNA recombination
CC   process to produce this polypeptide. The present invention also discloses
CC   applying the polypeptide to treat various diseases, such as malignant
CC   tumours, haemopathy, inflammations, immunological diseases, and human
CC   immunodeficiency virus (HIV) infection. The present invention also
CC   discloses an antagonist resisting the polypeptide and its treatment
CC   effect. The present invention also discloses application of the
CC   polynucleotide encoding the new RCCI protein 10.45. The current sequence
CC   represents a DNA binding RCCI protein 10.45 related PCR primer
XX
SQ   Sequence 24 BP; 0 A; 0 C; 6 G; 18 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 24;
  Best Local Similarity   84.2%;  Pred. No. 4.7e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                |||||  |||  ||||||||
Db         20 AAAAACAAACCAAAAAAAA 2


RESULT 4209
AAC95960
ID   AAC95960 standard; DNA; 25 BP.
XX
AC   AAC95960;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA HLA-B gene PCR primer #71.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 43; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 7 C; 0 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 4.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||   ||
Db          1 TTTTTTTTTTTTTTCCCAA 19


RESULT 4210
AAV06660/c
ID   AAV06660 standard; DNA; 25 BP.
XX
AC   AAV06660;
XX
DT   19-MAY-1998  (first entry)
XX
DE   Unlabeled oligonucleotide (P0).
XX
KW   Nucleoside analogue; polycyclic aromatic group; anthracene;
KW   phenanthracene; pyrene; stilbene; tetracene; pentacene;
KW   fluorescent label; ss.
XX
OS   Synthetic.
XX
PN   WO9743298-A1.
XX
PD   20-NOV-1997.
XX
PF   15-MAY-1997;   97WO-US008307.
XX
PR   15-MAY-1996;   96US-0017772P.
XX
PA   (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI   Kool ET;
XX
DR   WPI; 1998-008790/01.
XX
PT   Nucleoside derivatives comprising pyrene, anthracene or phenanthrene
PT   joined to C-1 atom of ribose or de:oxy:ribose sugar moiety - useful in
PT   preparation of fluorescently-labeled DNA.
XX
PS   Example 5; Fig 13; 114pp; English.
XX
CC   The present sequence represents an unlabeled oligonucleotide. The
CC   invention relates to a new nucleoside derivative comprising a pyrene,
CC   anthracene or phenanthrene joined to the C-1 atom of a sugar moiety
CC   through a carbon-carbon bond in either an alpha or a beta configuration,
CC   where the sugar moiety is ribose or deoxyribose. Also claimed is a
CC   phosphoramidite derivative of the above nucleoside derivative. The above
CC   nucleotide derivatives are useful in preparation of fluorescently-
CC   labeled DNA or RNA. These may be used in detection of target nucleic
CC   acids through hybridisation. The nucleoside analogues stack neatly into
CC   an RNA or DNA helix and do not interfere with binding properties of
CC   surrounding complementary bases
XX
SQ   Sequence 25 BP; 0 A; 6 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14.2;  DB 1;  Length 25;
  Best Local Similarity   84.2%;  Pred. No. 4.8e+03;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              ||| |||| ||||| ||||
Db         24 GAAGAAAAGAAAAAGAAAA 6


RESULT 4211
AAQ33508
ID   AAQ33508 standard; DNA; 14 BP.
XX
AC   AAQ33508;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1993  (first entry)
XX
DE   Sequence of microsatellite from clone AGLA206.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A1.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US000340.
XX
PR   15-JAN-1991;   91US-00642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification, gene
PT   mapping, and selective breeding.
XX
PS   Table 7; Page 131; 517pp; English.
XX
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a genomic library of bovine MboI DNA fragments of between 250
CC   and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of
CC   50 clones cross-hybridised. Assuming independent distribution of
CC   microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC   in the bovine genome is estimated at >100, 000. The sequence information
CC   for ca. 230 such bovine microsatellites is summarised in the
CC   specification and indexed herein (see below). The sequences upstream and
CC   downstream of the microsatellite sequence were used to generate the
CC   required PCR primers for in vitro amplification of the corresp.
CC   microsatellite (using the program OPTIPRIM). The microsatellites may be
```

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CC  used to identify individuals, for parentage testing, and in the genetic
CC  mapping of economic trait loci, or genes involved the determinism of
CC  economically important traits esp. in cattle, to allow selective
CC  breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC  field.)
XX
SQ  Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4212
AAQ33508/c
ID  AAQ33508 standard; DNA; 14 BP.
XX
AC  AAQ33508;
XX
DT  25-MAR-2003  (revised)
DT  02-FEB-1993  (first entry)
XX
DE  Sequence of microsatellite from clone AGLA206.
XX
KW  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW  genetic mapping; traits; amplification; ss.
XX
OS  Bos taurus.
XX
PN  WO9213102-A1.
XX
PD  06-AUG-1992.
XX
PF  15-JAN-1992;  92WO-US000340.
XX
PR  15-JAN-1991;  91US-00642342.
XX
PA  (GENM-) GENMARK.
XX
PI  Georges M,  Massey JM;
XX
DR  WPI; 1992-284684/34.
XX
PT  Polymorphic bovine DNA markers - used in genetic identification, gene
PT  mapping, and selective breeding.
XX
PS  Table 7; Page 131; 517pp; English.
XX
CC  The sequence is that of a bovine microsatellite sequence obtd. by
CC  screening a genomic library of bovine MboI DNA fragments of between 250
CC  and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of
CC  50 clones cross-hybridised. Assuming independent distribution of
CC  microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC  in the bovine genome is estimated at >100, 000. The sequence information
CC  for ca. 230 such bovine microsatellites is summarised in the
CC  specification and indexed herein (see below). The sequences upstream and
CC  downstream of the microsatellite sequence were used to generate the
CC  required PCR primers for in vitro amplification of the corresp.
CC  microsatellite (using the program OPTIPRIM). The microsatellites may be
CC  used to identify individuals, for parentage testing, and in the genetic
CC  mapping of economic trait loci, or genes involved the determinism of
CC  economically important traits esp. in cattle, to allow selective
CC  breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC  field.)
XX
SQ  Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 4213
AAV09230
ID  AAV09230 standard; DNA; 14 BP.
XX
AC  AAV09230;
XX
DT  07-JUL-1998  (first entry)
XX
DE  3' poly(T) primer 6.
XX
KW  3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW  oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
XX
OS  Synthetic.
XX
PN  WO9749832-A2.
XX
PD  31-DEC-1997.
XX
PF  23-JUN-1997;  97WO-CA000488.
XX
PR  21-JUN-1996;  96US-00667546.
PR  01-OCT-1996;  96US-00724466.
XX
PA  (TOOH ) UNIV QUEENS KINGSTON.
XX
PI  Petkovich PM;
XX
DR  WPI; 1998-077193/07.
XX
PT  Identifying DNA encoding inducible or suppressible cytochrome P450 - by
PT  screening for drugs which reduce the catabolism of retinoic acid, useful
PT  in cancer chemotherapy and the treatment of acne and psoriasis.
XX
PS  Example 1; Page 50; 113pp; English.
XX
CC  This is a 3' poly(T) PCR primer used in the amplification of the
CC  inducible cytochrome P450RAI gene which specifically metabolises a
CC  derivative of the retinoic acid (RA). The cytochrome P450 gene in general
CC  produces enzymes involved in the oxidative metabolism of endogenous and
CC  exogenous compounds. The cytochrome P450 nucleotide sequence can be used
CC  to induce or suppress the expression of its protein. P450RAI is highly
CC  induced by RA in cell lines and tissues. This allows for the development
CC  of a drug screen using promoters and nucleotide sequences to identify
CC  drugs which are useful for reducing the catabolism of RA
XX
SQ  Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTAA 14


RESULT 4214
AAV09234/c
ID  AAV09234 standard; DNA; 14 BP.
XX
AC  AAV09234;
XX
DT  07-JUL-1998  (first entry)
XX
DE  3' poly(T) primer 10.
```

XX
KW 3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
XX
OS Synthetic.
XX
PN WO9749832-A2.
XX
PD 31-DEC-1997.
XX
PF 23-JUN-1997; 97WO-CA000488.
XX
PR 21-JUN-1996; 96US-00667546.
PR 01-OCT-1996; 96US-00724466.
XX
PA (TOOH) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM;
XX
DR WPI; 1998-077193/07.
XX
PT Identifying DNA encoding inducible or suppressible cytochrome P450 - by
PT screening for drugs which reduce the catabolism of retinoic acid, useful
PT in cancer chemotherapy and the treatment of acne and psoriasis.
XX
PS Example 1; Page 51; 113pp; English.
XX
CC This is a 3' poly(T) PCR primer used in the amplification of the
CC inducible cytochrome P450RAI gene which specifically metabolises a
CC derivative of the retinoic acid (RA). The cytochrome P450 gene in general
CC produces enzymes involved in the oxidative metabolism of endogenous and
CC exogenous compounds. The cytochrome P450 nucleotide sequence can be used
CC to induce or suppress the expression of its protein. P450RAI is highly
CC induced by RA in cell lines and tissues. This allows for the development
CC of a drug screen using promoters and nucleotide sequences to identify
CC drugs which are useful for reducing the catabolism of RA
XX
SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAA 2797
||||||||||||||
Db 14 TGAAAAAAAAAAAA 1

RESULT 4215
AAV12222
ID AAV12222 standard; DNA; 14 BP.
XX
AC AAV12222;
XX
DT 22-JUN-1998 (first entry)
XX
DE Poly(T) oligonucleotide used in differential display PCR.
XX
KW Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid;
KW zebrafish; inhibitor; antisense; cancer; actinic keratosis;
KW oral leukoplakia; head tumour; neck tumour;
KW non-small cell lung carcinoma; basal cell carcinoma;
KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
KW therapy; diagnosis; screening; differential display; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9749815-A1.
XX
PD 31-DEC-1997.
XX
PF 23-JUN-1997; 97WO-CA000440.
XX
PR 21-JUN-1996; 96US-00667546.
PR 01-OCT-1996; 96US-00724466.
XX
PA (TOOH) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 1998-077178/07.
XX
PT Retinoid metabolising protein - useful to develop products to treat, e.g.
PT cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
PT ichthyosis.
XX
PS Disclosure; Page 14; 110pp; English.
XX
CC PolyT oligonucleotides (see AAV12217-28) were used in reverse
CC transcription reactions on polyA+ RNA isolated from the fins of control
CC or retinoic acid-treated zebrafish (Danio rerio). Several combinations of
CC the polyT primers were used with degenerate upstream primers (see
CC AAV12229-33) for differential display PCR. Bands demonstrating
CC reproducible differential amplifications were found using the primers
CC given in AAV12221 and AAV12231. This PCR product was reamplified (see
CC AAV12234-35). A differential display product (see AAV12213) which
CC exhibited a dependence on the presence of retinoic acid for its
CC expression was isolated, and was used to isolate a full-length clone (see
CC AAV12203) coding for a novel retinoid metabolising protein (see
CC AAW44159), designated zP450RAI
XX
SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAA 2188
||||||||||||||
Db 1 TTTTTTTTTTTTAA 14

RESULT 4216
AAV12226/c
ID AAV12226 standard; DNA; 14 BP.
XX
AC AAV12226;
XX
DT 22-JUN-1998 (first entry)
XX
DE Poly(T) oligonucleotide used in differential display PCR.
XX
KW Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid;
KW zebrafish; inhibitor; antisense; cancer; actinic keratosis;
KW oral leukoplakia; head tumour; neck tumour;
KW non-small cell lung carcinoma; basal cell carcinoma;
KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
KW therapy; diagnosis; screening; differential display; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9749815-A1.
XX
PD 31-DEC-1997.
XX
PF 23-JUN-1997; 97WO-CA000440.
XX
PR 21-JUN-1996; 96US-00667546.
PR 01-OCT-1996; 96US-00724466.
XX
PA (TOOH) UNIV QUEENS KINGSTON.
XX
PI Petkovich PM, White JA, Beckett BR, Jones G;
XX
DR WPI; 1998-077178/07.
XX

```
PT   Retinoid metabolising protein - useful to develop products to treat, e.g.
PT   cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
PT   ichthyosis.
XX
PS   Disclosure; Page 14; 110pp; English.
XX
CC   PolyT oligonucleotides (see AAV12217-28) were used in reverse
CC   transcription reactions on polyA+ RNA isolated from the fins of control
CC   or retinoic acid-treated zebrafish (Danio rerio). Several combinations of
CC   the polyT primers were used with degenerate upstream primers (see
CC   AAV12229-33) for differential display PCR. Bands demonstrating
CC   reproducible differential amplifications were found using the primers
CC   given in AAV12221 and AAV12231. This PCR product was reamplified (see
CC   AAV12234-35). A differential display product (see AAV12213) which
CC   exhibited a dependence on the presence of retinoic acid for its
CC   expression was isolated, and was used to isolate a full-length clone (see
CC   AAV12203) coding for a novel retinoid metabolising protein (see
CC   AAW44159), designated zP450RAI
XX
SQ   Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4217
AAT99552/c
ID   AAT99552 standard; DNA; 14 BP.
XX
AC   AAT99552;
XX
DT   08-JUN-1998  (first entry)
XX
DE   Oligo-dT primer used in epoxide hydrolase mEH gene RT-PCR.
XX
KW   Cell growth regulatory gene; mEH; microsomal epoxide hydrolase; rat;
KW   tumour; cancer; diagnosis; gene therapy; RT-PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9745542-A2.
XX
PD   04-DEC-1997.
XX
PF   29-MAY-1997;   97WO-US009584.
XX
PR   29-MAY-1996;   96US-0018557P.
XX
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Beaudry GA,  Bertelsen AH,  Galella E,  Madden SI;
XX
DR   WPI; 1998-032649/03.
XX
PT   DNA encoding mammalian growth response protein CGR11 or CGR19 - useful to
PT   suppress or diagnose cancer, also similar use of SM20 or mEH protein.
XX
PS   Example 2; Page 16; 46pp; English.
XX
CC   This oligo-dT primer was used with a random 10-mer primer (see AAT99553)
CC   in an RT-PCR amplification of rat embryo fibroblast REF-112 cell RNA.
CC   This was performed in order to identifying p53 regulated genes. One
CC   transcript that was upregulated specifically in cells harboring wild-type
CC   p53 protein was characterised. A previously known gene, mEH (microsomal
CC   epoxide hydrolase), was identified. 2 Novel cell growth regulatory genes,
CC   CGR11 (see AAV04008) and CGR19 (see AAV04010), were also isolated. These
CC   genes and the novel CGR11 and CGR19 growth regulatory proteins (see
CC   AAW38423 and AAW38425) can be used in methods for the diagnosis and
CC   treatment of cancer
XX
SQ   Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4218
AAX02696/c
ID   AAX02696 standard; DNA; 14 BP.
XX
AC   AAX02696;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Barley HPPD primer #2.
XX
KW   HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
KW   transgenic; plant cell; callus tissue, protoplast; electroporation;
KW   particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
KW   sunflower; tobacco; ss.
XX
OS   Hordeum vulgare.
XX
PN   DE19730066-A1.
XX
PD   21-JAN-1999.
XX
PF   14-JUL-1997;   97DE-01030066.
XX
PR   14-JUL-1997;   97DE-01030066.
XX
PA   (BADI ) BASF AG.
XX
PI   Seulberger H,  Lerchl J,  Schmidt R,  Kurpinska K,  Falk J;
XX
DR   WPI; 1999-096742/09.
XX
PT   DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing
PT   plants with increased vitamin E content, etc.
XX
PS   Example 1; Page 9; 26pp; German.
XX
CC   AAX02695-X02708 are primers used in the isolation of a novel barley
CC   (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
CC   protein is useful for plant transformation to produce transgenic plants
CC   especially where an expression cassette is introduced into a plant cell,
CC   callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
CC   transformation, electroporation or particle bombardment and where the
CC   plants are selected from soya, barley, wheat, oilseed rape, maize and
CC   sunflower, or where the DNA is expressed in tobacco plants, especially in
CC   leaves or seeds
XX
SQ   Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4219
AAX55057
ID   AAX55057 standard; DNA; 14 BP.
```

```
XX
AC   AAX55057;
XX
DT   05-JUL-1999  (first entry)
XX
DE   C/EBP-beta antisense oligonucleotide fragment.
XX
KW   Antisense oligonucleotide; multiple target; antisense treatment;
KW   impaired respiration; inflammation; lung disease;
KW   pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW   acute asthma; allergy; asthma; impeded respiration;
KW   respiratory distress syndrome; pain; cystic fibrosis;
KW   pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW   chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW   colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW   hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW   prostate cancer; ss.
XX
OS   Synthetic.
XX
PN   WO9913886-A1.
XX
PD   25-MAR-1999.
XX
PF   17-SEP-1998;   98WO-US019419.
XX
PR   17-SEP-1997;   97US-0059160P.
PR   09-JUN-1998;   98US-00093972.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 1999-229400/19.
XX
PT   New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT   vasoconstriction.
XX
PS   Disclosure; Page 70; 120pp; English.
XX
CC   The specification describes antisense oligonucleotides (AAX52869-X55271)
CC   directed against at least 2 mRNAs selected from target genes, coding and
CC   non-coding regions of RNAs corresponding to target genes, gene initiation
CC   codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
CC   -end and the juxta-section between coding and non-coding regions and all
CC   segments of RNAs encoding proteins associated with one or more diseases,
CC   conditions or mixtures. The antisense oligonucleotides may be derived
CC   from sequences AAX55272-74. These multiple target oligonucleotides
CC   (specifically AAX55180-271) can be used for the antisense treatment of
CC   diseases and conditions. Typical diseases and conditions are those
CC   associated with impaired respiration and inflammation, including lung
CC   diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC   acute asthma, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC   pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC   disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC   colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC   hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC   well as all types of cancers which may metastasize or have metastasized
CC   to the lungs, including breast and prostate cancer
XX
SQ   Sequence 14 BP; 0 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGG 66
              ||||||||||||||
Db          1 GGCGGGGGCGGCGG 14


RESULT 4220
AAX14689
ID   AAX14689 standard; DNA; 14 BP.
XX
AC   AAX14689;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix third strand of Esterase D gene nucleotides 962-975.
XX
KW   Triplex formation; DNA detection; triple helix; identification; bacteria;
KW   oncogene; virus; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 15-16; 168pp; English.
XX
CC   The present sequence represents a polynucleotide that is able to form a
CC   triple helix with a double stranded sequence. Cytosine bases in the
CC   present can be replaced with 5-methylcytosine for increased triplex
CC   stability. The present sequence is used in the assay of the invention,
CC   where it can be part of the anchor DNA or reporter DNA sequence. The
CC   assay comprises adding a sample containing double-stranded DNA test
CC   sequences to an aqueous medium containing at least one complex of anchor
CC   DNA, attached to a solid support, and reporter DNA, where either a part
CC   of the anchor DNA or reporter DNA is designed to form a triple-strand
CC   structure with part of the test sequence. Triplex formation results in
CC   displacement of the reporter DNA which is detected as an indication of
CC   the presence of the DNA test sequence. The method is used to detect DNA
CC   sequences, particularly for identification of bacteria (by detecting
CC   genes for ribosomal RNA) in clinical samples, but also detection of
CC   oncogenes and Hepatitis B virus
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4221
AAX14689/c
ID   AAX14689 standard; DNA; 14 BP.
XX
AC   AAX14689;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix third strand of Esterase D gene nucleotides 962-975.
XX
```

```
KW   Triplex formation; DNA detection; triple helix; identification; bacteria;
KW   oncogene; virus; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 15-16; 168pp; English.
XX
CC   The present sequence represents a polynucleotide that is able to form a
CC   triple helix with a double stranded sequence. Cytosine bases in the
CC   present can be replaced with 5-methylcytosine for increased triplex
CC   stability. The present sequence is used in the assay of the invention,
CC   where it can be part of the anchor DNA or reporter DNA sequence. The
CC   assay comprises adding a sample containing double-stranded DNA test
CC   sequences to an aqueous medium containing at least one complex of anchor
CC   DNA, attached to a solid support, and reporter DNA, where either a part
CC   of the anchor DNA or reporter DNA is designed to form a triple-strand
CC   structure with part of the test sequence. Triplex formation results in
CC   displacement of the reporter DNA which is detected as an indication of
CC   the presence of the DNA test sequence. The method is used to detect DNA
CC   sequences, particularly for identification of bacteria (by detecting
CC   genes for ribosomal RNA) in clinical samples, but also detection of
CC   oncogenes and Hepatitis B virus
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4222
AAX14688
ID   AAX14688 standard; DNA; 14 BP.
XX
AC   AAX14688;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 962-975 of Esterase D gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 15-16; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4223
AAX14688/c
ID   AAX14688 standard; DNA; 14 BP.
XX
AC   AAX14688;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 962-975 of Esterase D gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
```

```
PT   bacteria.
XX
PS   Disclosure; Col 15-16; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 4224
AAX57019
ID   AAX57019 standard; DNA; 14 BP.
XX
AC   AAX57019;
XX
DT   19-JUL-1999  (first entry)
XX
DE   WO9923258 oligonucleotide primer 1.
XX
KW   Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW   agglutination; bridging molecule; ss.
XX
OS   Synthetic.
XX
PN   WO9923258-A1.
XX
PD   14-MAY-1999.
XX
PF   30-OCT-1998;   98WO-US023267.
XX
PR   31-OCT-1997;   97US-0063969P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Weisburg WG,  Stull PD,  Reshatoff MR;
XX
DR   WPI; 1999-326994/27.
XX
PT   Optical detection of hybridization complexes for specific target nucleic
PT   acid sequences.
XX
PS   Example 1; Page 40; 46pp; English.
XX
CC   This invention describes a novel method for the visual detection of
CC   target nucleic acid presence in a sample. A preferred target is a
CC   Mycobacterium complex nucleic acid sequence. The detection method uses
CC   visual detection of a change in the hybridization without aid of
CC   instrumentation. Multiple copies of a target nucleic acid sequence are
CC   mixed with first and second detectable probes under hybridizing
CC   conditions favouring particle agglutination via a bridging molecule
CC   allowing for visual detection of the target nucleic acid sequence. The
CC   bridging molecule enhances or inhibits formation of a hybridization
CC   complex
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4225
AAX57019/c
ID   AAX57019 standard; DNA; 14 BP.
XX
AC   AAX57019;
XX
DT   19-JUL-1999  (first entry)
XX
DE   WO9923258 oligonucleotide primer 1.
XX
KW   Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW   agglutination; bridging molecule; ss.
XX
OS   Synthetic.
XX
PN   WO9923258-A1.
XX
PD   14-MAY-1999.
XX
PF   30-OCT-1998;   98WO-US023267.
XX
PR   31-OCT-1997;   97US-0063969P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Weisburg WG,  Stull PD,  Reshatoff MR;
XX
DR   WPI; 1999-326994/27.
XX
PT   Optical detection of hybridization complexes for specific target nucleic
PT   acid sequences.
XX
PS   Example 1; Page 40; 46pp; English.
XX
CC   This invention describes a novel method for the visual detection of
CC   target nucleic acid presence in a sample. A preferred target is a
CC   Mycobacterium complex nucleic acid sequence. The detection method uses
CC   visual detection of a change in the hybridization without aid of
CC   instrumentation. Multiple copies of a target nucleic acid sequence are
CC   mixed with first and second detectable probes under hybridizing
CC   conditions favouring particle agglutination via a bridging molecule
CC   allowing for visual detection of the target nucleic acid sequence. The
CC   bridging molecule enhances or inhibits formation of a hybridization
CC   complex
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4226
AAX19465
ID   AAX19465 standard; DNA; 14 BP.
XX
AC   AAX19465;
XX
```

DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:7.
XX
KW Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9907893-A1.
XX
PD 18-FEB-1999.
XX
PF 05-AUG-1998; 98WO-US016343.
XX
PR 08-AUG-1997; 97US-00908873.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Swisshelm K, Hosier S, Kubbies M;
XX
DR WPI; 1999-167454/14.
XX
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT polypeptide - useful for inducing a senescence phenotype in a cell.
XX
PS Example 1; Page 18; 44pp; English.
XX
CC The present invention describes human senescence factor p23. An
CC expression vector for p23 is useful for inducing a senescent phenotype in
CC a cell (preferably eukaryotic). This may help in regulating diseases,
CC including cancer, persistent inflammation, and various proliferative and
CC degenerative disorders. These transgenic cells are useful in gene therapy
CC for treating cancer, particularly where antisense oligonucleotides are
CC useful for blocking normal or mutant p23 expression in cancer cells or
CC other proliferating cells. Transgenic cells are also useful for producing
CC the p23 polypeptide in large quantities. The antibodies are useful for
CC raising antiserum against p23, and for identifying senescent cells in
CC culture and tissue biopsies. The p23 polynucleotides are useful for
CC modulating or altering p23 activity in a cell, and for identifying and
CC isolating the whole gene encoding p23, and variants of p23. Assays based
CC on p23 elements, which detect p23 levels and activity are useful as
CC diagnostic markers for staging tumours, determining prognosis, and/or
CC predicting therapeutic success. These elements also provide an assay for
CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The
CC isolation of the p23 polynucleotide permits the manipulation of malignant
CC growth in cancer. The present sequence represents a primer used in an
CC example from the present invention
XX
SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAA 2188
||||||||||||||
Db 1 TTTTTTTTTTTTAA 14

RESULT 4227
AAX19467/c
ID AAX19467 standard; DNA; 14 BP.
XX
AC AAX19467;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:9.
XX
KW Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9907893-A1.
XX
PD 18-FEB-1999.
XX
PF 05-AUG-1998; 98WO-US016343.
XX
PR 08-AUG-1997; 97US-00908873.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Swisshelm K, Hosier S, Kubbies M;
XX
DR WPI; 1999-167454/14.
XX
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT polypeptide - useful for inducing a senescence phenotype in a cell.
XX
PS Example 1; Page 18; 44pp; English.
XX
CC The present invention describes human senescence factor p23. An
CC expression vector for p23 is useful for inducing a senescent phenotype in
CC a cell (preferably eukaryotic). This may help in regulating diseases,
CC including cancer, persistent inflammation, and various proliferative and
CC degenerative disorders. These transgenic cells are useful in gene therapy
CC for treating cancer, particularly where antisense oligonucleotides are
CC useful for blocking normal or mutant p23 expression in cancer cells or
CC other proliferating cells. Transgenic cells are also useful for producing
CC the p23 polypeptide in large quantities. The antibodies are useful for
CC raising antiserum against p23, and for identifying senescent cells in
CC culture and tissue biopsies. The p23 polynucleotides are useful for
CC modulating or altering p23 activity in a cell, and for identifying and
CC isolating the whole gene encoding p23, and variants of p23. Assays based
CC on p23 elements, which detect p23 levels and activity are useful as
CC diagnostic markers for staging tumours, determining prognosis, and/or
CC predicting therapeutic success. These elements also provide an assay for
CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The
CC isolation of the p23 polynucleotide permits the manipulation of malignant
CC growth in cancer. The present sequence represents a primer used in an
CC example from the present invention
XX
SQ Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAA 2797
||||||||||||||
Db 14 TGAAAAAAAAAAAA 1

RESULT 4228
AAA34504
ID AAA34504 standard; DNA; 14 BP.
XX
AC AAA34504;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2193.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

```
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 540; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of the
CC   ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC   sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC   from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC   AAA33992) are specifically claimed ONs from the present invention. N.B.
CC   Sequences given in the disclosure of the present invention do not match
CC   up with their corresponding SEQ ID NO: sequences given in the sequence
CC   listing
XX
SQ   Sequence 14 BP; 0 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGG 66
              ||||||||||||||
Db          1 GGCGGGGGCGGCGG 14


RESULT 4229
AAF20626
ID   AAF20626 standard; DNA; 14 BP.
XX
AC   AAF20626;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human C/EBP polynucleotide fragment #2193.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US008020.
XX
PR   06-APR-1999;   99US-0127958P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not trigger
PT   adenosine receptors during metabolism, useful e.g. for treating cancers
PT   and respiratory obstructions.
XX
PS   Claim 14; Page 264; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 14 BP; 0 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGG 66
              ||||||||||||||
Db          1 GGCGGGGGCGGCGG 14
```

```
RESULT 4230
AAA62349
ID   AAA62349 standard; DNA; 14 BP.
XX
AC   AAA62349;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   10
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   12
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 16; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4231
AAA62349/c
ID   AAA62349 standard; DNA; 14 BP.
XX
AC   AAA62349;
XX
DT   06-NOV-2000  (first entry)
XX
DE   Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX
KW   Conformationally-locked oligonucleotide; antisense inhibitor;
KW   bicyclic sugar nucleoside analogue; gene probe; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   9
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   10
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
FT   modified_base   12
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX
PN   US6083482-A.
XX
PD   04-JUL-2000.
XX
PF   11-MAY-1999;   99US-00309742.
XX
PR   11-MAY-1999;   99US-00309742.
XX
PA   (ICNC ) ICN PHARM INC.
XX
PI   Wang G;
XX
DR   WPI; 2000-451496/39.
```

```
XX
PT   New conformationally restricted 3',5'-bridged nucleosides and
PT   oligonucleotides useful as antisense therapeutics or as gene-specific
PT   diagnostics.
XX
PS   Example 20; Col 16; 10pp; English.
XX
CC   The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
CC   C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in
CC   the sequence were incorporated by phosphoramidite chemistry using a DNA
CC   synthesiser. Bicyclic sugar nucleosides are conformationally restricted
CC   3',5'-bridged nucleosides which can be used as building blocks for
CC   oligonucleotides. Oligonucleotides can be produced that have certain,
CC   desired, geometrical shapes and entropy advantages. They may have
CC   superior hybridisation to DNA and RNA, and excellent biological
CC   stability. The conformationally-modified oligonucleotides may be useful
CC   as antisense inhibitors of gene expression or as gene probes, and may
CC   therefore be used in antisense therapeutics or gene-specific diagnostics
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4232
AAF84160
ID   AAF84160 standard; DNA; 14 BP.
XX
AC   AAF84160;
XX
DT   08-JUN-2001  (first entry)
XX
DE   Oligonucleotide #2.
XX
KW   Light responsive oligonucleotide; light irradiation; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200121637-A1.
XX
PD   29-MAR-2001.
XX
PF   20-SEP-2000; 2000WO-JP006415.
XX
PR   20-SEP-1999;   99JP-00304479.
XX
PA   (KOMI/) KOMIYAMA M.
XX
PI   Komiyama M,  Asanuma H,  Yoshida T;
XX
DR   WPI; 2001-266061/27.
XX
PT   Light-responsive oligonucleotides, useful in controlling DNA synthesis
PT   and gene expression, have structural isomerization on irradiation, and
PT   reversible change in melting temperature of the formed double or triple
PT   strands.
XX
PS   Example 3; Page 20; 43pp; Japanese.
XX
CC   The present invention relates to light responsive oligonucleotide, which
CC   contain one or more organic groups which can undergo structural
CC   isomerisation upon irradiation at a specific wavelength. The melting
CC   temperature of a double-strand formed by the light-responsive
CC   oligonucleotide, and another oligonucleotide complementary to the light-
CC   responsive oligonucleotide, reversibly changes depending on light
CC   irradiation. The oligonucleotides are useful in biotechnology, e.g. in
CC   controlling DNA elongation, gene expression, amplification and
CC   transcription, and for efficient gene diagnosis and gene therapy. The
CC   present sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4233
AAF84160/c
ID   AAF84160 standard; DNA; 14 BP.
XX
AC   AAF84160;
XX
DT   08-JUN-2001  (first entry)
XX
DE   Oligonucleotide #2.
XX
KW   Light responsive oligonucleotide; light irradiation; gene therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200121637-A1.
XX
PD   29-MAR-2001.
XX
PF   20-SEP-2000; 2000WO-JP006415.
XX
PR   20-SEP-1999;   99JP-00304479.
XX
PA   (KOMI/) KOMIYAMA M.
XX
PI   Komiyama M,  Asanuma H,  Yoshida T;
XX
DR   WPI; 2001-266061/27.
XX
PT   Light-responsive oligonucleotides, useful in controlling DNA synthesis
PT   and gene expression, have structural isomerization on irradiation, and
PT   reversible change in melting temperature of the formed double or triple
PT   strands.
XX
PS   Example 3; Page 20; 43pp; Japanese.
XX
CC   The present invention relates to light responsive oligonucleotide, which
CC   contain one or more organic groups which can undergo structural
CC   isomerisation upon irradiation at a specific wavelength. The melting
CC   temperature of a double-strand formed by the light-responsive
CC   oligonucleotide, and another oligonucleotide complementary to the light-
CC   responsive oligonucleotide, reversibly changes depending on light
CC   irradiation. The oligonucleotides are useful in biotechnology, e.g. in
CC   controlling DNA elongation, gene expression, amplification and
CC   transcription, and for efficient gene diagnosis and gene therapy. The
CC   present sequence is an oligonucleotide used in the present invention
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4234
AAC83821
```

```
ID   AAC83821 standard; RNA; 14 BP.
XX
AC   AAC83821;
XX
DT   28-FEB-2001  (first entry)
XX
DE   RNA oligonucleotide #1 used in a binding assay.
XX
KW   L-ribo-configurated Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.
XX
OS   Unidentified.
XX
PN   WO200066604-A2.
XX
PD   09-NOV-2000.
XX
PF   04-MAY-2000; 2000WO-DK000225.
XX
PR   04-MAY-1999;   99DK-00000603.
PR   01-SEP-1999;   99DK-00001225.
PR   11-JAN-2000; 2000DK-00000032.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J;
XX
DR   WPI; 2001-060972/07.
XX
PT   Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides, useful
PT   for therapeutic purposes e.g. in the construction of oligonucleotides, as
PT   substrates for nucleic acids polymerases and in RNA mediated catalytic
PT   processes.
XX
PS   Example 11; Page 56; 79pp; English.
XX
CC   The present invention relates to an oligomer comprising L-ribo-
CC   configurated Locked Nucleoside Analogues (L-ribo-LNA analogues). The
CC   present sequence is an RNA oligonucleotide. Binding studies of the L-ribo
CC   -LNA analogues towards the present sequence were carried out, to
CC   determine the thermostability of the L-ribo-LNA analogues. The analogs of
CC   the present invention have a variety of uses e.g. in the preparation of
CC   conjugates of the L-ribo-LNA modified oligonucleotides (oligomers)
XX
SQ   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4235
AAC83821/c
ID   AAC83821 standard; RNA; 14 BP.
XX
AC   AAC83821;
XX
DT   28-FEB-2001  (first entry)
XX
DE   RNA oligonucleotide #1 used in a binding assay.
XX
KW   L-ribo-configurated Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.
XX
OS   Unidentified.
XX
PN   WO200066604-A2.
XX
PD   09-NOV-2000.
XX
PF   04-MAY-2000; 2000WO-DX000225.
XX
PR   04-MAY-1999;   99DK-00000603.
PR   01-SEP-1999;   99DK-00001225.
PR   11-JAN-2000; 2000DK-00000032.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J;
XX
DR   WPI; 2001-060972/07.
XX
PT   Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides, useful
PT   for therapeutic purposes e.g. in the construction of oligonucleotides, as
PT   substrates for nucleic acids polymerases and in RNA mediated catalytic
PT   processes.
XX
PS   Example 11; Page 56; 79pp; English.
XX
CC   The present invention relates to an oligomer comprising L-ribo-
CC   configurated Locked Nucleoside Analogues (L-ribo-LNA analogues). The
CC   present sequence is an RNA oligonucleotide. Binding studies of the L-ribo
CC   -LNA analogues towards the present sequence were carried out, to
CC   determine the thermostability of the L-ribo-LNA analogues. The analogs of
CC   the present invention have a variety of uses e.g. in the preparation of
CC   conjugates of the L-ribo-LNA modified oligonucleotides (oligomers)
XX
SQ   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 4236
ABL88471
ID   ABL88471 standard; DNA; 14 BP.
XX
AC   ABL88471;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Oligo dT 3P1 primer 1.
XX
KW   Pain; analgesic; gene therapy; neurological disorder;
KW   neurodegenerative disease; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200212338-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-EP009011.
XX
PR   03-AUG-2000; 2000DE-01037759.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Gillen C,  Wetzels I,  Wnendt S,  Weihe E,  Schaefer MK;
XX
DR   WPI; 2002-257469/30.
XX
PT   Identifying pain-regulating compounds, useful for treating chronic pain
PT   and for diagnosis, by measuring binding of compounds to specific peptides
PT   and proteins.
XX
PS   Example 1; Page 62; 213pp; German.
XX
CC   The invention relates to identifying pain-regulating substances (A)
```

CC comprises (i) incubating a test substance with a cell (or preparation
CC from it) that has synthesised a peptide or protein (B) and (ii) measuring
CC either binding of the test substance to (B) or some functional parameter
CC that is altered by this binding. The method is useful for identifying
CC pain-regulating substances (A) with analgesic activity. (A) along with
CC nucleic acid (ABL88411-ABL88441) that encode proteins (B, ABB85006-
CC ABB85037) that interact with (A); (B); vectors containing the nucleic
CC acid; antibodies against (B); cells that express (B) and agents that bind
CC to (B), are all useful for treating pain, particularly chronic pain,
CC including use in gene therapy. The same materials can also be used for
CC diagnosis, e.g. of neurological and neurodegenerative diseases. The
CC present sequence is that of a PCR primer, used in examples of the
CC invention
XX
SQ Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAA 2188
||||||||||||||
Db 1 TTTTTTTTTTTTAA 14

RESULT 4237
ABQ83278
ID ABQ83278 standard; DNA; 14 BP.
XX
AC ABQ83278;
XX
DT 18-JAN-2003 (first entry)
XX
DE EGI cDNA tag related oligonucleotide SEQ ID NO:51.
XX
KW cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
PN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
XX
PA (KURE) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX
DR WPI; 2002-759896/82.
XX
PT Construction of cDNA tags for identifying expressed genes with specific
PT linkers and recognition sequences, applicable in gene expression
PT analysis, disease diagnosis and identifying target for gene therapy.
XX
PS Example 1; Page 24; 59pp; Japanese.
XX
CC The present invention describes a method for constructing a cDNA tag for
CC identifying an expressed gene. The method comprises: (a) preparation of
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC linker Y ligated material; and (e) cleaving the amplification product.
CC The method can be used for the construction of cDNA tags for identifying
CC expressed genes, which is applicable in gene expression analysis, disease
CC diagnosis and identifying target for gene therapy, including the
CC clarification of difference in function or morphology of cells under
CC physiological or pathological conditions. The cDNA or cells for assay can
CC be specifically expressed, with reproducibility and accuracy in the
CC detection of genes. The present sequence represents an expressed gene
CC identification (EGI) cDNA tag related oligonucleotide which is used in an
CC example from the present invention
XX
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTT 2179
||||||||||||||
Db 1 TTTTTTTTTTTTTT 14

RESULT 4238
ABQ83278/c
ID ABQ83278 standard; DNA; 14 BP.
XX
AC ABQ83278;
XX
DT 18-JAN-2003 (first entry)
XX
DE EGI cDNA tag related oligonucleotide SEQ ID NO:51.
XX
KW cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
PN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
XX
PA (KURE) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX
DR WPI; 2002-759896/82.
XX
PT Construction of cDNA tags for identifying expressed genes with specific
PT linkers and recognition sequences, applicable in gene expression
PT analysis, disease diagnosis and identifying target for gene therapy.
XX
PS Example 1; Page 24; 59pp; Japanese.
XX
CC The present invention describes a method for constructing a cDNA tag for
CC identifying an expressed gene. The method comprises: (a) preparation of
CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC linker Y ligated material; and (e) cleaving the amplification product.
CC The method can be used for the construction of cDNA tags for identifying
CC expressed genes, which is applicable in gene expression analysis, disease
CC diagnosis and identifying target for gene therapy, including the
CC clarification of difference in function or morphology of cells under
CC physiological or pathological conditions. The cDNA or cells for assay can
CC be specifically expressed, with reproducibility and accuracy in the
CC detection of genes. The present sequence represents an expressed gene
CC identification (EGI) cDNA tag related oligonucleotide which is used in an
CC example from the present invention
XX
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;

```
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4239
ABQ83276/c
ID   ABQ83276 standard; DNA; 14 BP.
XX
AC   ABQ83276;
XX
DT   18-JAN-2003  (first entry)
XX
DE   EGI cDNA tag related oligonucleotide SEQ ID NO:49.
XX
KW   cDNA tag; identification; gene expression analysis; linker;
KW   expressed gene identification; EGI; ss.
XX
OS   Synthetic.
XX
PN   WO200274951-A1.
XX
PD   26-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-JP002338.
XX
PR   15-MAR-2001; 2001JP-00073959.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
PA   (YAMA/) YAMAMOTO M.
PA   (YAMA/) YAMAMOTO N.
XX
PI   Yamamoto M,  Yamamoto N,  Hirose K,  Kasai J;
XX
DR   WPI; 2002-759896/82.
XX
PT   Construction of cDNA tags for identifying expressed genes with specific
PT   linkers and recognition sequences, applicable in gene expression
PT   analysis, disease diagnosis and identifying target for gene therapy.
XX
PS   Example 1; Page 24; 59pp; Japanese.
XX
CC   The present invention describes a method for constructing a cDNA tag for
CC   identifying an expressed gene. The method comprises: (a) preparation of
CC   complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC   cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC   fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC   linker Y ligated material; and (e) cleaving the amplification product.
CC   The method can be used for the construction of cDNA tags for identifying
CC   expressed genes, which is applicable in gene expression analysis, disease
CC   diagnosis and identifying target for gene therapy, including the
CC   clarification of difference in function or morphology of cells under
CC   physiological or pathological conditions. The cDNA or cells for assay can
CC   be specifically expressed, with reproducibility and accuracy in the
CC   detection of genes. The present sequence represents an expressed gene
CC   identification (EGI) cDNA tag related oligonucleotide which is used in an
CC   example from the present invention
XX
SQ   Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 4240
ABQ83275
ID   ABQ83275 standard; DNA; 14 BP.
XX
AC   ABQ83275;
XX
DT   18-JAN-2003  (first entry)
XX
DE   EGI cDNA tag related oligonucleotide SEQ ID NO:48.
XX
KW   cDNA tag; identification; gene expression analysis; linker;
KW   expressed gene identification; EGI; ss.
XX
OS   Synthetic.
XX
PN   WO200274951-A1.
XX
PD   26-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-JP002338.
XX
PR   15-MAR-2001; 2001JP-00073959.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
PA   (YAMA/) YAMAMOTO M.
PA   (YAMA/) YAMAMOTO N.
XX
PI   Yamamoto M,  Yamamoto N,  Hirose K,  Kasai J;
XX
DR   WPI; 2002-759896/82.
XX
PT   Construction of cDNA tags for identifying expressed genes with specific
PT   linkers and recognition sequences, applicable in gene expression
PT   analysis, disease diagnosis and identifying target for gene therapy.
XX
PS   Example 1; Page 24; 59pp; Japanese.
XX
CC   The present invention describes a method for constructing a cDNA tag for
CC   identifying an expressed gene. The method comprises: (a) preparation of
CC   complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC   cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC   fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC   linker Y ligated material; and (e) cleaving the amplification product.
CC   The method can be used for the construction of cDNA tags for identifying
CC   expressed genes, which is applicable in gene expression analysis, disease
CC   diagnosis and identifying target for gene therapy, including the
CC   clarification of difference in function or morphology of cells under
CC   physiological or pathological conditions. The cDNA or cells for assay can
CC   be specifically expressed, with reproducibility and accuracy in the
CC   detection of genes. The present sequence represents an expressed gene
CC   identification (EGI) cDNA tag related oligonucleotide which is used in an
CC   example from the present invention
XX
SQ   Sequence 14 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTA 2187
              ||||||||||||||
Db          1 TTTTTTTTTTTTTA 14


RESULT 4241
ABQ83271/c
ID   ABQ83271 standard; DNA; 14 BP.
XX
AC   ABQ83271;
XX
DT   18-JAN-2003  (first entry)
XX
DE   EGI cDNA tag related oligonucleotide SEQ ID NO:44.
XX
KW   cDNA tag; identification; gene expression analysis; linker;
```

```
KW   expressed gene identification; EGI; ss.
XX
OS   Synthetic.
XX
PN   WO200274951-A1.
XX
PD   26-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-JP002338.
XX
PR   15-MAR-2001; 2001JP-00073959.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
PA   (YAMA/) YAMAMOTO M.
PA   (YAMA/) YAMAMOTO N.
XX
PI   Yamamoto M,  Yamamoto N,  Hirose K,  Kasai J;
XX
DR   WPI; 2002-759896/82.
XX
PT   Construction of cDNA tags for identifying expressed genes with specific
PT   linkers and recognition sequences, applicable in gene expression
PT   analysis, disease diagnosis and identifying target for gene therapy.
XX
PS   Example 1; Page 24; 59pp; Japanese.
XX
CC   The present invention describes a method for constructing a cDNA tag for
CC   identifying an expressed gene. The method comprises: (a) preparation of
CC   complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC   cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC   fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC   linker Y ligated material; and (e) cleaving the amplification product.
CC   The method can be used for the construction of cDNA tags for identifying
CC   expressed genes, which is applicable in gene expression analysis, disease
CC   diagnosis and identifying target for gene therapy, including the
CC   clarification of difference in function or morphology of cells under
CC   physiological or pathological conditions. The cDNA or cells for assay can
CC   be specifically expressed, with reproducibility and accuracy in the
CC   detection of genes. The present sequence represents an expressed gene
CC   identification (EGI) cDNA tag related oligonucleotide which is used in an
CC   example from the present invention
XX
SQ   Sequence 14 BP; 13 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTT 2178
              ||||||||||||||
Db         14 CTTTTTTTTTTTTT 1


RESULT 4242
ABQ83269
ID   ABQ83269 standard; DNA; 14 BP.
XX
AC   ABQ83269;
XX
DT   18-JAN-2003  (first entry)
XX
DE   EGI cDNA tag related oligonucleotide SEQ ID NO:42.
XX
KW   cDNA tag; identification; gene expression analysis; linker;
KW   expressed gene identification; EGI; ss.
XX
OS   Synthetic.
XX
PN   WO200274951-A1.
XX
PD   26-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-JP002338.
XX
PR   15-MAR-2001; 2001JP-00073959.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
PA   (YAMA/) YAMAMOTO M.
PA   (YAMA/) YAMAMOTO N.
XX
PI   Yamamoto M,  Yamamoto N,  Hirose K,  Kasai J;
XX
DR   WPI; 2002-759896/82.
XX
PT   Construction of cDNA tags for identifying expressed genes with specific
PT   linkers and recognition sequences, applicable in gene expression
PT   analysis, disease diagnosis and identifying target for gene therapy.
XX
PS   Example 1; Page 24; 59pp; Japanese.
XX
CC   The present invention describes a method for constructing a cDNA tag for
CC   identifying an expressed gene. The method comprises: (a) preparation of
CC   complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC   cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC   fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC   linker Y ligated material; and (e) cleaving the amplification product.
CC   The method can be used for the construction of cDNA tags for identifying
CC   expressed genes, which is applicable in gene expression analysis, disease
CC   diagnosis and identifying target for gene therapy, including the
CC   clarification of difference in function or morphology of cells under
CC   physiological or pathological conditions. The cDNA or cells for assay can
CC   be specifically expressed, with reproducibility and accuracy in the
CC   detection of genes. The present sequence represents an expressed gene
CC   identification (EGI) cDNA tag related oligonucleotide which is used in an
CC   example from the present invention
XX
SQ   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4243
ABQ83269/c
ID   ABQ83269 standard; DNA; 14 BP.
XX
AC   ABQ83269;
XX
DT   18-JAN-2003  (first entry)
XX
DE   EGI cDNA tag related oligonucleotide SEQ ID NO:42.
XX
KW   cDNA tag; identification; gene expression analysis; linker;
KW   expressed gene identification; EGI; ss.
XX
OS   Synthetic.
XX
PN   WO200274951-A1.
XX
PD   26-SEP-2002.
XX
PF   13-MAR-2002; 2002WO-JP002338.
XX
PR   15-MAR-2001; 2001JP-00073959.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
PA   (YAMA/) YAMAMOTO M.
PA   (YAMA/) YAMAMOTO N.
XX
PI   Yamamoto M,  Yamamoto N,  Hirose K,  Kasai J;
XX
```

```
DR   WPI; 2002-759896/82.
XX
PT   Construction of cDNA tags for identifying expressed genes with specific
PT   linkers and recognition sequences, applicable in gene expression
PT   analysis, disease diagnosis and identifying target for gene therapy.
XX
PS   Example 1; Page 24; 59pp; Japanese.
XX
CC   The present invention describes a method for constructing a cDNA tag for
CC   identifying an expressed gene. The method comprises: (a) preparation of
CC   complementary deoxyribonucleic acid; (b) producing cDNA fragment by
CC   cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
CC   fragment ligated material; (d) amplification of the linker X-cDNA tag-
CC   linker Y ligated material; and (e) cleaving the amplification product.
CC   The method can be used for the construction of cDNA tags for identifying
CC   expressed genes, which is applicable in gene expression analysis, disease
CC   diagnosis and identifying target for gene therapy, including the
CC   clarification of difference in function or morphology of cells under
CC   physiological or pathological conditions. The cDNA or cells for assay can
CC   be specifically expressed, with reproducibility and accuracy in the
CC   detection of genes. The present sequence represents an expressed gene
CC   identification (EGI) cDNA tag related oligonucleotide which is used in an
CC   example from the present invention
XX
SQ   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         14 TTTTTTTTTTTTTT 1


RESULT 4244
AAD24496/c
ID   AAD24496 standard; DNA; 14 BP.
XX
AC   AAD24496;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Retinoid-regulated gene isolating poly(T) PCR primer #10.
XX
KW   Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW   cytochrome P450; prostate cancer; drug screening; PCR primer;
KW   retinoid-regulated gene; ss.
XX
OS   Unidentified.
XX
PN   US6306624-B1.
XX
PD   23-OCT-2001.
XX
PF   25-JUN-1997;   97US-00882164.
XX
PR   21-JUN-1996;   96US-00667546.
PR   01-OCT-1996;   96US-00724466.
PR   23-JUN-1997;   97WO-CA000440.
XX
PA   (TOOH ) UNIV QUEENS KINGSTON.
XX
PI   Petkovich PM,  White JA,  Beckett BR,  Jones G;
XX
DR   WPI; 2002-033254/04.
XX
PT   New DNA fragments having promoter activity, useful in retinoid
PT   metabolism, as well as in producing retinoic acid metabolizing cytochrome
PT   P450s that are useful as targets for the treatment of certain cancers.
XX
PS   Disclosure; Col 13; 75pp; English.
XX
CC   The present invention relates to retinoid (e.g., retinoic acid (RA),
CC   vitamin A) metabolising proteins and nucleic acid sequences encoding
CC   them. RA metabolising proteins contain a haeme-binding motif which is
CC   characteristic of the group of proteins known as cytochrome P450s. The
CC   sequences of the invention are useful in retinoid metabolism and in
CC   producing retinoic acid metabolising cytochrome P450s. They are
CC   particularly useful as targets for the treatment of certain cancers such
CC   as prostate cancer. The invention also relates to a method of screening
CC   drugs for their effect on activity of RA inducible proteins. The present
CC   DNA sequence is poly(T) PCR primer which is used for isolating retinoid
CC   regulating genes by differential display of mRNAs
XX
SQ   Sequence 14 BP; 1 A; 1 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match              0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4245
AAD24492
ID   AAD24492 standard; DNA; 14 BP.
XX
AC   AAD24492;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Retinoid-regulated gene isolating poly(T) PCR primer #6.
XX
KW   Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW   cytochrome P450; prostate cancer; drug screening; PCR primer;
KW   retinoid-regulated gene; ss.
XX
OS   Unidentified.
XX
PN   US6306624-B1.
XX
PD   23-OCT-2001.
XX
PF   25-JUN-1997;   97US-00882164.
XX
PR   21-JUN-1996;   96US-00667546.
PR   01-OCT-1996;   96US-00724466.
PR   23-JUN-1997;   97WO-CA000440.
XX
PA   (TOOH ) UNIV QUEENS KINGSTON.
XX
PI   Petkovich PM,  White JA,  Beckett BR,  Jones G;
XX
DR   WPI; 2002-033254/04.
XX
PT   New DNA fragments having promoter activity, useful in retinoid
PT   metabolism, as well as in producing retinoic acid metabolizing cytochrome
PT   P450s that are useful as targets for the treatment of certain cancers.
XX
PS   Disclosure; Col 13; 75pp; English.
XX
CC   The present invention relates to retinoid (e.g., retinoic acid (RA),
CC   vitamin A) metabolising proteins and nucleic acid sequences encoding
CC   them. RA metabolising proteins contain a haeme-binding motif which is
CC   characteristic of the group of proteins known as cytochrome P450s. The
CC   sequences of the invention are useful in retinoid metabolism and in
CC   producing retinoic acid metabolising cytochrome P450s. They are
CC   particularly useful as targets for the treatment of certain cancers such
CC   as prostate cancer. The invention also relates to a method of screening
CC   drugs for their effect on activity of RA inducible proteins. The present
CC   DNA sequence is poly(T) PCR primer which is used for isolating retinoid
CC   regulating genes by differential display of mRNAs
XX
```

```
SQ   Sequence 14 BP; 2 A; 0 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||||
Db          1 TTTTTTTTTTTTAA 14


RESULT 4246
ABA93701
ID   ABA93701 standard; DNA; 14 BP.
XX
AC   ABA93701;
XX
DT   30-APR-2002  (first entry)
XX
DE   Light responsive oligonucleotide (X1)T14.
XX
KW   Light responsive; detection; single nucleotide polymorphism; SNP;
KW   irradiation; ss.
XX
OS   Synthetic.
XX
PN   JP2001346579-A.
XX
PD   18-DEC-2001.
XX
PF   02-JUN-2000; 2000JP-00165441.
XX
PR   02-JUN-2000; 2000JP-00165441.
XX
PA   (KOMI/) KOMIYAMA S.
PA   (ASAN/) ASANUMA H.
XX
DR   WPI; 2002-145181/19.
XX
PT   Detecting single nucleotide polymorphism for expressing sensitivity
PT   information of diseases and drugs, comprises using a new oligonucleotide.
XX
PS   Example 3; Page 11; 14pp; Japanese.
XX
CC   The present invention describes a method for detecting single nucleotide
CC   polymorphisms (SNPs). ALso described is an oligonucleotide used in the
CC   detection of an SNP, prepared by binding an oligonucleotide having a
CC   complementary sequence or those devoid of up to several bases with 1 or
CC   more organic group(s) to be tested by light irradiation of a specific
CC   wave length to vary a double strand formation property of the
CC   oligonucleotide to be tested. The method is used for detecting SNPs. The
CC   present sequence represents a light responsive oligonucleotide which is
CC   used in an example from the present invention
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4247
ABA93701/c
ID   ABA93701 standard; DNA; 14 BP.
XX
AC   ABA93701;
XX
DT   30-APR-2002  (first entry)
XX
DE   Light responsive oligonucleotide (X1)T14.
XX
KW   Light responsive; detection; single nucleotide polymorphism; SNP;
KW   irradiation; ss.
XX
OS   Synthetic.
XX
PN   JP2001346579-A.
XX
PD   18-DEC-2001.
XX
PF   02-JUN-2000; 2000JP-00165441.
XX
PR   02-JUN-2000; 2000JP-00165441.
XX
PA   (KOMI/) KOMIYAMA S.
PA   (ASAN/) ASANUMA H.
XX
DR   WPI; 2002-145181/19.
XX
PT   Detecting single nucleotide polymorphism for expressing sensitivity
PT   information of diseases and drugs, comprises using a new oligonucleotide.
XX
PS   Example 3; Page 11; 14pp; Japanese.
XX
CC   The present invention describes a method for detecting single nucleotide
CC   polymorphisms (SNPs). ALso described is an oligonucleotide used in the
CC   detection of an SNP, prepared by binding an oligonucleotide having a
CC   complementary sequence or those devoid of up to several bases with 1 or
CC   more organic group(s) to be tested by light irradiation of a specific
CC   wave length to vary a double strand formation property of the
CC   oligonucleotide to be tested. The method is used for detecting SNPs. The
CC   present sequence represents a light responsive oligonucleotide which is
CC   used in an example from the present invention
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4248
ABZ96320
ID   ABZ96320 standard; DNA; 14 BP.
XX
AC   ABZ96320;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human C/EBP antisense fragment no.2180.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
```

```
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 11562; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 14 BP; 0 A; 3 C; 11 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         53 GGCGGGGGCGGCGG 66
              ||||||||||||||
Db          1 GGCGGGGGCGGCGG 14


RESULT 4249
ABX79769/c
ID   ABX79769 standard; cDNA; 14 BP.
XX
AC   ABX79769;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #94.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 343; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 14 BP; 0 A; 1 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 4250
AAT52140
ID   AAT52140 standard; RNA; 15 BP.
XX
AC   AAT52140;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2912).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
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PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
PT Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 175; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 0.0%; Pred. No. 2.3e+03;
Matches 0; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTT 2179
:::::::::::::
Db 1 UUUUUUUUUUUUUU 14

RESULT 4251
AAF16603
ID AAF16603 standard; DNA; 15 BP.
XX
AC AAF16603;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.
XX
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-AU000498.
XX
PR 24-MAY-1999; 99AU-00000510.
XX
PA (TACH/) TACHAS G.
XX
PI Tachas G;
XX
DR WPI; 2001-025093/03.
XX
PT Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX
PS Example 3; Page 148; 164pp; English.
XX
CC The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori
XX
SQ Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 2 AAAAAAAAAAAAAA 15

RESULT 4252
AAT52144/c
ID AAT52144 standard; RNA; 15 BP.
XX
AC AAT52144;
XX
DT 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX
DE Human ICAM hammerhead ribozyme target sequence (nt. position 2914).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9523225-A2.
XX

```
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 1 A; 1 C; 1 G; 0 T; 12 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4253
AAT52134
ID   AAT52134 standard; RNA; 15 BP.
XX
AC   AAT52134;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
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CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   0.0%;  Pred. No. 2.3e+03;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTT 2179
              :::::::::::::
Db          2 UUUUUUUUUUUUU 15


RESULT 4254
AAT52134/c
ID   AAT52134 standard; RNA; 15 BP.
XX
AC   AAT52134;
XX
DT   25-MAR-2003  (revised)
DT   25-MAR-1997  (first entry)
XX
DE   Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 175; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC   nucleotide base position indicated in the DE line. Regions of the mRNA
CC   that do not form secondary folding structures and that contain potential
CC   hammerhead and hairpin ribozyme cleavage sites were identified by
CC   computer analysis. Ribozymes directed against these mRNA sequences were
CC   designed and synthesised with modifications that improve their nuclease
CC   resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC   inhibit ICAM-1 expression, making them useful for reducing transplant
CC   rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC   asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         15 AAAAAAAAAAAAAA 2


RESULT 4255
AAX18361/c
ID   AAX18361 standard; DNA; 15 BP.
XX
AC   AAX18361;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 2.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
```

```
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 15 BP; 0 A; 2 C; 0 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 4256
AAA11718/c
ID   AAA11718 standard; DNA; 15 BP.
XX
AC   AAA11718;
XX
DT   14-JUL-2000  (first entry)
XX
DE   Human MIF gene D5k region primer #2.
XX
KW   MIF; migration inhibitory factor; D5k region; human; macrophage;
KW   diagnosis; primer; adenocarcinoma; metastasis; cancer; tumor cell; ss.
XX
OS   Homo sapiens.
XX
PN   US6043044-A.
XX
PD   28-MAR-2000.
XX
PF   15-JUL-1997;   97US-00893204.
XX
PR   15-JUL-1997;   97US-00893204.
XX
PA   (HUDS/) HUDSON P B.
PA   (HAKK/) HAKKY S I.
PA   (SIEG/) SIEGLER K M.
PA   (HAKK/) HAKKI A.
XX
PI   Hakky SI,  Hudson PB,  Siegler KM,  Hakki A;
XX
DR   WPI; 2000-292363/25.
XX
PT   A new method useful for diagnosing human adenocarcinoma and measuring
PT   metastatic potential comprises determining the levels of macrophage
PT   migration inhibitory factor within tumor cells.
XX
PS   Claim 11; Col 7-8; 6pp; English.
XX
CC   This invention describes a novel method for diagnosing adenocarcinoma and
CC   determining metastatic ability of human cancer in an individual by
CC   determining the increased levels of macrophage migration inhibitory
CC   factor (MIF) within tumor cells. The method is useful for diagnosing
CC   human adenocarcinoma, as well as for its prognosis. The method is also
CC   useful for measuring levels of macrophage migration inhibitory factor
CC   within tumor cells. The method provides better and more accurate
CC   prognostic markers for cancer. The method is also capable of
CC   distinguishing histological tumors from clinical cancers. This sequence
CC   represents a primer used to detect the human MIF gene D5k region which is
CC   described in the method of the invention
XX
SQ   Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         14 GAAAAAAAAAAAAA 1


RESULT 4257
AAF81549
ID   AAF81549 standard; DNA; 15 BP.
XX
AC   AAF81549;
XX
DT   05-JUN-2001  (first entry)
XX
DE   Dye-labeled molecule removal method related oligonucleotide #1.
XX
KW   Dye-labeled molecule removal; primer extension product purification;
KW   DNA sequencing; DNA analysis; ds.
XX
OS   Synthetic.
XX
PN   WO200125490-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US027765.
XX
PR   06-OCT-1999;   99US-0158188P.
PR   08-NOV-1999;   99US-0164050P.
PR   03-MAY-2000; 2000US-00564117.
XX
PA   (PROL-) PROLINX INC.
XX
PI   Spicer DA,  Hughes KA,  Kaiser RJ,  Mahoney JE,  Springer AL;
PI   Stolowitz ML,  Weissman CHD;
XX
DR   WPI; 2001-245064/25.
XX
PT   Removing unincorporated dye-labeled molecules associated with DNA
PT   sequencing, comprises using particles made of porous hydrophobic
PT   materials encapsulated in a hydrophilic matrix.
XX
PS   Example 1; Page 23; 57pp; English.
XX
CC   The present invention describes a method of removing unincorporated dye-
CC   labeled molecules from a mixture of the molecules and polymers. This is
CC   useful in the purification of primer extension products, for example in
CC   DNA sequencing and analysis. The present sequence was used to demonstrate
CC   the method of the invention
XX
SQ   Sequence 15 BP; 1 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              ||||||||||||| |
Db          1 GCTTTTTTTTTTTNA 15


RESULT 4258
AAF49041
ID   AAF49041 standard; DNA; 15 BP.
XX
AC   AAF49041;
XX
```

```
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #1.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 60; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4259
AAF49041/c
ID   AAF49041 standard; DNA; 15 BP.
XX
AC   AAF49041;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #1.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 60; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4260
AAF60455/c
ID   AAF60455 standard; DNA; 15 BP.
XX
AC   AAF60455;
XX
DT   27-APR-2001  (first entry)
XX
DE   Oligonucleotide clamp #10.
XX
KW   Oligonucleotide clamp; ds.
XX
OS   Unidentified.
XX
```

```
PN   US6180777-B1.
XX
PD   30-JAN-2001.
XX
PF   03-JAN-1997;   97US-00787321.
XX
PR   12-JAN-1996;   96US-0009918P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Horn T;
XX
DR   WPI; 2001-201911/20.
XX
PT   Synthesizing branched nucleic acids useful as diagnostic and molecular
PT   probes, involves combining first units having haloalkylamino groups and
PT   second units having thiol or phosphorothioate groups.
XX
PS   Example 5; Col 17-18; 20pp; English.
XX
CC   The present invention relates to a method for synthesising a branched or
CC   multiply connected macromolecular structure, comprising oligonucleotide
CC   clamps (OC). The macromolecular structure is capable of specifically
CC   binding to a target molecule, and can therefore be used as probes. At
CC   least one OC comprises a target binding sequence that binds specifically
CC   and stably with the target molecule, and at least two OCs comprise signal
CC   generation moieties capable of generating a detectable signal in the
CC   presence of the target molecule. In addition the OCs are connected to one
CC   another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC   present sequence is an OC used in the present invention
XX
SQ   Sequence 15 BP; 1 A; 2 C; 0 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4261
AAH23587
ID   AAH23587 standard; DNA; 15 BP.
XX
AC   AAH23587;
XX
DT   03-AUG-2001  (first entry)
XX
DE   Dye-labeled dideoxy terminators removal related oligonucleotide #1.
XX
KW   Dye-labeled dideoxy terminator; DNA sequencing;
KW   nucleic acid purification; hydrophilic polymeric matrix; ds.
XX
OS   Synthetic.
XX
PN   WO200125491-A1.
XX
PD   12-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US027895.
XX
PR   06-OCT-1999;   99US-0158188P.
PR   08-NOV-1999;   99US-0164050P.
PR   03-MAY-2000; 2000US-00564117.
XX
PA   (PROL-) PROLINX INC.
XX
PI   Spicer DA,  Hughes KA,  Kaiser RJ,  Mahoney JE,  Springer AL;
PI   Stolowitz ML,  Weissman CHD;
XX
DR   WPI; 2001-316173/33.
XX
PT   Removing unincorporated dye-labeled molecules from polymer incorporated
PT   with dye-labeled molecules, involves mixing and incubating the mixture
PT   with porous hydrophobic material entrapped within a hydrophilic matrix.
XX
PS   Example 1; Page 23; 58pp; English.
XX
CC   The present invention describes a method for removing unincorporated dye-
CC   labeled molecules from a mixture comprising dye-labeled molecules and a
CC   polymer into which dye-labeled molecules are incorporated, involving
CC   contacting the mixture with particles of a porous hydrophobic material
CC   entrapped within a hydrophilic matrix, incubating the mixture and
CC   removing the particles, thus removing the absorbed unincorporated dye-
CC   labeled molecules. This is useful for removing fluorescent and other dye-
CC   labeled molecules following procedures such as PCR
XX
SQ   Sequence 15 BP; 1 A; 1 C; 1 G; 11 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTGA 1783
              ||||||||||||||.|
Db          1 GCTTTTTTTTTTTNA 15


RESULT 4262
AAD30518
ID   AAD30518 standard; DNA; 15 BP.
XX
AC   AAD30518;
XX
DT   31-MAY-2002  (first entry)
XX
DE   Oligonucleotide used to identify human EER-7 cDNA.
XX
KW   Human; lysyl oxidase; LO gene; endothelial estrogen regulated gene; AAA;
KW   abdominal aortic aneurysms; EER-7 gene; myocardial infraction; elastin;
KW   fibrotic disease; gene therapy; cardiant; ss.
XX
OS   Unidentified.
XX
PN   WO200212470-A2.
XX
PD   14-FEB-2002.
XX
PF   08-AUG-2001; 2001WO-US024942.
XX
PR   08-AUG-2000; 2000US-0223763P.
PR   15-DEC-2000; 2000US-0255838P.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Evans MJ,  Scicchitano MS,  Bapat AR,  Beer E,  Bhat RA,  Ferris E;
PI   Mastroeni R,  Zhang J,  Karathanasis SK;
XX
DR   WPI; 2002-227150/28.
XX
PT   Novel isolated endothelial estrogen regulated gene protein comprising
PT   lysyl oxidase activity and conserved catalytic domain of lysyl oxidase,
PT   useful as target to treat abdominal aortic aneurysms, myocardial
PT   infarction.
XX
PS   Example 1; Page 46; 68pp; English.
XX
CC   The patent discloses novel lysyl oxidase (LO) genes, termed endothelial
CC   estrogen regulated (EER)-7 genes and their corresponding proteins. The
CC   invention also relates to an assay system to identify compounds that
CC   selectively modulate EER7 protein activity by interaction with estrogen
CC   receptors. Stimulation of LO enzyme activity of EER-7 acts as a target
CC   for abdominal aortic aneurysms (AAA) and myocardial infractions. Increase
CC   in EER-7 lysyl oxidase activity increases elastin cross-linking in the
```

CC inner elastic lamina which prevents development of aneurysms. Increased
CC EER-7 is also useful to increase collagen cross-linkings which increase
CC tensile strength of vessel wall which also prevents aneurysms. Myocardial
CC infraction is prevented by inhibiting rupture of fibrous cap that covers
CC plaque in the coronary vessels. Increased tensile strength of the cap,
CC resulting from increased LO activity helps preventing the infractions.
CC Inhibition of LO activity is useful for treating fibrotic diseases.
CC Stimulation of EER-7 proteins are useful for treating patients with
CC estrogen-related disease states. Genetic variants of EER-7 can be
CC detected to diagnose an EER-7 associated disease such as AAA or
CC myocardial infarction. EER-7 polynucleotides are useful in gene therapy.
CC The present DNA sequence is an oligonucleotide which is used to identify
CC human EER-7 cDNA
XX
SQ Sequence 15 BP; 1 A; 2 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1768 AGCTTTTTTTTTTT 1781
||||||||||||||
Db 1 AGCTTTTTTTTTTT 14

RESULT 4263
ABK98169
ID ABK98169 standard; DNA; 15 BP.
XX
AC ABK98169;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #39.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||| |||||||
Db 1 TTTTTTTNTTTTTTT 15

RESULT 4264
ABK98169/c
ID ABK98169 standard; DNA; 15 BP.
XX
AC ABK98169;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #39.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The

CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||| |||||||
Db 15 AAAAAAANAAAAAAA 1

RESULT 4265
ABK98187
ID ABK98187 standard; DNA; 15 BP.
XX
AC ABK98187;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #51.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention.
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||| |||||||
Db 1 TTTTTTTNTTTTTTT 15

RESULT 4266
ABK98187/c
ID ABK98187 standard; DNA; 15 BP.
XX
AC ABK98187;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #51.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,

CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||| |||||||
Db 15 AAAAAAANAAAAAAA 1

RESULT 4267
ABK98168
ID ABK98168 standard; DNA; 15 BP.
XX
AC ABK98168;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #38.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||| |||||||
Db 1 TTTTTTTNTTTTTTT 15

RESULT 4268
ABK98168/c
ID ABK98168 standard; DNA; 15 BP.
XX
AC ABK98168;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #38.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel

CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAA 2800
||||||| |||||||
Db 15 AAAAAAANAAAAAAA 1

RESULT 4269
ABK98167
ID ABK98167 standard; DNA; 15 BP.
XX
AC ABK98167;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #37.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTT 2180
||||||| |||||||
Db 1 TTTTTTTNTTTTTTT 15

RESULT 4270
ABK98167/c
ID ABK98167 standard; DNA; 15 BP.
XX
AC ABK98167;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #37.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide

CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| |||||||
Db         15 AAAAAAANAAAAAAA 1
```

RESULT 4271
ABK98186
ID ABK98186 standard; DNA; 15 BP.
XX
AC ABK98186;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #50.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.5%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||| |||||||
Db          1 TTTTTTTNTTTTTTT 15
```

RESULT 4272
ABK98186/c
ID ABK98186 standard; DNA; 15 BP.
XX
AC ABK98186;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #50.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targetting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming

```
CC   a triple-helix comprising a double helical nucleic acid comprising first
CC   and second substantially complementary strands, and an oligonucleotide
CC   bound to a purine-rich target sequence within the double helical nucleic
CC   acid, where the oligonucleotide binds in a parallel and antiparallel
CC   orientation, respectively, to target sequences on alternate strands of
CC   the double helical nucleic acid. The method has therapeutic applications,
CC   where gene expression is controlled by selective triple-helix formation
CC   within expression regulatory sequences of a target gene. The
CC   oligonucleotides can be used to form triple-helices, and are useful to
CC   detect the presence or absence of specific sequences within genomic DNA
CC   for diagnostic and therapeutic purposes. The oligonucleotides can be
CC   selected to specifically bind to pathogenic double-stranded DNA including
CC   specific sequences required by pathogenic bacteria or viruses for
CC   replication or virulence, reducing their pathogenicity. Alternatively,
CC   the oligonucleotide can be chosen to target a unique sequence of the
CC   pathogen which is not found in the genome of pathogen's host. The
CC   oligonucleotides can be used in cancer treatment by way of triple-helix
CC   suppression of specific oncogenes including those of endogenous or viral
CC   origin. Such therapeutic oligonucleotides are capable of forming triple-
CC   helices with such sequences in cancerous cells containing the activated
CC   oncogene, so preferentially killing or repressing the cancer causing
CC   cell. The present sequence represents an oligonucleotide used in the
CC   methods of the present invention
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match              0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||||||| |||||||
Db         15 AAAAAAANAAAAAAA 1


RESULT 4273
ABX79833
ID   ABX79833 standard; cDNA; 15 BP.
XX
AC   ABX79833;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #158.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 747; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match              0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTT 2180
              ||||||||||| |||
Db          1 TTTTTTTTTTTNTTT 15


RESULT 4274
ABX79833/c
ID   ABX79833 standard; cDNA; 15 BP.
XX
AC   ABX79833;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #158.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 747; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
```

```
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 2.3e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAA 2800
              ||| ||||||||||||
Db         15 AAANAAAAAAAAAAA 1


RESULT 4275
AAD44145/c
ID   AAD44145 standard; DNA; 16 BP.
XX
AC   AAD44145;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #5 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 4276
AAX18360
ID   AAX18360 standard; DNA; 16 BP.
XX
AC   AAX18360;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 1.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4277
AAX18368/c
ID   AAX18368 standard; DNA; 16 BP.
XX
AC   AAX18368;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 9.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
```

```
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         14 AAAAAAAAAAAAAA 1


RESULT 4278
AAX18365
ID   AAX18365 standard; DNA; 16 BP.
XX
AC   AAX18365;
XX
DT   11-MAY-1999  (first entry)
XX
DE   RT-PCR primer of the invention SEQ ID 6.
XX
KW   RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS   Synthetic.
XX
PN   JP11032765-A.
XX
PD   09-FEB-1999.
XX
PF   18-JUL-1997;   97JP-00208312.
XX
PR   18-JUL-1997;   97JP-00208312.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1999-183822/16.
XX
PT   Peptides having at least two new nucleotides - useful as primers in RT-
PT   PCR.
XX
PS   Disclosure; Page 10; 19pp; Japanese.
XX
CC   This sequence represents a primer of the invention. The invention relates
CC   to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC   -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC   a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC   natural number indicating the repetition of alpha; beta, delta = V or N;
CC   V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC   thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC   repetition of gamma, in which thymine expressed by gamma is composed of
CC   1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC   useful as primers for RT-PCR and determination of base sequences. The new
CC   sequences allow for reproductive and highly efficient analysis of gene
CC   sequences
XX
SQ   Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4279
AAD44147/c
ID   AAD44147 standard; DNA; 16 BP.
XX
AC   AAD44147;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #7 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 4280
AAD44149/c
ID   AAD44149 standard; DNA; 16 BP.
XX
AC   AAD44149;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Oligo-dT PCR primer #9 used to illustrate the method of the invention.
XX
KW   Sequential consensus region-directed amplification; gene expression;
KW   disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   US6277571-B1.
XX
PD   21-AUG-2001.
XX
PF   30-SEP-1998;   98US-00163485.
XX
PR   03-OCT-1997;   97US-00943162.
PR   03-OCT-1997;   97US-0108152P.
XX
PA   (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
XX
PI   Fillmore H,  Broaddus W,  Gillies G;
XX
DR   WPI; 2002-412824/44.
XX
PT   Sequential consensus region-directed amplification for sorting mixture of
PT   DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT   2 samples, useful for disease diagnosis and gene analysis.
XX
PS   Example; Fig 1C; 19pp; English.
XX
CC   The invention relates to a method of sequential consensus region-directed
CC   amplification for sorting a mixture of DNAs into 2 or more subsets or
CC   distinguishing gene expression patterns in 2 samples. The methods, kits
CC   and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC   more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC   for disease diagnosis and gene analysis. The present sequence is oligo dT
CC   PCR primer used to illustrate the method of the invention
XX
SQ   Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         16 AAAAAAAAAAAAAA 3


RESULT 4281
AAV33896
ID   AAV33896 standard; DNA; 16 BP.
XX
AC   AAV33896;
XX
DT   25-JAN-1999  (first entry)
XX
DE   PCR primer #6 for plant cyclin D-type genes.
XX
KW   D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW   CDC; Rb; retinoblastoma; germination; flowering; seed; fruit; PCR;
KW   root development; primer; amplification; ss.
XX
OS   Synthetic.
OS   Nicotiana tabacum.
OS   Helianthus tuberosus.
OS   Zea mays.
XX
PN   WO9842851-A1.
XX
PD   01-OCT-1998.
XX
PF   24-MAR-1998;   98WO-EP001701.
XX
PR   26-MAR-1997;   97EP-00302096.
XX
PA   (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI   Murray JAH;
XX
DR   WPI; 1998-532012/45.
XX
PT   Regulating growth and structure of plants by modulating protein that
PT   controls cell division - specifically a D-type cyclin, and related
PT   chimeric genes and transformed cells and plants, used to alter growth
PT   rate, flowering, seed production etc.
XX
PS   Disclosure; Page 61; 75pp; English.
XX
CC   Primers AAV33891-V33904 were used to PCR amplify cDNA sequence encoding
CC   plant D-type cyclin (AAV33884-V33889). The cyclin sequences can be used
CC   to alter the growth characteristics or architecture of plants by altering
CC   the (functional) level in the plant cells of a cell-division controlling
CC   protein that can bind to, or phosphorylate, an Rb-like protein, such as a
CC   D-type cyclin. Modulation of the cyclin gene is used to increase or
CC   decrease the growth rate, provide faster germination, reduce time to
CC   flowering, increase the number of flowers, seeds or fruits per plant,
CC   increase root development, reduce height and to delay flowering in a
CC   range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat,
CC   tomato, rice, barley, sunflower, carnation, chrysanthemum, rose, tulip,
CC   etc
XX
SQ   Sequence 16 BP; 2 A; 0 C; 6 G; 7 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2690 TGGAGATTTGGAATTG 2705
              |||:||||||||  |||
Db          1 TGGWGATTTGGATTTG 16


RESULT 4282
AAX69798/c
ID   AAX69798 standard; RNA; 17 BP.
XX
AC   AAX69798;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1093.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
```

```
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         17 AAAAAAAAAAAAAA 4


RESULT 4283
AAX69803
ID   AAX69803 standard; RNA; 17 BP.
XX
AC   AAX69803;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   0.0%;  Pred. No. 3e+03;
  Matches    0;  Conservative   14;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ::::::::::::::
Db          1 UUUUUUUUUUUUUU 14


RESULT 4284
AAX70117
ID   AAX70117 standard; RNA; 17 BP.
XX
AC   AAX70117;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1412.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 89; 218pp; English.
XX
```

```
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 5 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   64.3%;  Pred. No. 3e+03;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGA 1352
              :||:::|||||:||
Db          3 UCAUUUCAGCCUGA 16


RESULT 4285
AAX70116
ID   AAX70116 standard; RNA; 17 BP.
XX
AC   AAX70116;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1411.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 89; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 5 A; 4 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   64.3%;  Pred. No. 3e+03;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1339 TCATTTCAGCCTGA 1352
              :||:::|||||:||
Db          4 UCAUUUCAGCCUGA 17


RESULT 4286
AAX69438
ID   AAX69438 standard; RNA; 17 BP.
XX
AC   AAX69438;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #733.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 68; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 2 A; 2 C; 1 G; 0 T; 12 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   21.4%;  Pred. No. 3e+03;
  Matches    3;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1770 CTTTTTTTTTTGA 1783
              |::::::::::||
Db          1 CUUUUUUUUUUGA 14
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```
RESULT 4287
AAX69434
ID   AAX69434 standard; RNA; 17 BP.
XX
AC   AAX69434;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #729.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 68; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 1 A; 1 C; 3 G; 0 T; 12 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   21.4%;  Pred. No. 3e+03;
  Matches    3;  Conservative   11;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1769 GCTTTTTTTTTTTG 1782
              ||:::::::::::|
Db          4 GCUUUUUUUUUUG 17


RESULT 4288
AAA20469
ID   AAA20469 standard; RNA; 17 BP.
XX
AC   AAA20469;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Integrin alpha 6 subunit substrate sequence SEQ ID NO:3695.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  Mcswiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or stability
PT   of an mRNA encoding an angiogenic factors.
XX
PS   Claim 55; Page 147; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ   Sequence 17 BP; 1 A; 6 C; 3 G; 0 T; 7 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   50.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2629 GTCTCGTTCCTGTT 2642
              |:|:||::||:|::
Db          2 GUCUCGUUCCUGUU 15


RESULT 4289
AAA20470
ID   AAA20470 standard; RNA; 17 BP.
XX
AC   AAA20470;
XX
```

```
DT   19-JUN-2000  (first entry)
XX
DE   Integrin alpha 6 subunit substrate sequence SEQ ID NO:3696.
XX
KW   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW   integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW   hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
KW   ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW   dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW   age related macular degeneration; inflammation; neovascular glaucoma;
KW   myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW   tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW   Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   WO9950403-A2.
XX
PD   07-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006507.
XX
PR   27-MAR-1998;   98US-0079678P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Pavco PA,  Roberts E,  Jarvis T,  Coeshott C,  Mcswiggen JA;
XX
DR   WPI; 1999-591315/50.
XX
PT   Novel ribozymes for modulating the synthesis, expression and/or stability
PT   of an mRNA encoding an angiogenic factors.
XX
PS   Claim 55; Page 147; 305pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules with RNA
CC   cleaving activity, which specifically cleave RNA encoded by an aryl
CC   hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC   gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC   AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC   and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC   corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC   AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC   and AAA19155 to AAA19222 represent their corresponding target sequences;
CC   AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC   sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC   AAA21596 to AAA21688 represent their corresponding target sequences;
CC   AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC   for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC   AAA23422 represent their corresponding target sequences. The ribozymes of
CC   the invention are used for modulating the synthesis, expression and/or
CC   stability of an mRNA encoding angiogenic factor, especially ARNT,
CC   integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC   especially used to treat cancer, diabetic retinopathy, age related
CC   macular degeneration (ARMD), inflammation, and arthritis, as well as
CC   neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC   angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
CC   syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC   and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC   integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ   Sequence 17 BP; 0 A; 6 C; 3 G; 0 T; 8 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   50.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2629 GTCTCGTTCCTGTT 2642
              |:|:||::||:|::
Db          1 GUCUCGUUCCUGUU 14


RESULT 4290
```

```
AAA25447
ID   AAA25447 standard; DNA; 17 BP.
XX
AC   AAA25447;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1945.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db          4 TTTTTTTTTTTTTT 17


RESULT 4291
AAA25447/c
ID   AAA25447 standard; DNA; 17 BP.
```

```
XX
AC   AAA25447;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1945.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         17 AAAAAAAAAAAAAA 4


RESULT 4292
AAF03225
ID   AAF03225 standard; DNA; 17 BP.
XX
AC   AAF03225;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #1520.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 37; Page 90; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 3 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAA 1784
              ||||||||||||||
Db          2 TTTTTTTTTTTGAA 15


RESULT 4293
AAF03223
ID   AAF03223 standard; DNA; 17 BP.
XX
AC   AAF03223;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #1518.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
```

PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 90; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 4 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1771 TTTTTTTTTTTGAA 1784
||||||||||||||
Db 4 TTTTTTTTTTTGAA 17

RESULT 4294
AAF07018/c
ID AAF07018 standard; DNA; 17 BP.
XX
AC AAF07018;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #3275.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 54; Page 131; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 7 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2233 TGTTCCCTTAAGGT 2246
||||||||||||||
Db 17 TGTTCCCTTAAGGT 4

RESULT 4295
AAF03224
ID AAF03224 standard; DNA; 17 BP.
XX
AC AAF03224;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1519.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 90; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 4 A; 0 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1771 TTTTTTTTTTTGAA 1784
||||||||||||||
Db 3 TTTTTTTTTTTGAA 16

RESULT 4296
AAF03226
ID AAF03226 standard; DNA; 17 BP.
XX

```
AC   AAF03226;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #1521.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 37; Page 90; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 2 A; 0 C; 3 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAA 1784
              ||||||||||||||
Db          1 TTTTTTTTTTTGAA 14


RESULT 4297
ABK02792/c
ID   ABK02792 standard; RNA; 17 BP.
XX
AC   ABK02792;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human CD20 Hammerhead ribozyme #91.
XX
KW   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW   cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW   muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW   DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW   B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW   human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW   MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW   inflammatory arthropathy; central nervous system injury;
KW   cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW   chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW   Parkinson's disease; ataxia; Huntington's disease;
KW   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US004273.
XX
PR   11-FEB-2000; 2000US-0181797P.
PR   28-FEB-2000; 2000US-0185516P.
PR   06-MAR-2000; 2000US-0187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (CHOW/) CHOWRIRA B M.
XX
PI   Blatt L,  Mcswiggen J,  Chowrira BM;
XX
DR   WPI; 2001-607195/69.
XX
PT   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT   constructs, which down regulate expression of a CD20 gene or neurite
PT   growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT   central nervous system injury.
XX
PS   Claim 30; Page 141; 200pp; English.
XX
CC   The invention relates to a nucleic acid molecule which down regulates
CC   expression of a CD20 gene and a nucleic acid molecule which down
CC   regulates expression of a neurite growth inhibitor gene (NOGO). The
CC   nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC   DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC   possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC   an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC   with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC   of CD20 in the presence of a divalent cation that is preferably Mg^2^+.
CC   Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC   the cell and treat a patient having a condition associated with the level
CC   of CD20. The treatment may further comprise the use of one or more
CC   therapies. In particular, the CD20 targetting nucleic acid may be used to
CC   treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC   Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC   leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC   lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC   immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC   targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC   presence of a divalent cation that is preferably Mg^2^+. Furthermore, the
CC   nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC   cell and treat a patient having a condition associated with the level of
CC   NOGO. The treatment may further comprise the use of one or more
CC   therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC   treat central nervous system (CNS) injury and cerebrovascular accident
CC   (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC   chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC   Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC   disease, muscular dystrophy, and/or other neurodegenerative disease
CC   states which respond to the modulation of NOGO expression. The present
CC   sequence is a hammerhead ribozyme of the invention
XX
SQ   Sequence 17 BP; 7 A; 2 C; 0 G; 0 T; 8 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2465 AATTTTAATATTAA 2478
              ||||||||||||||
Db         14 AATTTTAATATTAA 1
```

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RESULT 4298
ABK02791/c
ID   ABK02791 standard; RNA; 17 BP.
XX
AC   ABK02791;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human CD20 Hammerhead ribozyme #90.
XX
KW   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW   cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW   muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW   DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW   B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW   human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW   MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW   inflammatory arthropathy; central nervous system injury;
KW   cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW   chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW   Parkinson's disease; ataxia; Huntington's disease;
KW   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US004273.
XX
PR   11-FEB-2000; 2000US-0181797P.
PR   28-FEB-2000; 2000US-0185516P.
PR   06-MAR-2000; 2000US-0187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (CHOW/) CHOWRIRA B M.
XX
PI   Blatt L,  Mcswiggen J,  Chowrira BM;
XX
DR   WPI; 2001-607195/69.
XX
PT   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT   constructs, which down regulate expression of a CD20 gene or neurite
PT   growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT   central nervous system injury.
XX
PS   Claim 30; Page 141; 200pp; English.
XX
CC   The invention relates to a nucleic acid molecule which down regulates
CC   expression of a CD20 gene and a nucleic acid molecule which down
CC   regulates expression of a neurite growth inhibitor gene (NOGO). The
CC   nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC   DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC   possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC   an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC   with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC   of CD20 in the presence of a divalent cation that is preferably Mg^2^+.
CC   Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC   the cell and treat a patient having a condition associated with the level
CC   of CD20. The treatment may further comprise the use of one or more
CC   therapies. In particular, the CD20 targetting nucleic acid may be used to
CC   treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC   Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC   leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC   lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC   immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC   targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC   presence of a divalent cation that is preferably Mg^2^+. Furthermore, the
CC   nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC   cell and treat a patient having a condition associated with the level of
CC   NOGO. The treatment may further comprise the use of one or more
CC   therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC   treat central nervous system (CNS) injury and cerebrovascular accident
CC   (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC   chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC   Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC   disease, muscular dystrophy, and/or other neurodegenerative disease
CC   states which respond to the modulation of NOGO expression. The present
CC   sequence is a hammerhead ribozyme of the invention
XX
SQ   Sequence 17 BP; 7 A; 2 C; 0 G; 0 T; 8 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2465 AATTTTAATATTAA 2478
              ||||||||||||||
Db         15 AATTTTAATATTAA 2

RESULT 4299
ABQ64252/c
ID   ABQ64252 standard; DNA; 17 BP.
XX
AC   ABQ64252;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Human KTOM1a portion (ABQ63232) probe # 965.
XX
KW   Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW   gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW   kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200224750-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-US029656.
XX
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   23-MAY-2001; 2001US-00864761.
PR   28-AUG-2001; 2001US-0315676P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Zhang J;
XX
DR   WPI; 2002-479509/51.
XX
PT   New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT   acids encoding the protein, useful for treating subjects having defects
PT   in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT   e.g., liver or bone.
XX
PS   Example 2; Page 284; 418pp; English.
XX
```

CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1740 GTGACAAGTACTGG 1753
||||||||||||||
Db 17 GTGACAAGTACTGG 4

RESULT 4300
ABQ64256/c
ID ABQ64256 standard; DNA; 17 BP.
XX
AC ABQ64256;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 969.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
DR WPI; 2002-479509/51.
XX
PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
PS Example 2; Page 284; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1739 GGTGACAAGTACTG 1752
||||||||||||||
Db 14 GGTGACAAGTACTG 1

RESULT 4301
ABQ99687/c
ID ABQ99687 standard; DNA; 17 BP.
XX
AC ABQ99687;
XX
DT 08-NOV-2002 (first entry)
XX
DE Murine Ikbkap exon 27 acceptor site.
XX
KW Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;
KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.
XX
OS Mus sp.
XX
PN WO200259381-A2.
XX
PD 01-AUG-2002.
XX
PF 07-JAN-2002; 2002WO-US000473.
XX
PR 06-JAN-2001; 2001US-0260080P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Slaugenhaupt S, Gusella JF;
XX
DR WPI; 2002-674806/72.
XX
PT New IKBKAP genes with mutations, useful for identifying a subject with
PT familial dysautonomia (FD), or for rapid carrier screening in the
PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or
PT prenatal diagnosis.
XX
PS Disclosure; Fig 11; 109pp; English.
XX
CC The present invention relates to methods and compositions useful for
CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day
CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM
CC 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565)
CC are associated with FD. The mutation associated with the major haplotype
CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine
CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced
CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD
CC patients, although they continue to express varying levels of wild-type
CC message in a tissue-specific manner. The mutation associated with the
CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine
CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.
CC This bp mutation causes an arginine to proline missense mutation (R696P)

```
CC   in the IKBKAP protein, which is predicted to disrupt a potential
CC   phosphorylation site. The IKBKAP nucleic acid sequences are useful for
CC   identifying a subject with FD and for rapid carrier screening. The IKBKAP
CC   gene maps to chromosome 9q31. A mouse model of FD was created in an
CC   example from the invention. Expression of murine Ikbkap was examined
CC   using both mouse embryo and adult mouse multiple tissue Northern blots.
CC   The blots were probes with a 1045bp PCR fragent that contains exons 2
CC   through 11, which was generated using PCR primers ABQ80563-ABQ80564.
CC   ABQ99662-ABQ99733 are the murine Ikbkap exon and intron boundaries
XX
SQ   Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAA 2797
              ||||||||||||||
Db         14 TGAAAAAAAAAAAA 1


RESULT 4302
ABS76198
ID   ABS76198 standard; DNA; 17 BP.
XX
AC   ABS76198;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Eb associated 17-mer SEQ ID 1724.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 302; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 0 A; 2 C; 5 G; 10 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGT 2330
              ||||||||||||||
Db          1 TTGTTGCTGCTTGT 14


RESULT 4303
ABS76197
ID   ABS76197 standard; DNA; 17 BP.
XX
AC   ABS76197;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human PAPP-Eb associated 17-mer SEQ ID 1723.
XX
KW   PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW   contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW   dysgenetic pregnancy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002102252-A1.
XX
PD   01-AUG-2002.
XX
PF   06-APR-2001; 2001US-00827998.
XX
PR   26-MAY-2000; 2000US-0207456P.
XX
PA   (GUYY/) GU Y.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Shannon ME;
XX
DR   WPI; 2002-697817/75.
XX
PT   New isolated nucleic acid encoding an isoform of human pregnancy
PT   associated plasma protein E, for preventing or aborting pregnancy.
XX
PS   Example 2; Page 301; 353pp; English.
XX
CC   This invention describes a novel isolated nucleic acid that encodes one
CC   of three new isoforms of human pregnancy associated plasma protein E,
CC   hPAPP-E. The products of the invention have abortive and contraceptive
CC   activity and can be used for gene therapy or in a vaccine. The nucleic
CC   acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC   used in pharmaceutical compositions or vaccines for preventing or
CC   aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC   dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC   the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC   antibodies can be used to assess the expression levels of PAPP-E isoform
CC   proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC   antenatally. This sequence represents an oligomer used in scanning the
CC   human PAPP-E genes described in the disclosure of the invention
XX
SQ   Sequence 17 BP; 0 A; 2 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2317 TTGTTGCTGCTTGT 2330
              ||||||||||||||
Db          2 TTGTTGCTGCTTGT 15


RESULT 4304
ACD55508
ID   ACD55508 standard; RNA; 17 BP.
```

```
XX
AC   ACD55508;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HBV amberzyme substrate sequence #92.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Example 1; Page 204; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HBV
CC   ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC   disclosed in the present invention
XX
SQ   Sequence 17 BP; 4 A; 2 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   57.1%;  Pred. No. 3e+03;
  Matches    8;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2117 GTTTTAGGAAACTT 2130
              |.:::|||||||::
Db          3 GUUUUAGGAAACUU 16


RESULT 4305
ACD50744
ID   ACD50744 standard; RNA; 17 BP.
XX
AC   ACD50744;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HBV hammerhead ribozyme substrate sequence #210.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Example 1; Page 140; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
```

```
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HBV
CC   ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC   disclosed in the present invention
XX
SQ   Sequence 17 BP; 4 A; 1 C; 4 G; 0 T; 8 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   57.1%;  Pred. No. 3e+03;
  Matches    8;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2117 GTTTTAGGAAACTT 2130
              |::::|||||||::
Db          4 GUUUUAGGAAACUU 17


RESULT 4306
ACD55509
ID   ACD55509 standard; RNA; 17 BP.
XX
AC   ACD55509;
XX
DT   23-SEP-2003  (first entry)
XX
DE   HBV amberzyme substrate sequence #93.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
PI   Blatt L,  Macejak D,  Mcswiggen J,  Morrissey D,  Pavco P,  Lee P;
PI   Draper K,  Roberts E;
XX
DR   WPI; 2003-229207/22.
XX
PT   Novel compound useful for treating cirrhosis, liver failure,
PT   hepatocellular carcinoma, or condition associated with hepatitis C virus
PT   infection.
XX
PS   Example 1; Page 204; 387pp; English.
XX
CC   The present invention relates to nucleic acid molecules which modulate
CC   the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC   Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC   and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC   inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC   are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC   transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC   as oligonucleotides that specifically bind the Enhancer I region of HBV
CC   DNA. The nucleic acids may be used to modulate the expression of HBV
CC   genes and HBV viral replication. Also disclosed is a method for screening
CC   compounds and/or potential therapies directed against HBV, and compounds
CC   that modulate the expression and/or replication of HCV. The compounds and
CC   methods of the invention are useful for the treatment of degenerative and
CC   disease states related to HBV and HCV infection, replication and gene
CC   expression such as cirrhosis, liver failure, and hepatocellular
CC   carcinoma. The present sequence represents a substrate for one of the HBV
CC   ribozyme, inozyme, G-cleaver, zinzyme, DNAzyme or amberzyme sequences
CC   disclosed in the present invention
XX
SQ   Sequence 17 BP; 4 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   57.1%;  Pred. No. 3e+03;
  Matches    8;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2117 GTTTTAGGAAACTT 2130
              |::::|||||||::
Db          2 GUUUUAGGAAACUU 15


RESULT 4307
ACD63827/c
ID   ACD63827 standard; RNA; 17 BP.
XX
AC   ACD63827;
XX
DT   30-SEP-2003  (first entry)
XX
DE   HCV minus strand DNAzyme substrate sequence #1242.
XX
KW   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW   RNA stability; RNA expression; RNA synthesis; antisense;
KW   enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW   HBV reverse transcriptase; Enhancer I region; viral replication;
KW   degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW   liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW   virucide; antiinflammatory; substrate; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO200281494-A1.
XX
PD   17-OCT-2002.
XX
PF   26-MAR-2002; 2002WO-US009187.
XX
PR   26-MAR-2001; 2001US-00817879.
PR   08-JUN-2001; 2001US-00877478.
PR   08-JUN-2001; 2001US-0296876P.
PR   24-OCT-2001; 2001US-0335059P.
PR   05-DEC-2001; 2001US-0337055P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MACE/) MACEJAK D.
PA   (MCSW/) MCSWIGGEN J.
PA   (MORR/) MORRISSEY D.
PA   (PAVC/) PAVCO P.
PA   (LEEP/) LEE P.
PA   (DRAP/) DRAPER K.
PA   (ROBE/) ROBERTS E.
XX
```

PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 297; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 1 A; 4 C; 9 G; 0 T; 3 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 515 CACCACGGGCGCCC 528
||||||||||||||
Db 14 CACCACGGGCGCCC 1

RESULT 4308
ACD58843
ID ACD58843 standard; RNA; 17 BP.
XX
AC ACD58843;
XX
DT 24-SEP-2003 (first entry)
XX
DE HCV DNAzyme substrate sequence #1037.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
DR WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 252; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNAzyme or minus strand DNAzyme sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 3 A; 10 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 515 CACCACGGGCGCCC 528
||||||||||||||
Db 1 CACCACGGGCGCCC 14

RESULT 4309
ACC63818
ID ACC63818 standard; DNA; 17 BP.
XX
AC ACC63818;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour supression, SEQ ID 1065.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX

PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 155; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2074 ATCTGACACACTCT 2087
||||||||||||||
Db 2 ATCTGACACACTCT 15

RESULT 4310
ADB40646
ID ADB40646 standard; DNA; 17 BP.
XX
AC ADB40646;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #969.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 145; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1865 CACTTAGCCATTGA 1878
||||||||||||||
Db 4 CACTTAGCCATTGA 17

RESULT 4311
ADB40890
ID ADB40890 standard; DNA; 17 BP.
XX
AC ADB40890;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #1213.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 173; 771pp; French.
XX

CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

```
  Query Match              0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTT 2178
              ||||||||||||||
Db          4 CTTTTTTTTTTTTT 17
```

RESULT 4312
ADB45762/c
ID ADB45762 standard; DNA; 17 BP.
XX
AC ADB45762;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #6085.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 743; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 3 A; 3 C; 3 G; 8 T; 0 U; 0 Other;

```
  Query Match              0.5%;  Score 14;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        883 ATACAAAGTGACAG 896
              ||||||||||||||
Db         17 ATACAAAGTGACAG 4
```

RESULT 4313
AAH74930/c
ID AAH74930 standard; DNA; 18 BP.
XX
AC AAH74930;
XX
DT 29-OCT-2001 (first entry)
XX
DE DNA sequence of cap adaptor.
XX
KW Nucleotide sequence signature; nucleotide sequencing; ss.
XX
OS Synthetic.
XX
PN WO200161044-A1.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-US005032.
XX
PR 15-FEB-2000; 2000US-0182454P.
PR 01-SEP-2000; 2000US-0654187P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Corcoran KC, Eletr S;
XX
DR WPI; 2001-522608/57.
XX
PT Determining nucleotide sequence signature, by obtaining optical values
PT for each nucleotide position in a group, adjusting them to get ratio of
PT final highest values near predetermined factor, generating base call.
XX
PS Disclosure; Page 19; 73pp; English.
XX
CC The specification describes a method for determining a nucleotide
CC sequence signature. The method comprises obtaining optical measurements
CC with values indicating each nucleotide in a group of nucleotide
CC positions, adjusting the values until the ratio of highest value in the
CC set to next highest values in the set is at least a predetermined factor,
CC and generating a base call for a position in the group based on results
CC after the adjustment of values. The method is used for determining a
CC signature of a nucleotide sequence, and for determining a nucleotide
CC sequence of a polynucleotide from a series of optical measurements. The
CC present sequence represents an adaptor, which is used in the course of

```
CC   the invention
XX
SQ   Sequence 18 BP; 14 A; 0 C; 3 G; 0 T; 0 U; 1 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
              ||||||||||||||
Db         18 TTTTTTTTTTTTTT 5


RESULT 4314
ADC64942/c
ID   ADC64942 standard; DNA; 18 BP.
XX
AC   ADC64942;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Camellia sinensis L. (O.) Kuntze related PCR primer T11C.
XX
KW   Camellia sinensis L.(O.) Kuntze; tea tree; PCR primer; ss.
XX
OS   Synthetic.
OS   Camellia sinensis.
XX
PN   CN1377966-A.
XX
PD   06-NOV-2002.
XX
PF   30-MAR-2001; 2001CN-00112459.
XX
PR   30-MAR-2001; 2001CN-00112459.
XX
PA   (SCIN-) SCI & IND RES COMMISSION.
XX
DR   WPI; 2003-230959/23.
XX
PT   Cloning of a new gene sequence expressed and inhibited during winter
PT   dormancy of a tea tree top plumelet, comprises identification, cloning
PT   and analysis of a new primer in the gene sequence.
XX
PS   Example 3; Page 32; 66pp; Chinese.
XX
CC   The present invention describes the cloning of a new gene sequence
CC   expressed and inhibited during hibernation of the top plumelet of a
CC   Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
CC   identification, cloning and analysis of a primer terminal in the gene
CC   sequence expressed and inhibited during hibernation of the top plumelet
CC   of the tea tree. The present sequence represents a PCR primer which is
CC   used in an example from the present invention.
XX
SQ   Sequence 18 BP; 2 A; 2 C; 1 G; 13 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAA 2798
              ||||||||||||||
Db         18 GAAAAAAAAAAAAA 5


RESULT 4315
AAV48547/c
ID   AAV48547 standard; DNA; 18 BP.
XX
AC   AAV48547;
XX
DT   15-OCT-1998  (first entry)
XX
DE   p53 gene antisense oligonucleotide p53-T-12.
XX
KW   p53; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP856579-A1.
XX
PD   05-AUG-1998.
XX
PF   31-JAN-1997;   97EP-00101531.
XX
PR   31-JAN-1997;   97EP-00101531.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen K,  Brysch W;
XX
DR   WPI; 1998-400910/35.
XX
PT   Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT   consecutive guanosine or inosine - and have specific ratio of residues
PT   able to form two or three hydrogen bonds, have greater activity and
PT   reduced toxicity, used therapeutically or to modulate growth of cells in
PT   culture.
XX
PS   Example 2; Fig 4b; 286pp; English.
XX
CC   AAV48485-564 represent antisense oligonucleotides directed against the
CC   p53 gene. Of these, only oligonucleotides AAV48485-517 resulted in
CC   effective downregulation of negative growth by p53 and increased cell
CC   proliferation, while AAV48518-64 had little effect. The oligonucleotides
CC   exemplify the invention. The specification describes oligonucleotides
CC   that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC   can each form three hydrogen bonds to cytosine; do not contain four
CC   consecutive nucleotides able to form three H-bonds each to four
CC   consecutive cytosines; do not contain two sequences of three consecutive
CC   nucleotides each able to form three H-bonds to three consecutive
CC   cytosines, and the ratio between residues able to form two H-bonds each
CC   (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC   oligonucleotides are used to modulate expression of genes, particularly
CC   the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC   proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC   kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC   oligonucleotides can also be used to analyse function of proteins (by
CC   altering their expression or activity) and therapeutically, e.g. in cases
CC   of cancer or (targeting TGF) for stimulating the immune system
XX
SQ   Sequence 18 BP; 1 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        431 CCCCTGCACCAGCC 444
              ||||||||||||||
Db         16 CCCCTGCACCAGCC 3


RESULT 4316
AAV48548/c
ID   AAV48548 standard; DNA; 18 BP.
XX
AC   AAV48548;
XX
DT   15-OCT-1998  (first entry)
XX
DE   p53 gene antisense oligonucleotide p53-T-13.
XX
KW   p53; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS   Synthetic.
```

OS Homo sapiens.
XX
PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-00101531.
XX
PR 31-JAN-1997; 97EP-00101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen K, Brysch W;
XX
DR WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of residues
PT able to form two or three hydrogen bonds, have greater activity and
PT reduced toxicity, used therapeutically or to modulate growth of cells in
PT culture.
XX
PS Example 2; Fig 4b; 286pp; English.
XX
CC AAV48485-564 represent antisense oligonucleotides directed against the
CC p53 gene. Of these, only oligonucleotides AAV48485-517 resulted in
CC effective downregulation of negative growth by p53 and increased cell
CC proliferation, while AAV48518-64 had little effect. The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in cases
CC of cancer or (targeting TGF) for stimulating the immune system
XX
SQ Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 431 CCCCTGCACCAGCC 444
||||||||||||||
Db 18 CCCCTGCACCAGCC 5

RESULT 4317
AAZ70573
ID AAZ70573 standard; DNA; 18 BP.
XX
AC AAZ70573;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:4929.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 1282; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 886 CAAAGTGACAGTGG 899
||||||||||||||
Db 4 CAAAGTGACAGTGG 17

RESULT 4318
ABX95294
ID ABX95294 standard; DNA; 18 BP.
XX
AC ABX95294;
XX
DT 18-JUN-2003 (first entry)
XX
DE Human ABCA7 associated RT-PCR primer #1.
XX
KW Human; ATP-binding cassette transporter protein A7; ABC transporter;
KW ABCA7; autoimmune disease; Sjogren's syndrome; inflammation;
KW abnormal lipid metabolism; arteriosclerosis; ABCA-SSN inhibitor;
KW immunomodulator; immunosuppressive; antiinflammatory;
KW antiarteriosclerotic; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003010315-A1.
XX
PD 06-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-JP007487.
XX
PR 25-JUL-2001; 2001JP-00224176.
PR 06-DEC-2001; 2001JP-00372530.

XX
PA (KYOW) KYOWA HAKKO KOGYG KK.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI Ueda K, Nakagawa S, Nagase T;
XX
DR WPI; 2003-239444/23.
XX
PT Novel ABC transporter protein, ABCA7 splicing variant, participating in
PT the immune system, applicable in diagnosis of and screening drugs for
PT e.g. autoimmune diseases, Sjoegren's syndrome and inflammations.
XX
PS Example 2; Page 162; 183pp; Japanese.
XX
CC The present invention relates to the isolation of human ATP-binding
CC cassette (ABC) transporter protein A7 (ABCA7) splice variants, and the
CC polynucleotide sequences encoding them. The protein is applicable in the
CC diagnosis and screening of drugs for autoimmune diseases, Sjogren's
CC syndrome, inflammations, abnormal lipid metabolism and arteriosclerosis.
CC It may also be used in a method for screening ABCA-SSN inhibitors. The
CC present sequence represents a reverse transcriptase (RT)-PCR primer used
CC in the examples of the present invention
XX
SQ Sequence 18 BP; 2 A; 10 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1667 CACCCGCCCCTGGA 1680
||||||||||||||
Db 4 CACCCGCCCCTGGA 17

RESULT 4319
ADE27175/c
ID ADE27175 standard; RNA; 19 BP.
XX
AC ADE27175;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:119.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 119; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 1 A; 3 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1978 GAAAAAAAGAAAAG 1991
||||||||||||||
Db 15 GAAAAAAAGAAAAG 2

RESULT 4320
ADE27465
ID ADE27465 standard; RNA; 19 BP.
XX
AC ADE27465;
XX
DT 29-JAN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:409.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KW antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KW atherosclerosis; cancer; viral infection; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN WO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
PS Example 3; SEQ ID NO 409; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 19 BP; 15 A; 0 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1978 GAAAAAAAGAAAAG 1991
||||||||||||||
Db 5 GAAAAAAAGAAAAG 18

RESULT 4321
AAZ59379/c
ID AAZ59379 standard; DNA; 19 BP.
XX
AC AAZ59379;
XX
DT 05-APR-2000 (first entry)
XX
DE Forward PCR primer 3 for STP2 exon 1A sequencing.
XX
KW Single nucleotide polymorphism; SNP; STP2; phenol sulphotransferase;
KW genotyping; human; drug metabolism; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO9964630-A1.
XX
PD 16-DEC-1999.
XX
PF 09-JUN-1999; 99WO-US013094.
XX
PR 10-JUN-1998; 98US-0088710P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Guida M, Kurth J;
XX
DR WPI; 2000-105892/09.
XX
PT Novel nucleic acid used for genotyping, e.g. to predict rate of drug
PT metabolism.
XX
PS Disclosure; Page 14; 46pp; English.
XX
CC This sequence represents a PCR primer used in the sequencing of the exon
CC 1A region of human phenol sulphotransferase 2 (STP2). The invention
CC relates to sequences AAZ59305-Z59352 which are fragments of the STP2
CC gene. The fragments are from the 8 exons, the promoter region, 3' and 5'
CC untranslated regions of the STP2 gene. Each of the sequences contains a
CC newly identified STP2 gene single nucleotide polymorphism (SNP). STP2 is
CC a phenol sulphotransferase. Substrates for STP2 include minoxidil,
CC acetaminophen, and paranitrophenol. Several of the nucleotide changes
CC identified at the polymorphism sites, give rise to an amino acid change.
CC Amino acid changes may result in altered enzyme activity. The sequences
CC can be used as probes for detecting STP2 polymorphisms. The polymorphic
CC probes are used in screening and genotyping, i.e. to predict the rate of
CC metabolism of STP2 substrates, potential drug-drug interactions and
CC adverse side effects. They can also be used to detect diseases resulting
CC from accidental or occupational exposure to toxins and to establish
CC animal, cell or in vitro models for drug metabolism
XX
SQ Sequence 19 BP; 13 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTT 2176
||||||||||||||
Db 17 TCCTTTTTTTTTTT 4

RESULT 4322
AAA86064/c
ID AAA86064 standard; DNA; 19 BP.
XX
AC AAA86064;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cdc 25 hs ribozyme binding site #172.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 102; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 13 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2179 TTTTTTTTAACTTT 2192
||||||||||||||
Db 18 TTTTTTTTAACTTT 5

RESULT 4323
AAA86065/c
ID AAA86065 standard; DNA; 19 BP.
XX
AC AAA86065;
XX
DT 04-DEC-2000 (first entry)
XX
DE Cdc 25 hs ribozyme binding site #173.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 102; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 12 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2179 TTTTTTTTAACTTT 2192
||||||||||||||
Db 17 TTTTTTTTAACTTT 4

RESULT 4324
AAH61226/c
ID AAH61226 standard; DNA; 19 BP.
XX
AC AAH61226;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3650.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 337; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 13 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2179 TTTTTTTTAACTTT 2192
||||||||||||||
Db 18 TTTTTTTTAACTTT 5

RESULT 4325
AAH61227/c
ID AAH61227 standard; DNA; 19 BP.
XX
AC AAH61227;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3651.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;

```
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 337; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 12 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2179 TTTTTTTTAACTTT 2192
                ||||||||||||||
Db         17 TTTTTTTTAACTTT 4


RESULT 4326
AAT73291
ID   AAT73291 standard; DNA; 20 BP.
XX
AC   AAT73291;
XX
DT   12-DEC-1997  (first entry)
XX
DE   Primer 1 for pUC19 DNA amplification.
XX
KW   primer; PCR; polymerase chain reaction; sequencing; walking;
KW   complementary extension reaction; low redundancy; universal primer; ss.
XX
OS   Synthetic.
XX
PN   EP767240-A2.
XX
PD   09-APR-1997.
XX
PF   17-SEP-1996;   96EP-00114907.
XX
PR   18-SEP-1995;   95JP-00238141.
PR   30-JAN-1996;   96JP-00013634.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K;
XX
DR   WPI; 1997-205424/19.
XX
PT   Efficient sequencing of long DNA by fragment walking - with simultaneous
PT   sequencing of restriction enzyme fragment and adjacent region of intact
PT   DNA, avoids the need for cloning and requires fewer primers.
XX
PS   Example 1; Page 11; 50pp; English.
XX
CC   A method for DNA analysis based on a complementary extension reaction
CC   using a DNA polymerase, comprises a combination of fragment walking and
CC   DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC   restriction enzyme and the targeted DNA sequence can be determined
CC   directly from the digested DNA fragments. By exploring the overlapping
CC   sequence of the determined base sequence, the overall base sequence of a
CC   lengthy DNA can be determined with low redundancy without cloning or
CC   subcloning. In addition, the method can be done with commercially
CC   available universal primers or with fewer primers than required in
CC   existing methods. AAT73291-92 are primers used in determination of the
CC   pUC19 sequence. Primer extension was carried out using 16 primers
CC   AAT73293
XX
SQ   Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTT 2179
                ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4327
AAT73292
ID   AAT73292 standard; DNA; 20 BP.
XX
AC   AAT73292;
XX
DT   12-DEC-1997  (first entry)
XX
DE   Primer 2 for pUC19 DNA amplification.
XX
KW   primer; PCR; polymerase chain reaction; sequencing; walking;
KW   complementary extension reaction; low redundancy; universal primer; ss.
XX
OS   Synthetic.
XX
PN   EP767240-A2.
XX
PD   09-APR-1997.
XX
PF   17-SEP-1996;   96EP-00114907.
XX
PR   18-SEP-1995;   95JP-00238141.
PR   30-JAN-1996;   96JP-00013634.
XX
PA   (HITA ) HITACHI LTD.
XX
```

PI Kambara H, Okano K;
XX
DR WPI; 1997-205424/19.
XX
PT Efficient sequencing of long DNA by fragment walking - with simultaneous
PT sequencing of restriction enzyme fragment and adjacent region of intact
PT DNA, avoids the need for cloning and requires fewer primers.
XX
PS Example 1; Page 11; 50pp; English.
XX
CC A method for DNA analysis based on a complementary extension reaction
CC using a DNA polymerase, comprises a combination of fragment walking and
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC restriction enzyme and the targeted DNA sequence can be determined
CC directly from the digested DNA fragments. By exploring the overlapping
CC sequence of the determined base sequence, the overall base sequence of a
CC lengthy DNA can be determined with low redundancy without cloning or
CC subcloning. In addition, the method can be done with commercially
CC available universal primers or with fewer primers than required in
CC existing methods. AAT73291-92 are primers used in determination of the
CC pUC19 sequence. Primer extension was carried out using 16 primers
CC AAT73293
XX
SQ Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTT 2179
||||||||||||||
Db 1 TTTTTTTTTTTTTT 14

RESULT 4328
AAF99302/c
ID AAF99302 standard; DNA; 20 BP.
XX
AC AAF99302;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #418.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 46; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799
||||||||||||||
Db 20 AAAAAAAAAAAAAA 7

RESULT 4329
ABS77947/c
ID ABS77947 standard; DNA; 20 BP.
XX
AC ABS77947;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #431.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

```
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         20 AAAAAAAAAAAAAA 7


RESULT 4330
ABL39308/c
ID   ABL39308 standard; DNA; 20 BP.
XX
AC   ABL39308;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 737.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 283; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         20 AAAAAAAAAAAAAA 7


RESULT 4331
ACD99727/c
ID   ACD99727 standard; DNA; 20 BP.
XX
AC   ACD99727;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #413.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 20; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         20 AAAAAAAAAAAAAA 7


RESULT 4332
```

```
ADB36804/c
ID   ADB36804 standard; DNA; 20 BP.
XX
AC   ADB36804;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #418.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 11; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 16 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db         20 AAAAAAAAAAAAAA 7


RESULT 4333
AAQ97488
ID   AAQ97488 standard; cDNA; 20 BP.
XX
AC   AAQ97488;
XX
DT   25-MAR-2003  (revised)
DT   22-DEC-1995  (first entry)
XX
DE   M. sexta alaserpin PCR primer.
XX
KW   Alaserpin; serpin; serine protease-inhibitor; elastase inhibitor;
KW   chymotrypsin-inhibitor; plant protectant; insect resistance;
KW   crop improvement; transgenic plant; alfalfa; Medicago sativa;
KW   Manduca sexta; primer; PCR; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   US5436392-A.
XX
PD   25-JUL-1995.
XX
PF   21-DEC-1992;   92US-00994133.
XX
PR   12-JAN-1990;   90US-00464310.
XX
PA   (ARIZ-) ARIZONA TECHNOLOGY DEV CORP.
XX
PI   Thomas JC,  Bohnert HJ,  Kanost MR;
XX
DR   WPI; 1995-268881/35.
XX
PT   Transgenic plant containing novel serine protease inhibitor gene of M.
PT   sexta - provides protection for the plant against attack by insects, e.g.
PT   alfalfa against thrips.
XX
PS   Example 7; Col 16; 24pp; English.
XX
CC   PCR primers given in AAQ97487-88, corresp. to nt. 73-92 and 835-854 of M.
CC   sexta alaserpin cDNA (AAQ97486) respectively, were used to generate a 782
CC   bp PCR fragment used as a DNA probe for the M. sexta alaserpin gene in
CC   transgenic alfalfa plants. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        861 CGCTCCTCAGCTCT 874
              ||||||||||||||
Db          1 CGCTCCTCAGCTCT 14


RESULT 4334
AAX33317/c
ID   AAX33317 standard; DNA; 20 BP.
XX
AC   AAX33317;
XX
DT   30-JUN-1999  (first entry)
XX
DE   PEBP2 alpha A gene expression regulating DNA PCR primer SEQ ID NO:76.
XX
KW   PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911787-A1.
XX
PD   11-MAR-1999.
XX
PF   02-SEP-1998;   98WO-JP003920.
XX
PR   02-SEP-1997;   97JP-00254250.
PR   15-OCT-1997;   97JP-00299407.
PR   08-APR-1998;   98JP-00114135.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Harada H,  Fujiwara M,  Tagashira S,  Ogawa S,  Katsumata T;
PI   Nakatsuka M;
XX
DR   WPI; 1999-243621/20.
XX
PT   DNA regulating expression of PEBP2 alphaA gene to produce regulator
PT   protein, useful as promoter for prevention or/and treatment of bone
PT   diseases e.g. osteoporosis.
XX
PS   Example 10; Page 46; 118pp; Japanese.
XX
CC   The present invention describes DNA which participates in the regulation
```

```
CC   of expression of PEBP2 alpha A gene. The DNA produces a regulator protein
CC   with the activity of promoting bone formation and can serve as a promoter
CC   for prevention and treatment of bone diseases including osteoporosis. The
CC   present sequence represents a PCR primer used in an example from the
CC   present invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        436 GCACCAGCCGGCGC 449
              ||||||||||||||
Db         18 GCACCAGCCGGCGC 5


RESULT 4335
AAX33251/c
ID   AAX33251 standard; DNA; 20 BP.
XX
AC   AAX33251;
XX
DT   30-JUN-1999  (first entry)
XX
DE   PEBP2 alpha A gene expression regulating DNA PCR primer SEQ ID NO:8.
XX
KW   PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911787-A1.
XX
PD   11-MAR-1999.
XX
PF   02-SEP-1998;   98WO-JP003920.
XX
PR   02-SEP-1997;   97JP-00254250.
PR   15-OCT-1997;   97JP-00299407.
PR   08-APR-1998;   98JP-00114135.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Harada H,  Fujiwara M,  Tagashira S,  Ogawa S,  Katsumata T;
PI   Nakatsuka M;
XX
DR   WPI; 1999-243621/20.
XX
PT   DNA regulating expression of PEBP2 alphaA gene to produce regulator
PT   protein, useful as promoter for prevention or/and treatment of bone
PT   diseases e.g. osteoporosis.
XX
PS   Example 1; Page 27; 118pp; Japanese.
XX
CC   The present invention describes DNA which participates in the regulation
CC   of expression of PEBP2 alpha A gene. The DNA produces a regulator protein
CC   with the activity of promoting bone formation and can serve as a promoter
CC   for prevention and treatment of bone diseases including osteoporosis. The
CC   present sequence represents a PCR primer used in an example from the
CC   present invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        436 GCACCAGCCGGCGC 449
              ||||||||||||||
Db         18 GCACCAGCCGGCGC 5


RESULT 4336
AAX33257/c
ID   AAX33257 standard; DNA; 20 BP.
XX
AC   AAX33257;
XX
DT   30-JUN-1999  (first entry)
XX
DE   PEBP2 alpha A gene expression regulating DNA PCR primer SEQ ID NO:14.
XX
KW   PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9911787-A1.
XX
PD   11-MAR-1999.
XX
PF   02-SEP-1998;   98WO-JP003920.
XX
PR   02-SEP-1997;   97JP-00254250.
PR   15-OCT-1997;   97JP-00299407.
PR   08-APR-1998;   98JP-00114135.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Harada H,  Fujiwara M,  Tagashira S,  Ogawa S,  Katsumata T;
PI   Nakatsuka M;
XX
DR   WPI; 1999-243621/20.
XX
PT   DNA regulating expression of PEBP2 alphaA gene to produce regulator
PT   protein, useful as promoter for prevention or/and treatment of bone
PT   diseases e.g. osteoporosis.
XX
PS   Example 2; Page 29; 118pp; Japanese.
XX
CC   The present invention describes DNA which participates in the regulation
CC   of expression of PEBP2 alpha A gene. The DNA produces a regulator protein
CC   with the activity of promoting bone formation and can serve as a promoter
CC   for prevention and treatment of bone diseases including osteoporosis. The
CC   present sequence represents a PCR primer used in an example from the
CC   present invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        436 GCACCAGCCGGCGC 449
              ||||||||||||||
Db         18 GCACCAGCCGGCGC 5


RESULT 4337
AAS10630/c
ID   AAS10630 standard; DNA; 20 BP.
XX
AC   AAS10630;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human caspase 3 antisense oligonucleotide 108954.
XX
KW   Human; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;
KW   viral infection; haematopoietic disorder; autoimmune disorder;
KW   atherosclerosis; neurological disorder; antisense; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

```
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate internucleotide linkages.
FT                   Some bases especially bases 1-5 and bases 16-20 are 2'-
FT                   methoxyethyl (2'-MOE) bases, bases 6-15 are 2'-
FT                   deoxynucleotides and all cytidine bases are 5'-
FT                   methylcytidines"
XX
PN   WO200153310-A1.
XX
PD   26-JUL-2001.
XX
PF   11-JAN-2001; 2001WO-US000888.
XX
PR   18-JAN-2000; 2000US-00484617.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Zhang H,  Cowsert LM;
XX
DR   WPI; 2001-442252/47.
XX
PT   New antisense compound to inhibit caspase 3 is useful for treating
PT   hepatitis and atherosclerosis.
XX
PS   Example 17; Page 87; 127pp; English.
XX
CC   The present sequence for human caspase 3 antisense oligonucleotide 108954
CC   is 1 of various novel antisense oligonucleotides (AAS10517-AAS10676)
CC   described in the present invention. Also described are methods of using
CC   these compounds for the modulation of caspase 3 expression. The caspase 3
CC   antisense oligonucleotides specifically hybridise with and inhibit the
CC   expression of caspase 3. Antisense compounds targeted to caspase 3 are
CC   useful to inhibit caspase 3 expression in cells or tissues and to
CC   modulate apoptosis. The caspase 3 antisense oligonucleotides are useful
CC   for treating disorders associated with expression of caspase 3. Such
CC   disorders include hyperproliferative disorders (e.g. cancer), viral
CC   infections (e.g. hepatitis), haematopoietic disorders, autoimmune
CC   disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
CC   disease)
XX
SQ   Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2000 TAGCTTCTTCAGAG 2013
              ||||||||||||||
Db         20 TAGCTTCTTCAGAG 7


RESULT 4338
AAF74765/c
ID   AAF74765 standard; DNA; 20 BP.
XX
AC   AAF74765;
XX
DT   17-MAY-2001  (first entry)
XX
DE   Human hDPP PCR primer SEQ ID NO:5.
XX
KW   Human; hDPP; diacylglycerol pyrophosphate phosphatase; DPP; detection;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1271009-A.
XX
PD   25-OCT-2000.
XX
PF   17-MAR-2000; 2000CN-00114952.
XX
PR   17-MAR-2000; 2000CN-00114952.
XX
PA   (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
XX
PI   Li N,  Xiao H,  Liu F;
XX
DR   WPI; 2001-081384/10.
XX
PT   New human diacyl glyceropyrophosphate phosphatase protein and its code
PT   sequence.
XX
PS   Example 1; Page 10; 19pp; Chinese.
XX
CC   The present invention describes a human diacylglycerol pyrophosphate
CC   phosphatase (DPP) designated hDPP. hDPP is expressed in normal tissue
CC   near cancerous liver cells of a human body. Also described are methods
CC   for the preparation and detection of hDPP nucleotide and protein
CC   sequences. The present sequence represents a PCR primer for human hDPP,
CC   which is used in an example from the present invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2608 TGTTCAGAAAGCAA 2621
              ||||||||||||||
Db         18 TGTTCAGAAAGCAA 5


RESULT 4339
AAD11975
ID   AAD11975 standard; DNA; 20 BP.
XX
AC   AAD11975;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human PTP1B antisense oligonucleotide (ISIS# 107784).
XX
KW   Human; PTP1B; protein phosphatase 1B inhibitor; antisense; gene therapy;
KW   infection; inflammation; tumour; prophylaxis; phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Methoxyethyl residues"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= m5c
FT   modified_base   10
FT                   /*tag=  e
FT                   /mod_base= m5c
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "Methoxyethyl residues"
FT   modified_base   17
FT                   /*tag=  f
FT                   /mod_base= m5c
XX
PN   US6261840-B1.
XX
```

PD 17-JUL-2001.
XX
PF 18-JAN-2000; 2000US-00487368.
XX
PR 18-JAN-2000; 2000US-00487368.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowsert LM, Wyatt J;
XX
DR WPI; 2001-432181/46.
XX
PT New antisense compounds capable of modulating expression of human protein
PT phosphatase 1B, useful for diagnosis, prophylaxis and treatment of
PT diseases associated with expression of protein phosphatase.
XX
PS Claim 1; Col 42; 71pp; English.
XX
CC The invention is directed to antisense compounds, particularly
CC oligonucleotides which are targetted to a DNA encoding protein
CC phosphatase 1B (PTP1B) to modulate its expression. The antisense
CC compounds are useful for diagnosis, prophylaxis and treatment of diseases
CC associated with the expression of PTP1B, to prevent or delay infection,
CC inflammation and tumour formation and as a research reagent. The PTP1B
CC DNA is useful in gene therapy. The present sequence is an antisense
CC oligonucleotide with a phosphorothioate backbone. This oligo is targetted
CC to human PTP1B to inhibit its expression
XX
SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2005 TCTTCAGAGATCAA 2018
||||||||||||||
Db 6 TCTTCAGAGATCAA 19

RESULT 4340
ABK85050
ID ABK85050 standard; DNA; 20 BP.
XX
AC ABK85050;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human PTP1B antisense oligonucleotide ISIS 107784.
XX
KW Antisense; protein phosphatase 1B; PTP1B; ss; probe; human;
KW type 2 diabetes; obesity; ovarian cancer; chronic myeloid leukaemia;
KW hyperproliferative disease; antidiabetic; anorectic; cytostatic;
KW blood glucose; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002055479-A1.
XX
PD 09-MAY-2002.
XX
PF 14-MAY-2001; 2001US-00854883.
XX
PR 18-JAN-2000; 2000US-00487368.
PR 31-JUL-2000; 2000US-00629644.
XX
PA (COWS/) COWSERT L M.
PA (WYAT/) WYATT J.
PA (FREI/) FREIER S M.
PA (MONI/) MONIA B P.
PA (BUTL/) BUTLER M M.
PA (MCKA/) MCKAY R.
XX
PI Cowsert LM, Wyatt J, Freier SM, Monia BP, Butler MM, Mckay R;
XX
DR WPI; 2002-462914/49.
XX
PT Compound for inhibiting the expression of protein phosphatase 1B (PTP1B)
PT and for treating diabetes, cancer, or obesity, comprises an antisense
PT oligonucleotide targeted to nucleic acid encoding PTP1B.
XX
PS Claim 3; Page 23; 133pp; English.
XX
CC The invention relates to a compound of 8-50 nucleobases in length
CC targeted to a nucleic acid encoding protein phosphatase 1B (PTP1B), where
CC the compound specifically hybridises with and inhibits the expression of
CC PTP1B (e.g. an antisense oligonucleotide). Also included are (1) a
CC compound of 8-50 nucleobases in length which specifically hybridises with
CC an 8 nucleobase portion of an active site on a nucleic acid encoding
CC PTP1B; (2) inhibiting the expression of PTP1B in cells or tissues
CC comprising contacting the cells or tissues with the compound; treating an
CC animal having or suspected of having a disease or condition associated
CC with PTP1B comprising administering the compound; (4) decreasing blood
CC sugar levels in an animal comprising administering the compound; (5)
CC preventing or delaying the onset of a disease or condition associated
CC with PTP1B in an animal comprising administering the compound; and (6)
CC preventing or delaying the onset of an increase in blood glucose levels
CC in an animal comprising administering the compound. The compound is used
CC to inhibit the expression of PTP1B in cells or tissues, to treat or
CC prevent or delay the onset of a disease or condition associated with
CC PTP1B, such as type 2 diabetes, obesity, cancer (especially ovarian
CC cancer, chronic myeloid leukaemia and hyperproliferative diseases in an
CC animal having or suspected of having the disease or condition, and for
CC decreasing blood sugar levels or preventing or delaying the onset of an
CC increase in blood glucose levels in an animal. The compound is also used
CC in diagnostics, therapeutics, prophylaxis, and in research reagents and
CC kits. The present sequence is an antisense compound of the invention
CC targetting human PTP1B
XX
SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2005 TCTTCAGAGATCAA 2018
||||||||||||||
Db 6 TCTTCAGAGATCAA 19

RESULT 4341
ABK37219
ID ABK37219 standard; DNA; 20 BP.
XX
AC ABK37219;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PTP1B mRNA level inhibition antisense DNA #16.
XX
KW Human; mouse; rat; protein tyrosine phosphatase 1B; PTP1B; ss; adipose;
KW liver; kidney; metabolic disease; type 2 diabetes; obesity; cancer;
KW hyperproliferative condition; blood serum; blood plasma; antidiabetic;
KW blood glucose level; cytostatic; anorectic; antisense gene therapy;
KW PTP1B mRNA level inhibition.
XX
OS Homo sapiens.
XX
PN WO200210378-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US023874.
XX
PR 31-JUL-2000; 2000US-00629644.
XX
PA (ISIS-) ISIS PHARM INC.

XX
PI Cowsert LM, Wyatt J, Freier SM, Monia BP, Butler MM, Mckay R;
XX
DR WPI; 2002-180079/23.
XX
PT Novel antisense compound useful for treating type 2 diabetes, cancer and
PT obesity, is targeted to nucleic acid encoding human protein phosphatase
PT 1B, and hybridizes and inhibits PTP1B expression.
XX
PS Claim 3; Page 67; 142pp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding protein phosphatase 1B (PTP1B), which specifically hybridises
CC with and inhibits the expression of PTP1B. The compounds of the invention
CC are useful for inhibiting the expression of PTP1B in liver, kidney or
CC adipose cells or tissues and for treating an animal, preferably human,
CC having a disease or condition associated with PTP1B, including metabolic
CC diseases or conditions, e.g. type 2 diabetes and obesity, or
CC hyperproliferative conditions such as cancer. The sequences are also
CC useful for decreasing blood (serum or plasma) glucose levels in an animal
CC e.g. a diabetic human or rodent, for preventing or delaying the onset of
CC a disease or condition associated with PTP1B , and for preventing or
CC delaying the onset of an increase in blood glucose levels. This sequence
CC represents a PTP1B mRNA level inhibition antisense oligonucleotide of the
CC invention
XX
SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2005 TCTTCAGAGATCAA 2018
||||||||||||||
Db 6 TCTTCAGAGATCAA 19

RESULT 4342
ABI96879
ID ABI96879 standard; DNA; 20 BP.
XX
AC ABI96879;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleptide Zip ID#3966 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC medinesis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 GGACTGCGAGGATC 218
||||||||||||||
Db 5 GGACTGCGAGGATC 18

RESULT 4343
ABZ89489/c
ID ABZ89489 standard; DNA; 20 BP.
XX
AC ABZ89489;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4731; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2174 TTTTTTTTTTTTTA 2187
||||||||||||||
Db 17 TTTTTTTTTTTTTA 4

RESULT 4344
ABZ90889
ID ABZ90889 standard; DNA; 20 BP.
XX
AC ABZ90889;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6131; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 6 A; 0 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1491 TGGAGAAAATGGAG 1504
||||||||||||||
Db 2 TGGAGAAAATGGAG 15

RESULT 4345
ABZ91792
ID ABZ91792 standard; DNA; 20 BP.
XX
AC ABZ91792;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7034; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 4 A; 2 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 948 TACTGGGAGGTGTT 961
||||||||||||||
Db 3 TACTGGGAGGTGTT 16

RESULT 4346
ADC51216/c
ID ADC51216 standard; DNA; 20 BP.
XX
AC ADC51216;
XX
DT 18-DEC-2003 (first entry)
XX
DE PCR primer #1 for DNA encoding Spirotrichonympha leidyi cellulase.
XX
KW Protozoa; cellulase; industrial enzyme agent; detergent; fodder additive;
KW textile processing industry; PCR; primer; ss.
XX
OS Spirotrichonympha leidyi.
XX
PN JP2003070475-A.
XX
PD 11-MAR-2003.
XX
PF 03-SEP-2001; 2001JP-00266454.
XX
PR 03-SEP-2001; 2001JP-00266454.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
XX
DR WPI; 2003-782806/74.
XX
PT Novel protein having cellulase activity obtained from termite symbiosis
PT protozoa, useful in textile processing, as fodder additive and detergent.
XX
PS Example; SEQ ID NO 3; 10pp; Japanese.
XX
CC The present invention relates to the isolation of a protozoa
CC (Spirotrichonympha leidyi) cellulase, and the polynucleotide sequence
CC encoding it. The protein is useful as an industrial enzyme agent, e.g.
CC detergents, fodder additive, and in textile processing industries. The
CC polynucleotide sequence encoding the cellulase is useful for producing
CC the protein by recombinant techniques. The present sequence represents a
CC PCR primer used in the examples of the present invention.
XX
SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1910 ATCAACAATACCTT 1923
||||||||||||||
Db 18 ATCAACAATACCTT 5

RESULT 4347
AAZ26249/c
ID AAZ26249 standard; DNA; 21 BP.
XX
AC AAZ26249;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 438.
XX
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS Homo sapiens.
XX
PN WO9841648-A2.
XX
PD 24-SEP-1998.
XX
PF 19-MAR-1998; 98WO-US005419.
XX
PR 20-MAR-1997; 97US-0041057P.
XX
PA (VARI-) VARIAGENICS INC.
XX
PI Housman D, Ledley FD, Stanton VP;
XX
DR WPI; 1998-521232/44.
XX
PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
PS Disclosure; Fig 7; 605pp; English.
XX
CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC human polymorphic sites described in the method of the invention

```
XX
SQ   Sequence 21 BP; 13 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||||
Db         21 TTTTTTTTTTTTAA 8


RESULT 4348
AAQ71292
ID   AAQ71292 standard; DNA; 21 BP.
XX
AC   AAQ71292;
XX
DT   12-MAY-1995  (first entry)
XX
DE   Feline zona pellucida (FZP)-2 PCR primer-5.
XX
KW   Feline zona pellucida; FZP-2; contraceptive vaccine antigen; ss.
XX
OS   Synthetic.
XX
PN   JP06217777-A.
XX
PD   09-AUG-1994.
XX
PF   29-JAN-1993;   93JP-00013496.
XX
PR   29-JAN-1993;   93JP-00013496.
XX
PA   (TOFU ) TONEN CORP.
XX
DR   WPI; 1994-305384/38.
XX
PT   New DNA sequence coding feline zona pellucida (FZP) 2 - used for prodn.
PT   of contraceptive vaccine antigen for cats.
XX
PS   Example 2; Page 5; 10pp; Japanese.
XX
CC   The feline zona pellucida (FZP)-2 coding sequence was obtained by PCR
CC   amplification of cDNA synthesised from mRNA isolated from cat ovaries.
CC   PCR primers 3, 4 and 5 (AAQ71290-Q71292) were used to amplify cDNA
CC   corresponding to codons 477-716 of FZP-2. Subfragments of the FZP-2
CC   protein can be expressed for use as antigens in contraceptive vaccines
CC   for cats
XX
SQ   Sequence 21 BP; 3 A; 4 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTT 1780
              ||||||||||||||
Db          8 AAGCTTTTTTTTTT 21


RESULT 4349
AAZ26403/c
ID   AAZ26403 standard; DNA; 21 BP.
XX
AC   AAZ26403;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human polymorphic region 592.
XX
KW   Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW   cell viability; loss of heterozygosity; precancerous condition; ASI;
KW   allele specific inhibitor; somatic cell; diagnosis; prevention;
KW   atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW   dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW   graft versus host disease; malignant cell removal; bone marrow; ss.
XX
OS   Homo sapiens.
XX
PN   WO9841648-A2.
XX
PD   24-SEP-1998.
XX
PF   19-MAR-1998;   98WO-US005419.
XX
PR   20-MAR-1997;   97US-0041057P.
XX
PA   (VARI-) VARIAGENICS INC.
XX
PI   Housman D,  Ledley FD,  Stanton VP;
XX
DR   WPI; 1998-521232/44.
XX
PT   Identifying target genes for allele-specific drugs - used for diagnosis,
PT   prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT   dysplastic lesions, endometriosis or graft versus host disease.
XX
PS   Disclosure; Fig 7; 605pp; English.
XX
CC   This invention describes a novel method for identifying an inhibitor
CC   potentially useful for treatment of cancer, where the inhibitor is active
CC   on a gene vital for cell growth or viability, and where the gene is
CC   subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC   used for preventing the development of cancer in a patient having a
CC   precancerous condition, by administering to the patient a first allele
CC   specific inhibitor (ASI) targeted to an allele of a first essential gene
CC   present in cells of the precancerous condition, where the normal somatic
CC   cells of the patient are heterozygous for the first gene, the inhibitor
CC   is active on at least one but less than all allelic forms of the gene
CC   present in a population and targets only one allelic form present in the
CC   normal somatic cells, and the first gene. The products and methods can be
CC   used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC   cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC   lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC   graft versus host disease. The method can also be used to remove
CC   malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
CC   human polymorphic sites described in the method of the invention
XX
SQ   Sequence 21 BP; 12 A; 2 C; 0 G; 7 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAA 2188
              ||||||||||||||
Db         21 TTTTTTTTTTTTAA 8


RESULT 4350
AAF96504/c
ID   AAF96504 standard; DNA; 21 BP.
XX
AC   AAF96504;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1265.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,C)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 136; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 12 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTT 2170
              ||||||||||||||
Db         19 TTTTTCTCCTTTTT 6


RESULT 4351
AAH22316/c
ID   AAH22316 standard; DNA; 22 BP.
XX
AC   AAH22316;
XX
DT   21-AUG-2001  (first entry)
XX
DE   Brain ankyrin-2 hybridisation probe SEQ ID NO:62.
XX
KW   Human; differentially expressed gene; angiogenesis; diagnosis;
KW   angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KW   vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KW   rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KW   neovascularisation; restenosis; hypertension; aneurysm; angina;
KW   myocardial infarction; chronic heart condition; osteoporosis; PCR primer;
KW   hybridisation; probe; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200132926-A2.
XX
PD   10-MAY-2001.
XX
PF   01-NOV-2000; 2000WO-US030051.
XX
PR   01-NOV-1999;   99US-0162699P.
PR   13-APR-2000; 2000US-0196802P.
PR   31-OCT-2000; 2000US-00703350.
XX
PA   (CURA-) CURAGEN CORP.
PA   (GETH ) GENENTECH INC.
XX
PI   Mehraban F,  Gerritsen M,  Rastelli L;
XX
DR   WPI; 2001-291056/30.
XX
PT   Differentially expressed genes involved in angiogenesis, useful for
PT   treating e.g. vascular tumors, atherosclerosis and/or restenosis
PT   subsequent to balloon angioplasty.
XX
PS   Example 19; Page 148; 182pp; English.
XX
CC   The present invention describes differentially expressed genes involved
CC   in angiogenesis (I), and the polypeptides that encode them. (I) have
CC   cardiovascular activity, and can be used in the modulation of
CC   angiogenesis. The nucleic acids and polypeptides may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate angiogenesis. The polypeptides may also be used as antigens
CC   in the production of antibodies against them and in assays to identify
CC   modulators of their expression and activity. The antibodies and
CC   antagonists may also be used to down regulate expression and activity and
CC   modulate angiogenesis. The antibodies may also be used as diagnostic
CC   agents for detecting the presence of the polypeptides in samples.
CC   Disorders that may be prevented, diagnosed and/or treated by the above
CC   methods include, for example vascular tumours, proliferative tumours,
CC   proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC   atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC   associated with neovascularisation, restenosis subsequent to balloon
CC   angioplasty, scar tissue over production. peripheral vascular disease,
CC   hypertension, inflammatory vasculitides, Reynaud's disease and Reynaud's
CC   phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC   lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC   reperfusion injury, angina, myocardial infarctions, chronic heart
CC   conditions, heart failure such as congestive heart failure, age-related
CC   macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322
CC   to AAB98325 represent sequence used in the exemplification of the present
CC   invention
XX
SQ   Sequence 22 BP; 8 A; 9 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 22;
  Best Local Similarity   77.3%;  Pred. No. 4.5e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2562 TGGGCTCTGTTCTTGGCTTGGA 2583
              |||   ||||||||||||  ||
Db         22 TGGTGGCTGTTCTTGGCTGCGA 1


RESULT 4352
AAX81611
ID   AAX81611 standard; DNA; 23 BP.
XX
AC   AAX81611;
XX
DT   26-AUG-1999  (first entry)
XX
DE   PCR primer used to amplify erythrovirus V9 nucleotide sequences.
XX
KW   Erythrovirus V9; differential diagnosis; parvovirus; infection;
KW   erythrovirus screening; typing; immunoassay; PCR primer; ss.
```

XX
OS Synthetic.
OS Erythrovirus.
XX
PN FR2771751-A1.
XX
PD 04-JUN-1999.
XX
PF 03-DEC-1997; 97FR-00015197.
XX
PR 03-DEC-1997; 97FR-00015197.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX
PI Nguyen QT, Garbarg CA, Auguste V;
XX
DR WPI; 1999-349543/30.
XX
PT Erythrovirus V9 and its nucleic acid sequences - can be used in the
PT diagnosis of its infections.
XX
PS Claim 3; Page 27; 80pp; French.
XX
CC AAX81588-X81630 represent PCR primers used to amplify erythrovirus V9
CC polynucleotide sequences. Probes and primers derived from erythrovirus V9
CC polynucleotide sequences (AAX81580) can be used for differential
CC diagnosis of erythrovirus (parvovirus) infections by a combination of
CC amplification and hybridisation assay. The probes can also be used to
CC assess susceptibility to erythrovirus infection and for erythrovirus
CC screening and typing. The antibodies can be used in immunoassays for
CC diagnosis of erythrovirus V9 infections
XX
SQ Sequence 23 BP; 16 A; 1 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 23;
Best Local Similarity 77.3%; Pred. No. 4.7e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAAA 2804
|| ||||| | |||||| |||
Db 1 TTAAAAAATATAAAAAATGAAA 22

RESULT 4353
ABN86867/c
ID ABN86867 standard; DNA; 24 BP.
XX
AC ABN86867;
XX
DT 23-JUL-2002 (first entry)
XX
DE Human macroprotein 11.88 PCR primer 2 SEQ ID NO:4.
XX
KW Human; macroprotein 11.88; embryo development disorder; tumour;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1331201-A.
XX
PD 16-JAN-2002.
XX
PF 30-JUN-2000; 2000CN-00116908.
XX
PR 30-JUN-2000; 2000CN-00116908.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292867/34.
XX
PT Polypeptide-human macroprotein 11.88 and polynucleotide for coding it.
XX
PS Example 2; Page 19 (Disclosure); 34pp; Chinese.
XX
CC The present invention describes human macroprotein 11.88 (I). Also
CC described is a process for preparing (I) using DNA recombination
CC techniques. (I) and the polynucleotide encoding it can be used in the
CC treatment of diseases such as embryo development disorders and tumours.
CC The present sequence represents a PCR primer for human macroprotein
CC 11.88, which is used in an example from the present invention
XX
SQ Sequence 24 BP; 4 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 24;
Best Local Similarity 77.3%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAAA 2804
|| || ||| |||||||||||
Db 24 TTTAATAAACCCAAAAAAAAAA 3

RESULT 4354
AAC95962
ID AAC95962 standard; DNA; 25 BP.
XX
AC AAC95962;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-B gene PCR primer #73.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 43; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 7 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 14; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTT 2179

```
                    ||||||||||||||
Db          1 TTTTTTTTTTTTTT 14


RESULT 4355
AAC95680/c
ID   AAC95680 standard; DNA; 25 BP.
XX
AC   AAC95680;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DPB1 gene PCR primer #15.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 38; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 25;
  Best Local Similarity   77.3%;  Pred. No. 5e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAA 2797
              | | | | | ||||||||||||
Db         22 GCTCGTAGTTAAAAAAAAAAAA 1


RESULT 4356
ABL35095
ID   ABL35095 standard; DNA; 30 BP.
XX
AC   ABL35095;
XX
DT   04-APR-2002  (first entry)
XX
DE   RNA/DNA hybrid control oligonucleotide SEQ ID NO: 1.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .30
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4357
ABL35096
ID   ABL35096 standard; DNA; 30 BP.
XX
AC   ABL35096;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 2.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .30
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
FT   misc_RNA        1. .12
FT                   /*tag=  b
FT   misc_RNA        19. .30
FT                   /*tag=  c
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4358
ABL35097
ID   ABL35097 standard; DNA; 30 BP.
XX
AC   ABL35097;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 3.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .30
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
FT   misc_RNA        13. .18
FT                   /*tag=  b
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4359
ABL35105
ID   ABL35105 standard; DNA; 30 BP.
XX
AC   ABL35105;
XX
DT   04-APR-2002  (first entry)
XX
DE   RNA/DNA hybrid assay control oligonucleotide SEQ ID NO: 11.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .30
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 30; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4360
ABL35098
ID   ABL35098 standard; RNA; 30 BP.
XX
AC   ABL35098;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA SEQ ID NO: 4.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .30
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.5%;  Score 14;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAA 2799
              ||||||||||||||
Db          1 AAAAAAAAAAAAAA 14


RESULT 4361
AAX69804
ID   AAX69804 standard; RNA; 17 BP.
XX
AC   AAX69804;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
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PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 79; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   11.8%;  Pred. No. 3.2e+03;
  Matches    2;  Conservative   13;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              :::::::::::::  ||
Db          1 UUUUUUUUUUUUUCCAA 17


RESULT 4362
AAA25454/c
ID   AAA25454 standard; DNA; 17 BP.
XX
AC   AAA25454;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 77; Page 79; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              ||  ||||||||||||||
Db         17 ATACAAAAAAAAAAAAA 1


RESULT 4363
AAQ20006/c
ID   AAQ20006 standard; DNA; 17 BP.
XX
AC   AAQ20006;
XX
DT   01-APR-1992  (first entry)
XX
DE   Oligonucleotide #2 able to covalently cross-link to target DNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   aziridinylcytosine; cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   8
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   modified_base   14
FT                   /*tag=  c
FT                   /mod_base= m5c
FT   modified_base   17
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346.
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
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XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 2; Page 20; 42pp; English.
XX
CC   The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is
CC   one of four oligonucleotides which were designed to specifically bind and
CC   cross-link to the duplex target sequence AAQ20004. Oligo #2 has the
CC   covalent cross-linking group, i.e. N4N4-ethanocytosine, at its 3' end. An
CC   assay for crosslinked triple helix showed considerable reaction with
CC   Oligo #2 and with Oligo #1 (see AAQ20005) which has the crosslinking
CC   group at the 5' end. The most complete reaction was seen with Oligo #3
CC   (see AAQ20007) having N4N4-ethanocytosine at both the 5' and 3' termini.
CC   A control oligo with no cross-linking group showed no reaction. The half-
CC   life of the cross-linking reaction for Oligo #2 was ca. 1 hr (1 microM);
CC   Oligo #1 showed a rate four times slower. See also AAQ20008
XX
SQ   Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              ||| ||||| |||||||
Db         17 GAAGAAAAAGAAAAAAA 1


RESULT 4364
AAQ20005
ID   AAQ20005 standard; DNA; 17 BP.
XX
AC   AAQ20005;
XX
DT   01-APR-1992  (first entry)
XX
DE   Oligonucleotide #1 able to covalently cross-link to target DNA.
XX
KW   deoxyribonucleic acid; major groove; ethanoamino group;
KW   aziridinylcytosine; cross-linking group; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N4N4-ethanocytosine"
FT   modified_base   9
FT                   /*tag=  b
FT                   /mod_base= m5c
FT   modified_base   15
FT                   /*tag=  c
FT                   /mod_base= m5c
XX
PN   WO9118997-A.
XX
PD   12-DEC-1991.
XX
PF   25-MAY-1990;   90US-00529346..
XX
PR   25-MAY-1990;   90US-00529346.
PR   14-JAN-1991;   91US-00640654.
XX
PA   (GILE-) GILEAD SCIE INC.
XX
PI   Matteucci MD,  Krawczyk S;
XX
DR   WPI; 1992-007480/01.
XX
PT   New sequence-specific non-photo-activated crosslinking agents - bind to
PT   the major groove of duplex DNA and are esp. useful for treating latent
PT   infections e.g. HIV.
XX
PS   Example 2; Page 20; 42pp; English.
XX
CC   The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is
CC   one of four oligonucleotides which were designed to specifically bind and
CC   cross-link to the duplex target sequence AAQ20004. Oligo #1 has the
CC   covalent cross-linking group, i.e. N4N4-ethanocytosine, at its 5' end. An
CC   assay for crosslinked triple helix showed considerable reaction with
CC   Oligo #1 and with Oligo #2 (see AAQ20006) which has the crosslinking
CC   group at the 3' end. The most complete reaction was seen with Oligo #3
CC   (see AAQ20007) having N4N4-ethanocytosine at both the 5' and 3' termini.
CC   A control oligo with no cross-linking group showed no reaction. The half-
CC   life of the cross-linking reaction for Oligo #2 was ca. 1 hr (1 microM);
CC   Oligo #1 showed a rate four times slower. See also AAQ20008
XX
SQ   Sequence 17 BP; 0 A; 3 C; 0 G; 14 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              |||||||| ||||| ||
Db          1 CTTTTTTTCTTTTTCTT 17


RESULT 4365
AAQ25487/c
ID   AAQ25487 standard; DNA; 17 BP.
XX
AC   AAQ25487;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Purine rich HUMIL2 target duplex sequence.
XX
KW   Target; human interleukin-2 gene; AIDS; triplex; HIV; hepatitis;
KW   malignancy; inflammation; ds.
XX
OS   Synthetic.
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
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```
XX
PS   Claim 11; Page 64; 77pp; English.
XX
CC   The sequence depicts a HUMIL2 (interleukin-2) sequence beginning at
CC   nucleotide 1114. The sequence is a viral duplex sequence contg. a purine-
CC   rich region concentrated on one chain of the duplex. The sequence may be
CC   prepd. by standard DNA synthesis. The HUMIL2 duplex sequence is used as a
CC   target for novel oligomers which are capable of forming a triplex at
CC   physiological pH by coupling into the major groove of the DNA duplex. Six
CC   such oligomers IL2 401-6 are capable of forming a triplex with this
CC   sequence. The oligomers are used in the treatment of inflammation.
CC   Similar oligomers may be used to target viral DNA duplexes specific for
CC   HIV, herpes and other viruses. The triple helices form under mild
CC   conditions thus assays may be carried out without subjecting the test
CC   specimen to harsh conditions. The oligomer is able to inhibit gene
CC   expression, as verified by in vitro systems. See also AAQ25452-25501 and
CC   AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 17 BP; 12 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTT 2172
              ||||| ||||||| |||
Db         17 TTTTTCCTCCTTTCTTT 1


RESULT 4366
AAT32744
ID   AAT32744 standard; DNA; 17 BP.
XX
AC   AAT32744;
XX
DT   28-NOV-1996  (first entry)
XX
DE   Hepatitis C virus ribozyme target sequence.
XX
KW   Hepatitis C virus; ribozyme; treatment; liver; disease; tPA; uPA;
KW   tissue plasminogen activator; urokinase plasminogen activator;
KW   adenoviral vector; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9618419-A1.
XX
PD   20-JUN-1996.
XX
PF   14-DEC-1995;   95WO-US016347.
XX
PR   14-DEC-1994;   94US-00357508.
PR   07-JUN-1995;   95US-00476257.
PR   11-SEP-1995;   95US-00534220.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Kay MA,  Lieber A;
XX
DR   WPI; 1996-300395/30.
XX
PT   Prodn. of gene prods. in a patient's liver - by transducing hepatocyte(s)
PT   with adenoviral vectors expressing molecules which induce hepatocyte
PT   regeneration, e.g. tPA, useful for e.g. for treatment of hepatitis C.
XX
PS   Claim 24; Page 56; 74pp; English.
XX
CC   A gene product can be produced in a patient's liver by transducing
CC   hepatocytes in situ with an adenoviral vector (AV) encoding the gene
CC   product desired and which also comprises a sequence encoding tissue
CC   plasminogen activator (tPA) or urokinase plasminogen activator (uPA)
CC   which promote rapid liver regeneration. The method is particularly useful
CC   for the treatment of hepatitis C virus since the AV can be made to encode
CC   one or more ribozymes specific for HCV RNA. HCV ribozyme target sequences
CC   are described in AAT32741-46. This target sequence corresponds to
CC   nucleotides 385-401 of HCV RNA
XX
SQ   Sequence 17 BP; 4 A; 9 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 3.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        439 CCAGCCGGCGCCCACAG 455
              ||| ||| |||||||||
Db          1 CCAACCGTCGCCCACAG 17


RESULT 4367
AAX71549
ID   AAX71549 standard; RNA; 17 BP.
XX
AC   AAX71549;
XX
DT   28-JUL-1999  (first entry)
XX
DE   Human KDR VEGF receptor hammerhead ribozyme substrate #561.
XX
KW   Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW   KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW   tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW   fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW   foetal liver kinase 1; ss.
XX
OS   Homo sapiens.
XX
PN   WO9715662-A2.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;   96WO-US017480.
XX
PR   26-OCT-1995;   95US-0005974P.
PR   11-JAN-1996;   96US-00584040.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (CHIR ) CHIRON CORP.
XX
PI   Pavco P,  Mcswiggen J,  Stinchcomb D,  Escobedo J;
XX
DR   WPI; 1997-259017/23.
XX
PT   Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT   stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT   rheumatoid arthritis, etc., in a human patient.
XX
PS   Claim 4; Page 114; 218pp; English.
XX
CC   The present invention describes nucleic acid molecules which modulate the
CC   synthesis, expression and/or stability of a mRNA encoding 1 or more
CC   receptors of vascular endothelial growth factor (VEGF). A patient
CC   (preferably human) having a condition associated with the level of the
CC   fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC   receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC   angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC   treated by administering the nucleic acid molecule or the expression
CC   vector to the patient. AAX67275 to AAX75752 represent specific examples
CC   of nucleic acid molecules from the present invention
XX
SQ   Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             0.5%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   64.7%;  Pred. No. 3.2e+03;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2553 AGAGGATGCTGGGCTCT 2569
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